ReadMe.docx presents the descriptions of 11 files in DAEM folder. The proposed DAEM model employs two drug attributes, molecular structure and side effect for ADDI modeling. In the experiments, we totally extract 673,458 distinct adverse drug pairs from Twosides [1] to construct adverse interaction matrix  and adverse interaction tensor , which are associated with  drugs and  adverse interactions. This folder contains the experimental dataset and source code of the proposed model. All experiments are executed on a PC server with two Nvidia GTX 1080Ti GPUs and 64G real memory in Windows platform. The source codes of DAEM are public available at https://github.com/AdverseDDI/DAEM.git.

Except for ReadMe.docx, the detailed descriptions of the 11 files in this folder are given in the following:

1. MolecularStructureMatrix.txt is the hand-designed molecular structure matrix of drugs, which is built based on DrugBank database [2]. Each drug is in relevance to an 881 dimensional binary vector () such that if drug  owns the *i*-th molecular substructure, then; otherwise. In MolecularStructureMatrix.txt, the first row represents the identifiers of 555 drugs with the prefix of CID, and the second row indicates the 881 dimensional binary vectors of 555 drugs.
2. SiderEffectMatrix.txt is the hand-designed side effect matrix of drugs , which is extracted from SIDER database [3]. Each drug is coded as a 1,656 dimensional binary vector () such that  or  denotes whether that drug  can result in the *r*-th side effect or not. In SiderEffectMatrix.txt, the first row represents the identifiers of 555 drugs with the prefix of CID, and the second row indicates the 1,656 dimensional binary vectors of 555 drugs.
3. AdverseInteractionMatrix.txt records the adverse interaction matrix of drugs , in which if drug pair  results in adverse interactions, then; otherwise. Therefore, AdverseInteractionMatrix.txt owns 555 rows and 555 columns.
4. AdverseInteractionTensor.txt presents the detailed adverse interaction information caused by adverse drug pairs, which can be utilized to construct the adverse interaction tensor of drugs (,). To be specific, the first two columns denote the indexes of drugs corresponding to the first column in DrugCID-DrugName.txt, and the third column indicates the index of adverse interactions in consistence with the first column in AdverseInteractionID-AdverseInteractionName.txt. In this way, adverse interaction tensor  can be established by first initiating a three-dimensional tensor with the size of , and then filling the tensor based on the each row in AdverseInteractionTensor.txt.
5. DrugCID-DrugName.txt records the brief information of 555 drugs, in which the first column presents the index of drugs that is used in the first two columns in AdverseInteractionTensor.txt, the second column is the identifiers of drugs with the prefix of CID, and the last column indicates the name of drugs.
6. AdverseInteractionID-AdverseInteractionName.txt contains the brief descriptions of 1318 adverse interactions, in which the first column indicates the index of adverse interactions presented in the last column in AdverseInteractionTensor.txt, the second column is the identifiers of adverse interactions with the prefix of C0, and the last column indicates the name of adverse interactions.
7. LowDimensionalMolecularStructureRepresentation.txt is the derived molecular structure embeddings of drugs  output by source code file DeepAttributeEmbedding.py. Since the auto-encoder designed for deep molecular structure embedding employs  layers with one third layer size for each successive higher layer in the encoders, the embedding dimensionality for molecular structure  is set to be 97.
8. LowDimensionalSideEffectRepresentation.txt is the captured side effect embeddings of drugs  output by source code file DeepAttributeEmbedding.py. Likewise, the auto-encoder devised for deep side effect embedding employs  layers with one third layer size for each successive higher layer in the encoders, the embedding dimensionality for side effect  is set to be 184.
9. DeepAttributeEmbedding.py is the source code of deep attributed embedding, composed of attributed embedding capturing, adverse relationship preservation, and attribute dependence modeling. The inputs of DeepAttributeEmbedding.py are the hand-designed molecular structure and side effect matrices of drugs  and  (i.e., MolecularStructureMatrix.txt and SiderEffectMatrix.txt). The outputs of this file are the derived molecular structure and side effect embeddings of drugs  and  presented in LowDimensionalMolecularStructureRepresentation.txt and LowDimensionalSideEffectRepresentation.txt, respectively. One can directly run ‘Python DeepAttributeEmbedding.py’ in the cmd windows to conduct deep attributed embedding.
10. Multi-taskLearningADDIPrediction.py is the source code of multi-task learning for ADDI prediction. The inputs of this file are the learned molecular structure and side effect embeddings of drugs  and  presented in LowDimensionalMolecularStructureRepresentation.txt and LowDimensionalSideEffectRepresentation.txt, and adverse interaction dataset given in AdverseInteractionTensor.txt. This source code file is to explore the underlying relationship between the concatenated attribute representation  (,) and the adverse interactions among drugs. One can directly run ‘Python Multi-taskLearningADDIPrediction.py’ in the cmd windows to conduct multi-task learning for ADDI prediction. Note that it may take 2-3 hours to output the final evaluation results.

**Reference**

[1] Tatonetti, N. P., Ye, P. P., Roxana, D. et al (2012). Data-driven prediction of drug effects and interactions. Science Translational Medicine, 4, 1-14.

[2] Wishart, D. S., Knox, C., Guo, A. C. et al. (2008). DrugBank: A knowledgebase for drugs, drug actions and drug targets. Nucleic Acids Research, 36, 901-906.

[3] Kuhn, M., Letunic, I., Jensen, L. J. et al. (2016). The SIDER database of drugs and side effects. Nucleic Acids Research, 44, 1075-1079.