

The source codes of NCRR are written by C++. Because there may exist compatibility problems in different C++ development tools (such as Visual C++ 6.0, Visual Studio 2012 or Visual Studio 2015), we have uploaded the complete source codes and detailed instructions in the website. In this study, the authors used Visual C++ 6.0 to run the NCRR codes. The detailed process of running NCRR codes using Visual C++ 6.0 is described as follows:

- (1) Create a project: click button “File” → click button “New” → click button “Win32 Console Application” → click button “OK” → click button “Finish”;
- (2) Create “C++ source file”: click button “File” → click button “New” → click button “C++ Source File”. Then, users copy the source codes of NCRR into the programming box;
- (3) Run the codes: click button “Rebuild All” → click button “Execute Program”.
- (4) In the input file, the first raw is the sample label and the first column is the gene ID (see “LUAD input example.csv” in the uploaded folder).
- (5) The output file is named as “Net.csv” in which the first and second columns represent the IDs of two genes linking by an edge and the third column represents the edge weight.