INPUT: training data (set of RNA sequences) test data (set of RNA sequences)

OUTPUT: SVM class probability for each of test data

(1) Training

for each sequence $x$ in training data
  compute a base-pairing probability matrix $P_x$;
  for each position $i$ in $x$
    compute a base-pairing profile {$P_{xL}(i)$, $P_{xR}(i)$, $P_{xU}(i)$};
  end for
end for

for each sequence $x$ in training data
  for each sequence $y$ in training data
    compute a value of BPLA kernel $K_{train}(x, y)$;
  end for
end for

Train a SVM classifier using $K_{train}$;

(2) Test

for each sequence $x$ in test data
  compute a base-pairing probability matrix $P_x$;
  for each position $i$ in $x$
    compute a base-pairing profile {$P_{xL}(i)$, $P_{xR}(i)$, $P_{xU}(i)$};
  end for
end for

for each sequence $x$ in test data
  for each sequence $y$ in training data
    compute a value of BPLA kernel $K_{test}(x, y)$;
  end for
end for

for each sequence $x$ in test data
  compute a SVM class probability for $x$ using $K_{test}$ and the trained classifier;
end for

function COMPUTE_AVERAGED_BP_MATRIX($X$)
  for each sequence $X_k$ in $X$
    compute a base-pairing probability matrix $P_{X_k}$;
  end for
  return the averaged matrix of $P_{X_k}$;
end function

(b) Profile BPLA kernel

INPUT: training data (set of RNA alignments) test data (set of RNA alignments)

OUTPUT: SVM class probability for each of test data

(1) Training

for each alignment $X$ in training data
  $P_X$ = COMPUTE_AVERAGED_BP_MATRIX($X$);
  for each column $i$ in $X$
    compute a base-pairing profile {$P_{X_L}(i)$, $P_{X_R}(i)$, $P_{X_U}(i)$};
  end for
end for

for each alignment $X$ in training data
  for each alignment $Y$ in training data
    compute a value of Profile BPLA kernel $K_{train}^{pair}(X, Y)$;
  end for
end for

Train a SVM classifier using $K_{train}^{pair}$;

(2) Test

for each alignment $X$ in test data
  $P_X$ = COMPUTE_AVERAGED_BP_MATRIX($X$);
  for each column $i$ in $X$
    compute a base-pairing profile {$P_{X_L}(i)$, $P_{X_R}(i)$, $P_{X_U}(i)$};
  end for
end for

for each alignment $X$ in test data
  for each alignment $Y$ in training data
    compute a value of Profile BPLA kernel $K_{test}^{pair}(X, Y)$;
  end for
end for

for each alignment $X$ in test data
  compute a SVM class probability for $X$ using $K_{test}^{pair}$ and the trained classifier;
end for

function COMPUTE_AVERAGED_BP_MATRIX($X$)
  for each sequence $X_k$ in $X$
    compute a base-pairing probability matrix $P_{X_k}'$;
  end for
  return the averaged matrix of $P_{X_k}'$;
end function