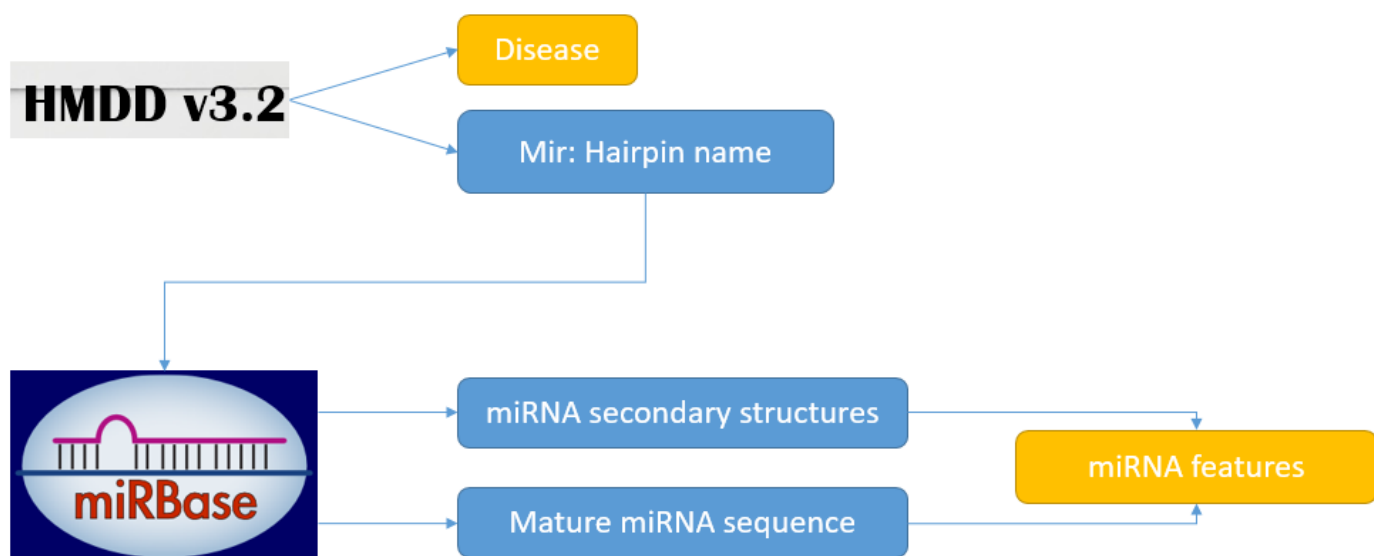
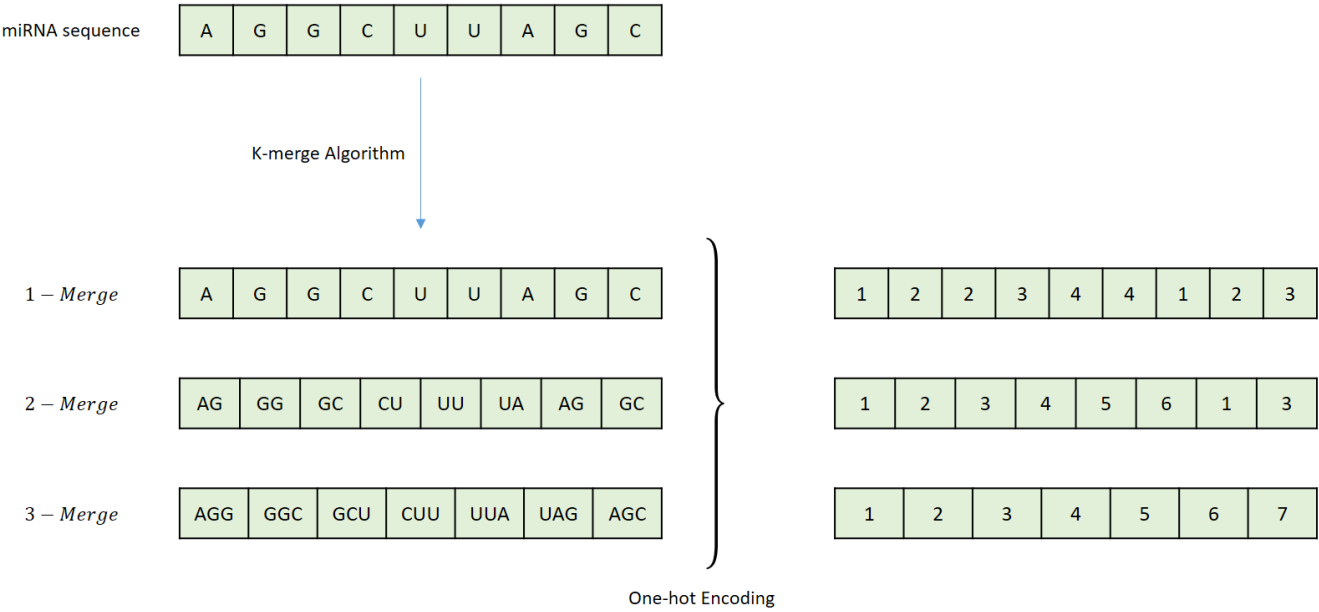
