

```
In [21]: import os
import pandas as pd
import json
import imgkit
import io
import base64
import matplotlib.pyplot as plt
```

```
In [47]: # Function to create a small plot and return it as a base64-encoded image
def create_plot(data, title):
    fig, ax = plt.subplots()
    ax.plot(['k2', 'k3', 'k4', 'k5'], data, marker='*', color='red', linewidth=10)
    ax.set_title(title)
    ax.set_ylim(0, 1)
    buf = io.BytesIO()
    plt.savefig(buf, format='png')
    plt.close(fig)
    buf.seek(0)
    img_base64 = base64.b64encode(buf.read()).decode('utf-8')
    return f"<img src='data:image/png;base64,{img_base64}' width='100' height='50'>"
```

```
In [59]: def generate_metrics_table(metrics_folder, output_image_path, split=False):
    rows = []
    files = os.listdir(metrics_folder)
    metric_files = [file for file in files if file.startswith("binary_classifier_") and file.endswith(".json")]
    k_metrics = [None, None, None, None]

    # Read metrics from each file and store in k_metrics list
    for file in metric_files:
        k_value = int(file.split("_")[2].split(".")[0])
        with open(os.path.join(metrics_folder, file), 'r') as f:
            metrics = json.load(f)
            k_metrics[k_value-2] = metrics

    # Iterate through gene families and metrics for each k value
    for gene_family, metrics_data_k2 in k_metrics[0].items():
        metrics_data_k3 = k_metrics[1][gene_family]
        metrics_data_k4 = k_metrics[2][gene_family]
        metrics_data_k5 = k_metrics[3][gene_family]

        # Find the max values for each metric
        max_accuracy = max(metrics_data_k2['accuracy'], metrics_data_k3['accuracy'], metrics_data_k4['accuracy'], metrics_data_k5['accuracy'])
        max_precision = max(metrics_data_k2['precision'], metrics_data_k3['precision'], metrics_data_k4['precision'], metrics_data_k5['precision'])
        max_recall = max(metrics_data_k2['recall'], metrics_data_k3['recall'], metrics_data_k4['recall'], metrics_data_k5['recall'])
        max_f1 = max(metrics_data_k2['f1'], metrics_data_k3['f1'], metrics_data_k4['f1'], metrics_data_k5['f1'])

        # Construct HTML row for each gene family
        row = f"<tr><td>{gene_family}</td><td>"
```

- # Accuracy metrics
 

```
row += f"<td>{metrics_data_k2['accuracy']:.3f}</td>" if metrics_data_k2['accuracy'] != max_accuracy else f"<td>{max_accuracy:.3f}</td>"
```

```
row += f"<td>{metrics_data_k3['accuracy']:.3f}</td>" if metrics_data_k3['accuracy'] != max_accuracy else f"<td>{max_accuracy:.3f}</td>"
```

```
row += f"<td>{metrics_data_k4['accuracy']:.3f}</td>" if metrics_data_k4['accuracy'] != max_accuracy else f"<td>{max_accuracy:.3f}</td>"
```

```
row += f"<td>{metrics_data_k5['accuracy']:.3f}</td>" if metrics_data_k5['accuracy'] != max_accuracy else f"<td>{max_accuracy:.3f}</td>"
```

```
row += f"<td>{create_plot([metrics_data_k2['accuracy'], metrics_data_k3['accuracy'], metrics_data_k4['accuracy'], metrics_data_k5['accuracy']])}</td>"
```
- # Precision metrics
 

