With the proper installation of the Python and PyTorch environments, the simplified steps for implementing the source codes of the proposed model are

1. Run **MultiAttributeRepresentationLearning.py** in . \Source Codes of MAMK\Multi-Attribute Representation Learning and obtain the shared and specific attribute representations of drugs in Subfolder . \Source Codes of MAMK\Multi-Attribute Representation Learning\SharedSpecificAttributeRepresentations and the recovered multi-attribute absent information in Subfolder . \Source Codes of MAMK\Multi-Attribute Representation Learning\RecoveredMultiAttributeRepresentations
2. Copied the the shared and specific attribute representations of drugs with the suffix of ‘.npy’ from Subfolder . \Source Codes of MAMK\Multi-Attribute Representation Learning\SharedSpecificAttributeRepresentations to the Subfolder .\ Source Codes of MAMK\Multi-Kernel Representation Learning for ADDI prediction\SharedSpecificAttributeRepresentations.
3. Run ‘KernelFunctionLearning.py’ to output the metrics of the model shown in the console.

