1. **Association matrix** - Matrix representing circRNA,disease associations.

2. **integrated CircRNA Similarity** - Integrated CircRNA similarity calculated based on

circRNA functional and GIP similarities, as described in the paper.

3. **integrated Disease Similarity** - Integrated disease similarity calculated based on

disease semantic and GIP similarities, as described in the paper.

4. **main**- Calculates integrated similarities of circRNA and diseases.

5. **miRNASS**-Calculates circRNA functional similarity.

6. **gkl**-Calculates GIP similarities of circRNA and diseases.

7. **AE-RF.py- Code for the implementation of AE-RF.**

For any queries, please feel free to contact: deepthi523@gmail.com