```
row += f"<td class='lc'>{metrics_data_k2['precision']:.3f}</td>" if metrics_data_k2['precision'] != max_precision else f"<td>{max_precision:.3f}</td>"
```

```
row += f"<td>{metrics_data_k3['precision']:.3f}</td>" if metrics_data_k3['precision'] != max_precision else f"<td>{max_precision:.3f}</td>"
```

```
row += f"<td>{metrics_data_k4['precision']:.3f}</td>" if metrics_data_k4['precision'] != max_precision else f"<td>{max_precision:.3f}</td>"
```

```
row += f"<td>{metrics_data_k5['precision']:.3f}</td>" if metrics_data_k5['precision'] != max_precision else f"<td>{max_precision:.3f}</td>"
```

```
row += f"<td>{create_plot([metrics_data_k2['precision'], metrics_data_k3['precision'], metrics_data_k4['precision'], metrics_data_k5['precision']])}</td>"
```
- # Recall metrics
 

```
row += f"<td class='lc'>{metrics_data_k2['recall']:.3f}</td>" if metrics_data_k2['recall'] != max_recall else f"<td>{max_recall:.3f}</td>"
```

```
row += f"<td>{metrics_data_k3['recall']:.3f}</td>" if metrics_data_k3['recall'] != max_recall else f"<td>{max_recall:.3f}</td>"
```

```
row += f"<td>{metrics_data_k4['recall']:.3f}</td>" if metrics_data_k4['recall'] != max_recall else f"<td>{max_recall:.3f}</td>"
```

```
row += f"<td>{metrics_data_k5['recall']:.3f}</td>" if metrics_data_k5['recall'] != max_recall else f"<td>{max_recall:.3f}</td>"
```

```
row += f"<td>{create_plot([metrics_data_k2['recall'], metrics_data_k3['recall'], metrics_data_k4['recall'], metrics_data_k5['recall']])}</td>"
```
- # F1 metrics
 

```
row += f"<td class='lc'>{metrics_data_k2['f1']:.3f}</td>" if metrics_data_k2['f1'] != max_f1 else f"<td>{max_f1:.3f}</td>"
```

```
row += f"<td>{metrics_data_k3['f1']:.3f}</td>" if metrics_data_k3['f1'] != max_f1 else f"<td>{max_f1:.3f}</td>"
```

```
row += f"<td>{metrics_data_k4['f1']:.3f}</td>" if metrics_data_k4['f1'] != max_f1 else f"<td>{max_f1:.3f}</td>"
```

```
row += f"<td>{metrics_data_k5['f1']:.3f}</td>" if metrics_data_k5['f1'] != max_f1 else f"<td>{max_f1:.3f}</td>"
```

```
row += f"<td>{create_plot([metrics_data_k2['f1'], metrics_data_k3['f1'], metrics_data_k4['f1'], metrics_data_k5['f1']])}</td>"
```

```
row += "</tr>"
rows.append(row)

# Function to construct HTML for table
def construct_html_table(rows):
    return f"""
<html>
<head>
<style>
    table {
        width: 100%;
        border-collapse: collapse;
        border: 1px solid black;
    }
    th, td {
        border: 1px solid black;
        padding: 8px;
        text-align: center;
        font-size: 14px;
    }
    th {
        background-color: #f2f2f2;
    }
    .main-col {
        text-align: center;
        background-color: #e6f7ff; /* Soft background color for main columns */
    }
    .sub-col {
        background-color: #f2f2f2; /* Light background color for sub-columns */
    }
    thead, tbody {
        border: 1px solid;
    }
    .lc {
        border-left: 1px solid !important;
    }
    .metric_style{
        text-align: center !important;