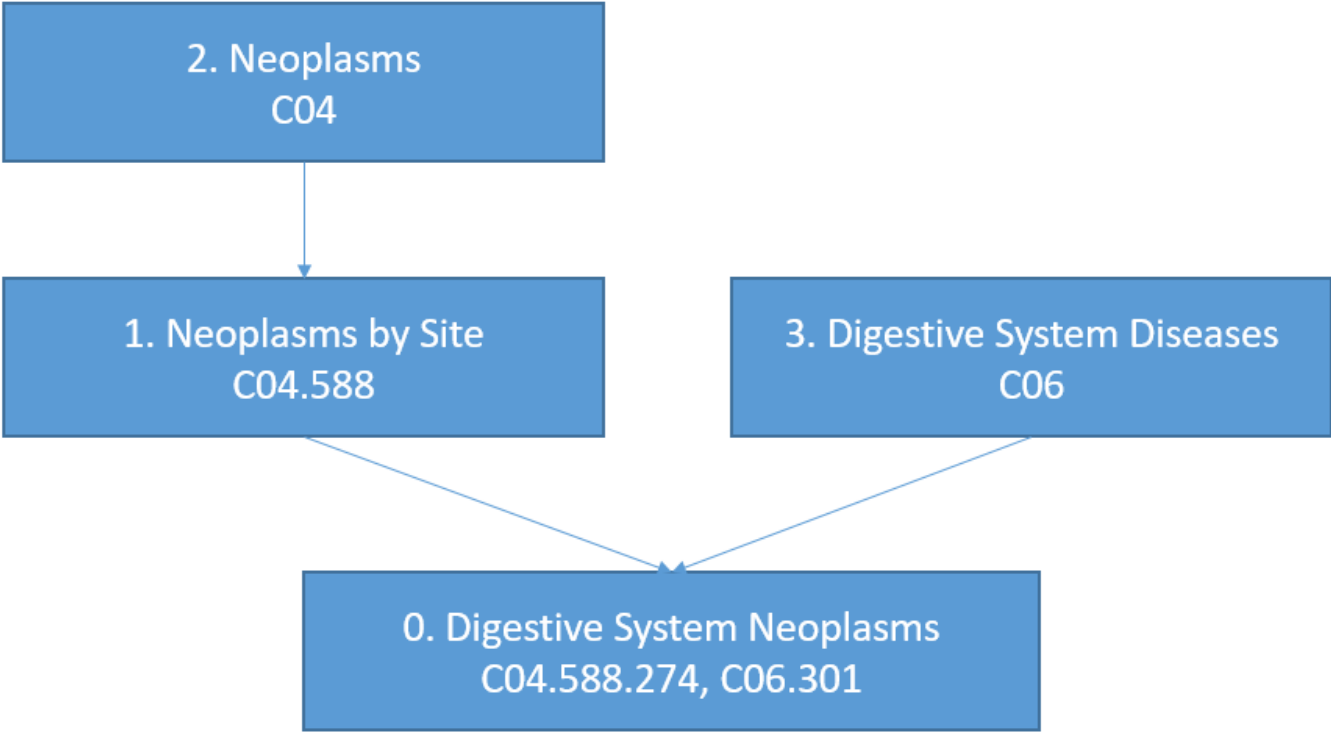




