**Algorithm 2: FVTLDA with ANN**

**Input**: Known miRNA-lncRNA associations matrix *ML*, known miRNA-disease associations matrix *MD*, known lncRNA-disease associations matrix *LD*, disease MESH descriptors, parameter *r*1, *r*2, *k*1, *k*2, *rate*.

**Output**: The association probability fraction vector of candidate lncRNA-disease pairs.

**Step 1**: Generate the miRNA Gaussian interaction profile kernel similarity matrix KM by Eq (4);

**Step 2**: Generate the disease semantic similarity matrix DSMD and DSLD by Eq (8);

**Step 3**: Generate the miRNA function similarity matrix *FM* and lncRNA function similarity matrix *FL* by Eq (9) and Eq (10) respectively;

The training process of the FVTLDA with ANN is as follows:

**Step 4**: Generate feature vector *FVij* for each pair of lncRNA *li* and disease *dj* in the training set by Eq (17);

**Step 5**: Generate the association probability fraction *OUTPUT*(*i*,*j*) for each pair of lncRNA *li* and disease *dj* in the training set by Eq (18);

**Step 6**: Take the *FVij* as input values and *OUTPUT*(*i*,*j*) as the target values to generate the weights and biases of ANN according to the four major steps described above;

After obtaining weights and biases of ANN, the testing process of the FVTLDA with

ANN is as follows:

**Step 7**: Generate feature vector *FVij* for each pair of lncRNA *li* and disease *dj* in the testing set;

**Step 8**: Take the *FVij* as input values to calculate the association probability fraction *scoreij* for each pair of lncRNA *li* and disease *dj* in the testing set;

(Here, scoreij is the output values of the ANN.)

**Step 9**: Sort all candidate lncRNA-disease pairs by the value of association probability fractions obtained by step 8 in the descending order;

**Step 10**: Output the sorted candidate lncRNA-disease pairs;

**Algorithm 1: FVTLDA with MLR**

**Input**: Known miRNA-lncRNA associations matrix *ML*, known miRNA-disease associations matrix *MD*, known lncRNA-disease associations matrix *LD*, disease MESH descriptors, parameter *r*1, *r*2, *k*1, *k*2, *rate*.

**Output**: The association probability fractions vector of candidate lncRNA-disease pairs.

**Step 1**: Generate the miRNA Gaussian interaction profile kernel similarity matrix KM by Eq (4);

**Step 2**: Generate the disease semantic similarity matrix DSMD and DSLD by Eq (8);

**Step 3**: Generate the miRNA function similarity matrix *FM* and lncRNA function similarity matrix *FL* by Eq (9) and Eq (10) respectively;

The training process of the FVTLDA with MLR is as follows:

**Step 4**: Generate feature vector *FVij* for each pair of lncRNA *li* and disease *dj* in the training set by Eq (17);

**Step 5**: Generate the association probability fractions *OUTPUT*(*i*,*j*) for each pair of lncRNA *li* and disease *dj* in the training set by Eq (18);

**Step 6**: Obtain the optimal regression coefficients W∗ by Eq (24);

After obtaining W\*, the testing process of the FVTLDA with MLR is as follows:

**Step 7**: Generate feature vector *FVij* for each pair of lncRNA *li* and disease *dj* in the testing set;

**Step 8**: Calculate the association probability fraction *scoreij* for each pair of lncRNA *li* and disease *dj* in the testing set as follows: *scoreij* =*W*\*×*FVij* ;

**Step 9**: Sort all candidate lncRNA-disease pairs by the value of association probability fractions obtained by step 8 in the descending order;

**Step 10**: Output the sorted candidate lncRNA-disease pairs;