

## DeNovo: Work Flow

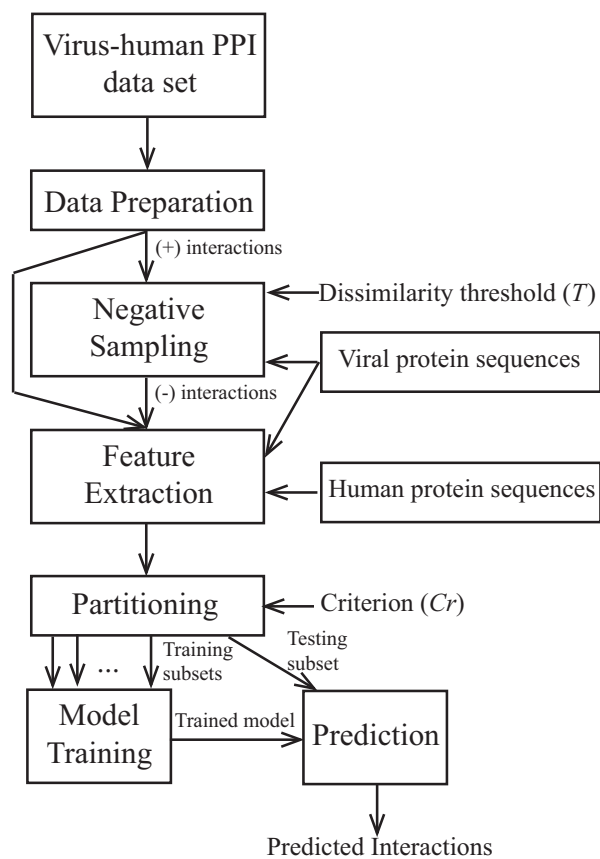


Figure 1: DeNovo work flow. Virus-human PPIs are first cleaned, negative interactions are generated, and features are extracted from the protein sequences of the positive and negative interaction pairs. The feature vectors of the interactions are partitioned into multiple pairs of training and testing subsets based on a criterion  $Cr$ . A machine learning model is trained on the feature vectors from a training subset and tested on the corresponding testing subset.