TopNet is an automated web tool designed to calculate topological parameters and compare different sub-networks for any given network. TopNet takes as input an adjacency matrix or network and a set of nodes chosen to create sub-networks. Then, it computes all topological parameters mentioned above and shows the power-law degree distribution for each sub-network. TopNet also enables the user to explore the complex networks part by part. First, all first neighbors of a certain node could be shown as a simple graph. Secondly, after the user defines two nodes of interest and a maximum path length, the sub-network between these two nodes with all the nodes on the path within the maximum path length will be drawn as an independent graph.

**What is TopNet?**
TopNet is an automated web tool designed to calculate topological parameters and compare different sub-networks for any given network. TopNet takes as input an adjacency matrix or network and a set of nodes chosen to create sub-networks. Then, it computes all topological parameters mentioned above and shows the power-law degree distribution for each sub-network. TopNet also enables the user to explore the complex networks part by part. First, all first neighbors of a certain node could be shown as a simple graph. Secondly, after the user defines two nodes of interest and a maximum path length, the sub-network between these two nodes with all the nodes on the path within the maximum path length will be drawn as an independent graph.

**Start to use TopNet**
- Upload your own dataset here. Both category dataset and interaction dataset can be accepted.
- Calculate the topology parameters: diameter, average path length, and clustering coefficient. The data to be calculated can be freely selected from gene datasets or datasets uploaded by the user.
- Navigate within the interaction network. Select all the neighbours of one node. Links from different interaction datasets are separated by different colors.
- Visualize all the possible paths of every two nodes. The maximum length of the path is defined by the user.

- Click [here](#) to enter the download page
- Click [here](#) to enter the reference page

*Last updated: 07/06/2021*
Nodes in sub-network $A$

Nodes in sub-network $B$

Shortest path in the whole network

Shortest path in sub-network $A$

Degree of $s$ is 4, not 3

Distance between $s$ and $t$ is 2, not 3
$K = 10.82 \ln(E) + 27.56$

$R^2 = 0.9099$

$P < 10^{-8}$
**Figure 6**

(A) Plot showing the relationship between the fraction of helices (H) and the average degree (K). The regression line is given by $K = -100.9S + 46.35$ with $R^2 = 0.9416$ and $P < 10^{-12}$.

(B) Plot showing the relationship between the fraction of strands (S) and the average degree (K). The regression line is given by $K = -76.67M + 66.05$ with $R^2 = 0.8769$ and $P < 10^{-5}$.

(C) Plot showing the relationship between the fraction of random coil (M) and the average degree (K). The regression line is given by $K = -76.67M + 66.05$ with $R^2 = 0.8769$ and $P < 10^{-5}$. 
Proteins with functional annotations

Proteins without functional annotations

Average degree (K)

P < 10^{-12}
A. $K = 0.0186N + 19.09$
   $R^2 = 0.8553$
   $P < 10^{-6}$

B. $K = 0.0063N + 44.56$
   $R^2 = 0.1318$
   $P = 0.2329$

C. $K = 0.0063N + 44.56$
   $R^2 = 0.1318$
   $P = 0.2329$

D. $K = 0.0015N + 2.261$
   $R^2 = 0.7345$
   $P < 10^{-4}$

Figure 8