        border: 1px solid !important;
    }
</style>
</head>
<body>
<!-- Metrics Table -->
<table>
<thead>
<tr>
<th colspan="2" class="main-col">Gene (Family)</th>
<th colspan="5" class="metric_style">Accuracy</th>
<th colspan="5" class="main-col metric_style">Precision</th>
<th colspan="5" class="main-col metric_style">Recall</th>
<th colspan="5" class="main-col metric_style">F1</th>
</tr>
<tr>
<th class="sub-col lc">k=2</th>
<th class="sub-col">k=3</th>
<th class="sub-col">k=4</th>
<th class="sub-col">k=5</th>
<th class="sub-col">trend</th>
<th class="sub-col lc">k=2</th>
<th class="sub-col">k=3</th>
<th class="sub-col">k=4</th>
<th class="sub-col">k=5</th>
<th class="sub-col">trend</th>
<th class="sub-col lc">k=2</th>
<th class="sub-col">k=3</th>
<th class="sub-col">k=4</th>
<th class="sub-col">k=5</th>
<th class="sub-col">trend</th>
<th class="sub-col lc">k=2</th>
<th class="sub-col">k=3</th>
<th class="sub-col">k=4</th>
<th class="sub-col">k=5</th>
<th class="sub-col">trend</th>
</tr>
</thead>
<tbody>
{rows}
</tbody>
</table>
</body>
</html>
"""

# Save HTML table to PNG
if split:
    # Split rows into two parts
    mid_index = len(rows) // 2
    rows_part1 = rows[:mid_index]
    rows_part2 = rows[mid_index:]

    # Generate HTML content for both parts
    table_html_part1 = construct_html_table(rows_part1)
    table_html_part2 = construct_html_table(rows_part2)

    # Save both parts as separate PNG images
    imgkit.from_string(table_html_part1, output_image_path.replace(".png", "_part1.png"))
    imgkit.from_string(table_html_part2, output_image_path.replace(".png", "_part2.png"))

    return table_html_part1, table_html_part2
else:
    # Generate HTML content for the whole table
    table_html = construct_html_table(rows)

    # Save as single PNG image
    imgkit.from_string(table_html, output_image_path)

return table_html
```

```
In [60]: # Example usage:
metrics_folder = "./metrics"
output_image_path = "metrics_table_anova.png"
metrics_table = generate_metrics_table(metrics_folder, output_image_path, split=True)
```

```
Loading page (1/2)
Rendering (2/2)
Done
Loading page (1/2)
Rendering (2/2)
Done
```

```
In [61]: # Display the HTML table
from IPython.display import display, HTML
display(HTML(metrics_table[0]))
display(HTML(metrics_table[1]))
```

Gene (Family)	Accuracy	Precision	Recall	F1
k=2 k=3 k=4 k=5 trend				
AP2	0.9850.9840.9930.987	0.4840.4710.6580.512	0.9670.9830.9840.950	0.6450.6370.7890.665
ARF	0.9881.0001.0001.000	0.5400.9950.9981.000	1.0000.9960.9980.997	0.7010.9950.9980.998
ARRB	0.9970.9990.9950.993	0.7130.8960.5950.526	0.9640.9750.9950.983	0.8190.9340.7420.685
B3	0.9940.9950.9960.993	0.8490.9330.9170.931	0.9830.9190.9690.865	0.9110.9260.9420.897
BBR BPC	0.9931.0001.0001.000	0.3641.0000.9961.000	0.9880.9921.0000.984	0.5310.9960.9980.992
BEST	0.9701.0001.0001.000	0.1371.0001.0000.997	0.9941.0001.0000.994	0.2411.0001.0000.995
C2H2	0.9840.9880.9960.991	0.7880.9810.9840.995	0.9660.8030.9440.841	0.8680.8830.9630.913
