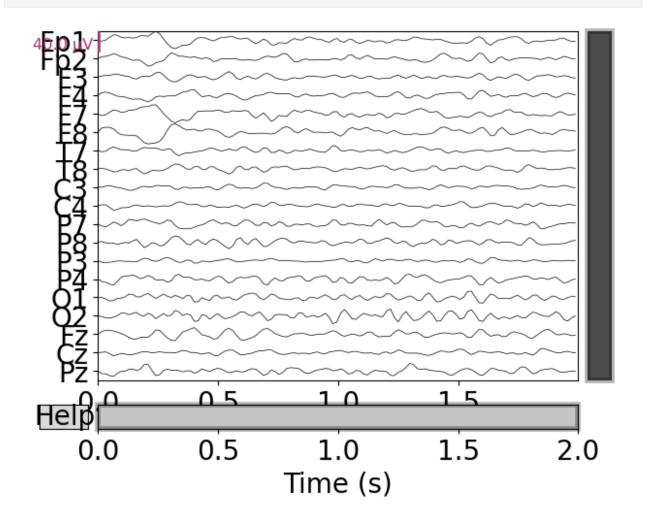
## Microstate analysis

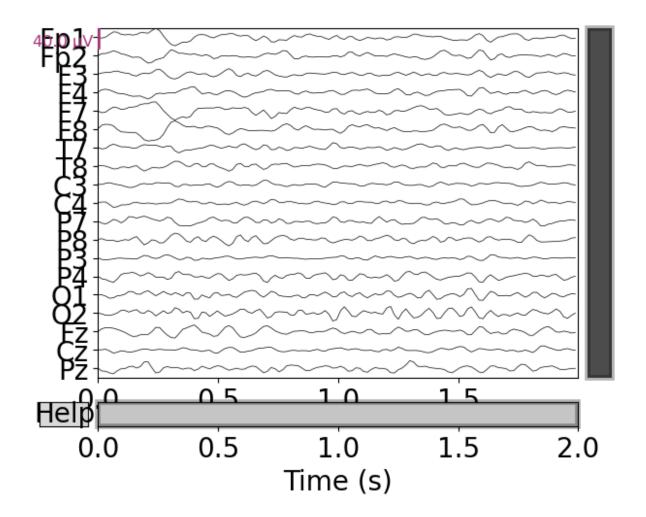
```
# Library import
import mne
import numpy as np
from sklearn.cluster import KMeans
import matplotlib.pyplot as plt
import nbconvert
import pandoc
import networkx as nx
import matplotlib.patches as mpatches
import warnings
warnings.filterwarnings('ignore')
# Load the EEG data from the provided EDF file
eeg data = mne.io.read raw edf("data/data Subject01 2 10.edf",
preload=True)
eeg data.info
Extracting EDF parameters from /Users/sid/Documents/GitHub/EEG
analysis/EEG-analysis/Dataset 4/data/data Subject01 2 10.edf...
EDF file detected
Setting channel info structure...
Creating raw.info structure...
Reading 0 \dots 999 = 0.000 \dots 1.998 \text{ secs...}
<Info | 7 non-empty values</pre>
bads: []
 ch names: Fp1, Fp2, F3, F4, F7, F8, T7, T8, C3, C4, P7, P8, P3, P4,
01, ...
 chs: 19 EEG
 custom ref applied: False
 highpass: 0.0 Hz
 lowpass: 250.0 Hz
meas date: 2020-10-05 18:33:44 UTC
nchan: 19
projs: []
sfreq: 500.0 Hz
# Apply bandpass filter to retain frequencies between 1 and 20 Hz
eeg data filtered = eeg data.copy().filter(l freg=1, h freg=20)
eeg data filtered.plot(duration=2, n channels=19)
Filtering raw data in 1 contiguous segment
Setting up band-pass filter from 1 - 20 Hz
FIR filter parameters
```

