

(a) Original BPLA kernel

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  $\{P_x^L(i), P_x^R(i), P_x^U(i)\}$ ;
  end for
end for
```

```
for each sequence x in training data
  for each sequence y in training data
    compute a value of BPLA kernel  $K^{\text{train}}(\mathbf{x}, \mathbf{y})$ ;
  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  $\{P_x^L(i), P_x^R(i), P_x^U(i)\}$ ;
  end for
end for
```

```
for each sequence x in test data
  for each sequence y in training data
    compute a value of BPLA kernel  $K^{\text{test}}(\mathbf{x}, \mathbf{y})$ ;
  end for
end for
```

```
for each sequence x in test data
  compute a SVM class probability for x \
  using  $K^{\text{test}}$  and the trained classifier;
end for
```

(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
   $P_x = \text{COMPUTE\_AVERAGED\_BP\_MATRIX}(\mathbf{X})$ ;
  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  $K^{\text{train}}(\mathbf{X}, \mathbf{Y})$ ;
  end for
end for
```

Train a SVM classifier using K^{train} ;

(2) Test

```
for each alignment X in test data
   $P_x = \text{COMPUTE\_AVERAGED\_BP\_MATRIX}(\mathbf{X})$ ;
  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  $K^{\text{test}}(\mathbf{X}, \mathbf{Y})$ ;
  end for
end for
```

```
for each alignment X in test data
  compute a SVM class probability for X \
  using  $K^{\text{test}}$  and the trained classifier;
end for
```

```
function COMPUTE_AVERAGED_BP_MATRIX(X)
  for each sequence  $\mathbf{X}^k$  in X
    compute a base-pairing probability matrix  $P'_{\mathbf{x}^k}$ ;
  end for
  return the averaged matrix of  $P'_{\mathbf{x}^k}$ ;
end function
```