## DF Creation

October 20, 2025

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[]: import pandas as pd
     pd.set_option('display.max_columns', None)
     # Load CSV
     df = pd.read_csv('mimic_cohort.csv')
     # Save as Parquet
     df.to_parquet('mimic_cohort.parquet')
[]: mimic_cohort = pd.read_parquet('mimic_cohort.parquet')
     mimic cohort.head()
[]: one_df = pd.read_csv("elixhauser_onehot.csv")
     one_df.to_parquet("elixhauser_onehot.parquet")
[]: onehot_cohort = pd.read_parquet("elixhauser_onehot.parquet")
     onehot cohort.head()
[]: first_comorbidity_col = 'chf'
     comorbidity_cols = onehot_cohort.columns[onehot_cohort.columns.
      →get_loc(first_comorbidity_col):].tolist()
     X = onehot_cohort[comorbidity_cols].values
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[]: from sklearn.preprocessing import StandardScaler
     from sklearn.cluster import KMeans
     # Standardize, since some papers do (binary columns usually don't need, butu
     ⇔follow paper's method if specified)
     n_clusters = 6  # Set to number of clusters used in the paper
     kmeans = KMeans(n_clusters=n_clusters, random_state=42)
     cluster_labels = kmeans.fit_predict(X)
     onehot_cohort['cluster'] = cluster_labels
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[]: # Compute the mean presence of each comorbidity feature in each cluster cluster_summary = onehot_cohort.groupby('cluster')[comorbidity_cols].mean() print(cluster_summary)
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[]: import networkx as nx
     import matplotlib.pyplot as plt
     # Example: Build a simple co-occurrence graph for one cluster
     G = nx.Graph()
     for comorb in comorbidity_cols:
         G.add node(comorb)
     # Add edges based on co-occurrence rates (customize logic to match paper)
     # Example: link every pair of comorbidities if they co-occur in >10% of \Box
     ⇔patients in the cluster
     threshold = 0.1
     cluster = 0 # Example: focus on first cluster
     df_cluster = onehot_cohort[onehot_cohort['cluster'] == cluster]
     for i, c1 in enumerate(comorbidity_cols):
         for c2 in comorbidity_cols[i+1:]:
             co_occur_rate = ((df_cluster[c1] == 1) & (df_cluster[c2] == 1)).mean()
             if co_occur_rate > threshold:
                 G.add_edge(c1, c2, weight=co_occur_rate)
     nx.draw(G, with_labels=True)
     plt.show()
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