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

2. **Association Matrix.xlsx -** Association matrix with corresponding circRNA,

disease names.

3. **integrated CircRNA Similarity.txt** - Integrated CircRNA similarity

calculated based on circRNA functional and GIP similarities, as described in

the paper.

4. **integrated Disease Similarity.txt** - Integrated disease similarity calculated

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

5. **main.m** - Calculates integrated similarities of circRNA and diseases.

6. **miRNAs.m** -Calculates circRNA functional similarity.

7. **gkl.m** -Calculates GIP similarities of circRNA and diseases.

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

For any queries, please feel free to contact: [deepthi523@gmail.com](mailto:deepthi523@gmail.com)

**Researchers can use the code with proper citation.**