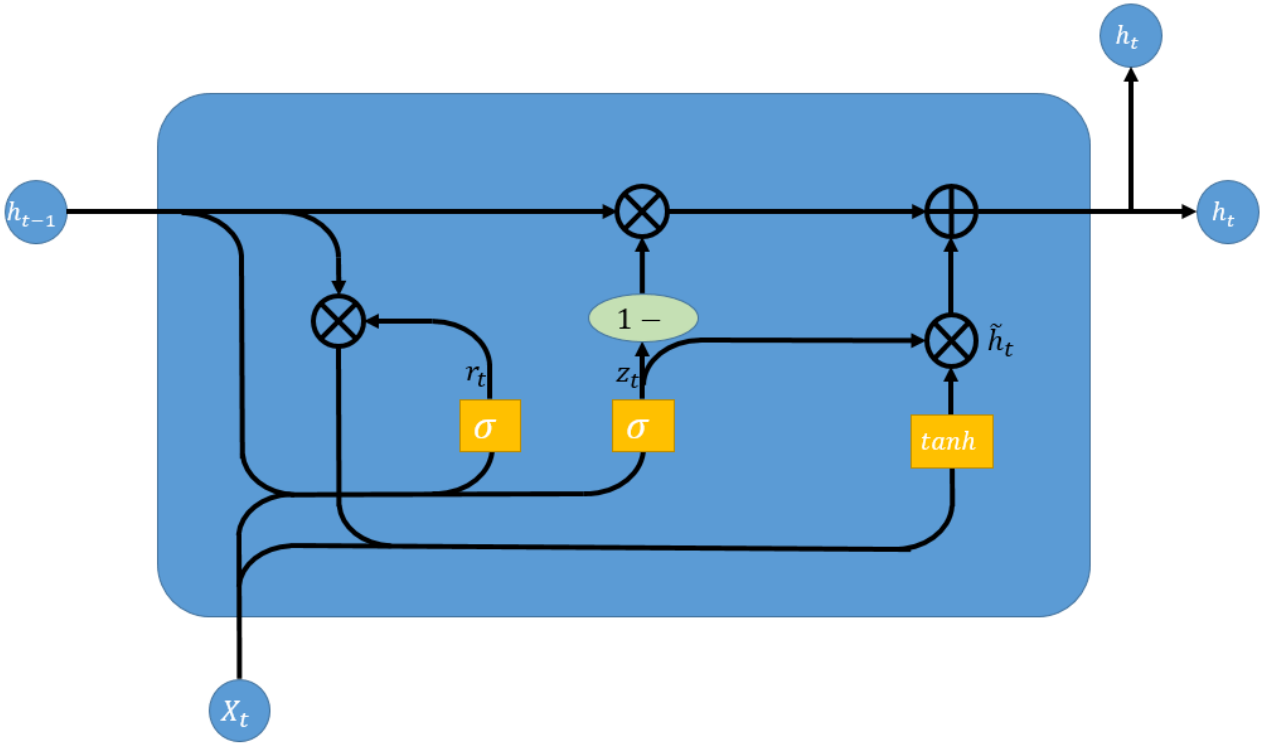
Supplementary Figure 1. Process for miRNA feature. The blue boxes represent keywords crawling and the yellow boxes represent the features of input disease and miRNAs.



Supplementary Figure 2. Example of K-merge algorithm for genetic data preprocessing. In 1-Merge, A, G, C, and U were replaced by 1, 2, 3, and 4. In 2-Merge, AG, GG, GC, CU, UU, UA were replaced by 1, 2, 3, 4, 5, and 6. In 3-merge, AGG, GGC, GCU, CUU, UUA, UAG, and AGC were replaced by 1, 2, 3, 4, 5, 6, and 7.



Supplementary Figure 3. The directed acyclic graph of MeSH descriptor for Digestive System Neoplasms.



$$\begin{aligned}
 z_t &= \text{sigmoid}(W_z^x x_t + W_z^h h_{t-1} + b_z) \\
 r_t &= \text{sigmoid}(W_r^x x_t + W_r^h h_{t-1} + b_r) \\
 \tilde{h}_t &= \tanh(W_h^x x_t + W_h^h (z_t \circ r_t) + b_h) \\
 h_t &= z_t \circ \tilde{h}_t + (1 - z_t) \circ h_{t-1}
 \end{aligned}$$

$$r_t, z_t \in [0,1]$$

Supplementary Figure 4. Gated recurrent unit.