------

Designing a one-pass, zero-phase, non-causal bandpass filter:

- Windowed time-domain design (firwin) method
- Hamming window with 0.0194 passband ripple and 53 dB stopband attenuation
- Lower passband edge: 1.00
- Lower transition bandwidth: 1.00 Hz (-6 dB cutoff frequency: 0.50 Hz)
- Upper passband edge: 20.00 Hz
- Upper transition bandwidth: 5.00 Hz (-6 dB cutoff frequency: 22.50 Hz)
- Filter length: 1651 samples (3.302 sec)





## Segmentation

This is typically done by identifying the time points with peak global field power (GFP) since these are moments of highest "synchrony" in the EEG data. At each of these peak GFP time points, the scalp topography is treated as a potential microstate.

```
# Calculate the Global Field Power (GFP) for the EEG data
gfp = np.std(eeg_data_filtered._data, axis=0)

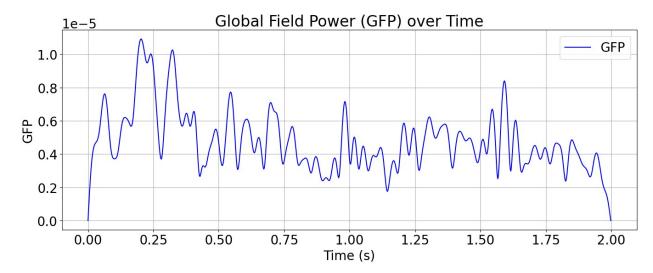
# Identify the time points with peak GFP
peak_indices = (gfp[:-2] < gfp[1:-1]) & (gfp[1:-1] > gfp[2:])

# Extract the time points of these peaks
peak_times = eeg_data_filtered.times[1:-1][peak_indices]

# Extract the topographies at these peak time points
peak_topographies = eeg_data_filtered._data[:, 1:-1][:, peak_indices]

peak_times, peak_topographies.shape
```

```
(array([0.064, 0.14 , 0.202, 0.24 , 0.322, 0.376, 0.404, 0.44 , 0.488,
        0.546, 0.606, 0.652, 0.698, 0.78, 0.832, 0.872, 0.91, 0.942,
        0.982, 1.018, 1.052, 1.092, 1.118, 1.168, 1.208, 1.244, 1.304,
        1.364, 1.42 , 1.458, 1.51 , 1.546, 1.592, 1.634, 1.674, 1.708,
        1.748, 1.79 , 1.85 , 1.944]),
 (19, 40)
# Adjust the font size for all text elements
plt.rcParams.update({'font.size': 20})
# Plot the Global Field Power (GFP)
plt.figure(figsize=(14, 6))
plt.plot(eeg_data_filtered.times, gfp, color='blue', label='GFP')
plt.xlabel('Time (s)')
plt.ylabel('GFP')
plt.title('Global Field Power (GFP) over Time')
plt.legend()
plt.grid(True)
plt.tight layout()
plt.show()
```



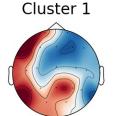
# Clustering

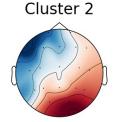
Group these potential microstates into clusters. We're looking to group them into 4 clusters corresponding to the predefined microstate classes A, B, C, and D.

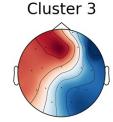
We'll use the k-means clustering algorithm for this purpose. Once we've identified these 4 cluster centroids, we can visually inspect them to determine their correspondence to the predefined microstate classes.

