

The detail of our bootstrap method

The bootstrap method was used in our paper to determine the threshold which we used to construct the correlation network R. Non-parameter bootstrap method, with $n=1000$ and $p\text{-value}=0.05$, was used in our study. The details of the method are described as follows.

The absolute Pearson correlation coefficient of each miRNA pairs in the 203 miRNAs across samples of 12 cancers formed the original dataset S. The dataset S consisted of 20503 data points and we assumed these data points in S as s_i ($i = 1 \cdots 20503$). Then, our bootstrap method was performed as steps below

Step one: We resampled the data to obtain a bootstrap resample R_i , which came from sampling with replacement from the original dataset S. The number of data points in the bootstrap resample was equal to the number of data points in the original dataset. We assumed the data points in the resample as r_{ij} ($j = 1 \cdots 20503$). It should be noted that different data points in R_i can equal to the same data point in S. Then we computed the mean of this resample as the bootstrap mean a_i by using the following equation.

$$a_i = \frac{\sum_{j=1}^{20503} r_{ij}}{20503}$$

Step two: We repeated step one 1000 times and the bootstrap mean of each resample ($a_i, i = 1 \cdots 1000$) formed a distribution A. This distribution was used to determine the threshold of our network in next step.

Step three: We chosen threshold of p-value as 0.05 and used the 95 percentile which is 0.1551881 in our case as the threshold. The mathematic formula of this step is as follows.

$$\text{threshold}(p - \text{value} = 0.05) = \{x | \text{pr}(x \leq A) = 0.05\}$$