C3H	0.9870.9940.9990.996	0.7090.9940.9840.997	0.9620.7970.9740.875	0.8170.8850.9790.932
CAM	0.9741.0001.0001.000	0.1400.9820.9960.997	0.9960.9890.9961.000	0.2460.9850.9960.998
CO-like	0.9921.0001.0001.000	0.4430.9610.9530.991	0.9880.9910.9950.998	0.6110.9760.9740.998
CPP	0.9911.0001.0001.000	0.3490.9790.9441.000	0.9880.9940.9940.972	0.5160.9860.9680.986
DBB	0.9590.9970.9960.995	0.1110.9530.5440.528	0.9880.4290.9970.985	0.1990.5920.7040.688
Dof	0.9981.0001.0001.000	0.9010.9901.0001.000	0.9890.9950.9970.996	0.9430.9930.9990.998
E2F	0.9931.0001.0001.000	0.4420.9940.9751.000	0.9750.9831.0000.994	0.6080.9890.9880.997
EIL	0.9690.9981.0001.000	0.1090.6740.9921.000	0.9840.7130.9840.984	0.1970.6930.9880.997
ERF	0.9930.9980.9950.997	0.9100.9760.9290.958	0.9850.9960.9960.998	0.9460.9860.9610.977
FAR	0.9840.9970.9980.998	0.6020.8810.9330.972	0.9790.9840.9750.936	0.7450.9300.9530.954
G2-like	0.9850.9980.9930.992	0.6730.9560.8190.806	0.9730.9740.9880.987	0.7950.9650.8960.887
GATA	0.9861.0001.0001.000	0.5480.9950.9970.998	0.9830.9780.9960.984	0.7040.9870.9970.991
GRAS	0.9960.9990.9990.999	0.8840.9920.9940.998	0.9770.9700.9870.978	0.9280.9810.9990.988
GRF	0.9981.0001.0001.000	0.7440.9971.0001.000	0.9970.9951.0000.997	0.8520.9961.0000.999
GeB	0.9620.9990.9990.998	0.1110.9330.8290.694	0.9580.9390.9960.962	0.1980.9360.8910.806
HB-PHD	0.9931.0001.0001.000	0.1820.9691.0001.000	1.0000.9900.9901.000	0.3080.9790.9951.000
HB-other	0.9670.9920.9840.979	0.1650.9460.2940.224	0.9030.6640.8860.798	0.2790.5450.4420.350
HD-ZIP	0.9920.9990.9990.998	0.7770.9790.9820.948	0.9910.9940.9960.998	0.8710.9860.9890.972
HRT-like	0.9431.0001.0001.000	0.0130.9801.0001.000	0.9601.0000.9801.000	0.0260.9900.9901.000
HSF	0.9951.0001.0001.000	0.7310.9980.9981.000	0.9900.9980.9990.997	0.8410.9980.9980.998
LBD	0.9780.9990.9990.999	0.5110.9920.9750.981	0.9790.9820.9900.979	0.6720.9870.9820.980
LFY	0.9651.0001.0001.000	0.0210.9781.0001.000	0.9610.8630.9800.941	0.0410.9170.9900.970

Gene (Family)	Accuracy	Precision	Recall	F1
k=2 k=3 k=4 k=5 trend				
LSD	0.9801.0001.0001.000	0.1280.9840.9460.910	0.9900.9430.9951.000	0.2260.9630.9700.953
M-type	0.9450.9940.9840.994	0.2920.8550.5990.807	0.9530.9060.9950.972	0.4470.8800.7450.882
MIK	0.9450.9980.9950.994	0.8110.9440.8290.777	0.9960.9860.9960.997	0.8940.9650.9050.874
MYB	0.9880.9900.9970.994	0.8580.9660.9730.938	0.9930.8890.9880.984	0.9210.9260.9810.960
MYB	0.9480.9810.9770.974	0.3140.9890.7070.676	0.9320.6910.8960.866	0.4700.7810.7900.759
NAC	0.9950.9980.9990.997	0.9360.9980.9920.995	0.9810.9720.9880.958	0.9580.9850.9900.976
NF-X1	0.9881.0001.0001.000	0.0920.9531.0001.000	1.0000.0001.0000.997	0.1690.9761.0000.988
NF-YA	0.9971.0001.0001.000	0.6960.9940.9960.976	0.9920.9960.9980.996	0.8180.9950.9970.986
NF-YB	0.9781.0001.0001.000	0.3060.9950.9890.970	0.9740.9920.9950.994	0.4650.9940.9920.982
NF-YC	0.9470.9991.0001.000	0.1240.9860.9880.997	0.9840.8880.9920.957	0.2200.9340.9900.977
NZZ	0.9610.0001.0001.000	0.0090.5641.0001.000	1.0000.0000.9550.955	0.0170.7210.