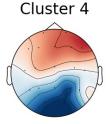
```
# Perform k-means clustering
n_clusters = 4
```

```
kmeans = KMeans(n clusters=n clusters,
random state=0).fit(peak topographies.T)
# Extract the cluster centroids (mean topographies for each cluster)
cluster topographies = kmeans.cluster centers
# Set the "standard 1020" montage for the EEG data
montage = mne.channels.make standard montage('standard 1020')
eeg data filtered.set montage(montage)
# Adjust the font size for all text elements
plt.rcParams.update({'font.size': 20})
# Plot the mean topographies for each cluster again
fig, axs = plt.subplots(1, n_clusters, figsize=(15, 3))
for i, ax in enumerate(axs):
    mne.viz.plot topomap(cluster topographies[i],
eeg_data_filtered.info, axes=ax, show=False)
    ax.set title(f'Cluster {i+1}')
plt.tight layout()
plt.show()
```









## **Assignment**

Assign each microstate to one of the predefined classes based on similarity to the mean topography of each cluster.

```
# Assign each peak GFP time point to one of the clusters
labels = kmeans.predict(peak_topographies.T)

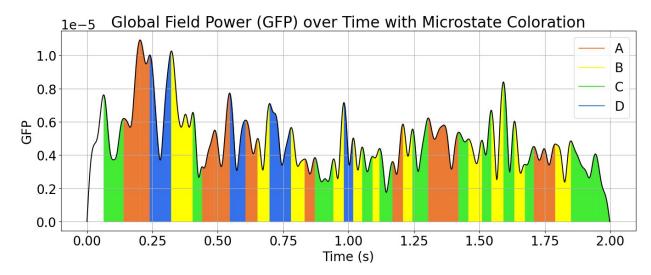
# Create a mapping based on the provided assignments
mapping = {0: 'A', 1: 'B', 3: 'C', 2: 'D'}
assigned_classes = [mapping[label] for label in labels]

assigned_classes

['C',
    'A',
    'A',
    'D',
```

```
'B',
 'B',
 'C',
 'Α',
 'Α',
 'D',
 'A',
 'B',
 'D',
 'Β',
'Α',
 'C',
 'C',
 'B',
 'D',
 'B',
 'C',
 'B',
 'C',
 'A',
 'B',
 'C',
 'A',
 'Α',
 'C',
 'B',
 'C',
 'B',
 'C',
'B',
 'C',
 'A',
 'Α',
 'B',
 'C',
 'C']
# Adjust the font size for all text elements
plt.rcParams.update({'font.size': 20})
# Define colors for each microstate class
color_map = {
    'Ā': '#eb7a34',
    'B': 'yellow',
    'C': '#43eb34',
    'D': '#3471eb'
# Correctly plot the Global Field Power (GFP) with color coding for
microstates
plt.figure(figsize=(14, 6))
```

```
for i, time in enumerate(peak times):
    if i == len(peak times) - 1:
        next time = eeg data filtered.times[-1]
    else:
        next time = peak times[i + 1]
    times slice = (eeg data filtered.times >= time) &
(eeg data filtered.times < next time)
    plt.fill between(eeg data filtered.times[times slice], 0,
gfp[times slice], color=color map[assigned classes[i]])
plt.plot(eeg_data_filtered.times, gfp, color='black', label='GFP')
plt.xlabel('Time (s)')
plt.ylabel('GFP')
plt.title('Global Field Power (GFP) over Time with Microstate
Coloration')
handles = [plt.Line2D([0], [0], color=color map[class label],
label=class label) for class label in ['A', 'B', 'C', 'D']]
plt.legend(handles=handles)
plt.grid(True)
plt.tight layout()
plt.show()
```



#### **Metrics**

- 1. **Average Duration or Lifespan**: This is the average time duration a microstate lasts.
- 2. **Frequency of Occurrence**: This is the number of times a microstate occurs divided by the total recording time.
- 3. **Coverage**: This is the fraction of total recording time that the microstate is dominant.
- 4. **Amplitude**: This is the average GFP during microstate dominance.
- 5. **Global Explained Varianc**e: This is the percentage of total variance explained by a given microstate.

6. **Transition Probabilities**: This is the probability of transitioning from one microstate to any other.

```
# Compute the average duration or lifespan for each microstate class
sampling freq = eeg data filtered.info['sfreq']
durations = np.diff(peak times, prepend=0) # Time durations between
successive peaks
# Calculate average duration for each class
average durations = {}
for microstate class in ['A', 'B', 'C', 'D']:
    durations class = durations[np.array(assigned_classes) ==
microstate classl
    average durations[microstate class] = np.mean(durations class) if
len(durations class) > 0 else 0
average durations # in seconds
{'A': 0.0525454545454545454,
 'B': 0.047500000000000001,
 'C': 0.047230769230769236,
 'D': 0.0455}
# Compute the frequency of occurrence for each microstate class
total time = eeg data filtered.times[-1]
frequency of occurrence = {}
for microstate class in ['A', 'B', 'C', 'D']:
    count class = sum(np.array(assigned classes) == microstate class)
    frequency of occurrence[microstate class] = count class /
total time
frequency of occurrence
{'A': 5.505505505505505,
 'B': 6.006006006006006.
 'C': 6.506506506506507,
 'D': 2.002002002002002}
# Compute the coverage for each microstate class
coverage = {}
for microstate class in ['A', 'B', 'C', 'D']:
    durations class = durations[np.array(assigned classes) ==
microstate classl
    coverage[microstate class] = sum(durations class) / total time
coverage
{'A': 0.2892892892892892,
 'B': 0.2852852852852853,
```

```
'C': 0.3073073073073074,
 'D': 0.091091091091091
# Correctly compute the amplitude (average GFP) for each microstate
class
amplitude = {}
for microstate class in ['A', 'B', 'C', 'D']:
    gfp class = gfp[1:-1][peak indices][np.array(assigned classes) ==
microstate classl
    amplitude[microstate class] = np.mean(gfp class) if len(gfp class)
> 0 else 0
amplitude
{'A': 5.4857346620798096e-06,
 'B': 5.693117492798647e-06,
 'C': 5.083266519798649e-06,
 'D': 8.005346887514641e-06}
# Correctly compute the global explained variance for each microstate
class
global variance = np.var(eeg data filtered. data)
explained variance = {}
inverse_mapping = {v: k for k, v in mapping.items()} # Invert the
mapping for proper indexing
explained variance = {}
for microstate class in ['A', 'B', 'C', 'D']:
    topographies_class = peak_topographies[:,
np.array(assigned classes) == microstate class]
    mean topography =
cluster topographies[inverse mapping[microstate class]]
    variance class = np.var(topographies class - mean topography[:,
np.newaxis], ddof=1)
    explained variance[microstate class] = (global variance -
variance_class) / global_variance * 100
explained variance
{'A': 30.483877136547143,
 'B': 28.79389538979006,
 'C': 39.00399757313737,
 'D': 24.37164385315286}
# Compute the transition probabilities for each microstate class
transition matrix = np.zeros((4, 4))
# Iterate over the assigned classes to count transitions
for i in range(1, len(assigned classes)):
    prev class = assigned classes[i - 1]
```

```
current class = assigned classes[i]
   transition matrix[inverse mapping[prev class],
inverse mapping[current class]] += 1
# Normalize the transition counts to get probabilities
transition probabilities = transition matrix /
transition matrix.sum(axis=1, keepdims=True)
# Convert to dictionary for readability
transition probabilities dict = {}
for i, microstate class i in enumerate(['A', 'B', 'C', 'D']):
   for j, microstate class j in enumerate(['A', 'B', 'C', 'D']):
       transition_probabilities_dict[f"{microstate_class_i} ->
{microstate class j}"] = transition probabilities[i, j]
transition probabilities dict
{'A -> A': 0.36363636363636363,
 'A -> B': 0.27272727272727,
 'A -> C': 0.18181818181818182,
 'A -> D': 0.18181818181818182,
 'C -> A': 0.25.
 'C -> B': 0.75,
 'C -> C': 0.0,
 ^{\prime}C \rightarrow D^{\prime}: 0.0.
 'D -> A': 0.4166666666666667,
 'D -> B': 0.416666666666667,
 'D -> C': 0.0,
 # Adjust the font size for all text elements
plt.rcParams.update({'font.size': 20})
# Create a directed graph
G = nx.DiGraph()
# Add nodes and edges to the graph based on transition probabilities
for transition, probability in transition probabilities dict.items():
   source, target = transition.split(' -> ')
   if probability > 0: # Only add edges with non-zero probabilities
       G.add edge(source, target, weight=probability)
# Define edge colors based on transitions
edge colors = {
   ^A -> B': 'blue',
   'B -> A': 'red',
```

```
'A -> C': 'green',
    'C -> A': 'purple'
    'A -> D': '#eb347d',
    'D -> A': 'orange',
    'B -> C': '#eb34c9'
    'C -> B': '#eb4c34',
    'B -> D': 'brown',
    'D -> B': 'lime',
    'C -> D': 'gray',
    'D -> C': 'olive',
    'A -> A': 'black',
    'B -> B': 'black',
    'C -> C': 'black',
    'D -> D': 'black'
}
# Draw the graph
pos = nx.spring layout(G)
# Function to adjust the annotation position to avoid overlap
def adjust position(pos source, pos target, offset=0.2):
    delta x = pos target[0] - pos source[0]
    delta y = pos target[1] - pos source[1]
    # Calculate normalized direction vector for the edge
    length = (delta_x^{**2} + delta_y^{**2})^{**0.5}
    direction = (delta x/length, delta y/length)
    # Adjust the position by the offset value
    x = (pos\_source[0] + pos\_target[0]) / 2 + direction[1] * offset
    y = (pos_source[1] + pos_target[1]) / 2 - direction[0] * offset
    return x, y
# Function to adjust the annotation position for self-looping arrows
def adjust self loop position(pos node, offset=0.3):
    return pos_node[0], pos_node[1] + offset
# Draw the graph with adjusted annotated transition probabilities for
self-looping arrows
fig, ax = plt.subplots(figsize=(12, 10))
# Draw the nodes and edges
nx.draw networkx nodes(G, pos, ax=ax, node size=2000,
node color='lightblue')
nx.draw_networkx_labels(G, pos, ax=ax, font size=20,
font weight='bold')
# Draw the edges with annotated probabilities
for edge in G.edges(data=True):
```

```
source, target = edge[0], edge[1]
    weight = edge[2]['weight']
    color = edge colors[f"{source} -> {target}"]
    # Determine the curvature of the edge based on transition
direction
    if source < target:</pre>
        curve = 0.2 # Curve the edge for one direction (e.g., A -> B)
        curve = 0.2 # Use a negative curve for the opposite direction
(e.g., B -> A)
    # Draw the edge with curvature
    nx.draw networkx edges(G, pos, edgelist=[(source, target)], ax=ax,
edge color=color, width=weight * 10,
connectionstyle=f'arc3, rad={curve}')
    # Adjust the position for the annotation
    if source == target: # Handle self-looping arrows
        x, y = adjust self loop position(pos[source])
    else:
        x, y = adjust position(pos[source], pos[target], offset=0.25)
    # Annotate the edge with the probability value
    ax.text(x, y, f"{weight:.2f}", fontsize=20,
verticalalignment='center', horizontalalignment='center', color=color)
# Legend positioned to the right of the plot
legend handles = [mpatches.Patch(color=color, label=f'{transition}')
for transition, color in edge_colors.items() if
G.has edge(transition.split(' -> ')[0], transition.split(' -> ')[1])]
ax.legend(handles=legend handles, loc='center left', fontsize='x-
small', bbox to anchor=(1, 0.5))
plt.title("Microstate Transition Probabilities")
plt.axis('off')
plt.tight_layout()
plt.show()
```

#### Microstate Transition Probabilities

