

MiRduplexSVM – miRNA: miRNA* duplex prediction.

It predicts the most probable miRNA duplex on a given miRNA hairpin.
It has two modes of operation.

- You can upload a txt file with your sequences in fasta format, (include fasta file header).
- You can paste your sequences (include fasta file header) in fasta format in the textbox, which is the default operation.

Output is a three columns tab delimited table. The first column specifies the sequences' IDs as they were specified by the user, the second and the third columns shows the most probable matures from the 5' and the 3' strand of the hairpin respectively. Entries for which the RNAfold output is not a hairpin or consists of multiple stems are filtered out and "Multibranch - No prediction" is returned as an output at the respective line.

An e-mail could be provided in order to receive your results.

Thank you for using MiRduplexSVM.

Input example:

```
>MI0000060
UGGGAUGAGGUAGUAGGUUGUAUAGUUUUAGGGUCACACCCACCACUGGGA
GAUAACUAUACAAUCUACUGUCUUUCCUA
>MI0000061
AGGUUGAGGUAGUAGGUUGUAUAGUUUAGAAUUACAUCAAGGGAGAUAACUG
UACAGCCUCCUAGCUUUCCU
>MI0000065
CCUAGGAAGAGGUAGUAGGUUGCAUAGUUUUAGGGCAGGGAUUUUGCCCAC
AAGGAGGUAACUAUACGACCUGCUGCCUUUCUAGG
>MI0003603
UCUUAUCAAUGAGGUAGACCAUGGGUUCUCAUUGUAAUAGUGUAGAAUGUUG
GUUAACUGUGGACUCCUGGCUCUGUCUCAAUUCUACUGAUUC
>MI0000070
GUCAGCAGUGCCUUAGCAGCACGUAUUUUGGCGUUAAGAUUCUAAAAUUA
UCUCCAGUAUUUACUGUGCUGCUGAAGUAAGGUUGAC
>MI0003681
GUGUAGUAGAGCUAGGAGGAGAGGGUCCUGGAGAAGCGUGGACCGGUCCGG
GUGGGUCCGGCAGGUUCUCACCCUCUCUAGGCCCCAUUCUCCUCUG
>MI0000071
GUCAGAAUAAUGUCAAGUGCUUACAGUGCAGGUAGUGAUUUGUGCAUCUAC
UGCAGUGAAGGCACUUGUAGCAUUAUGGUGAC
```

Output example:

sequenceID	5strandMature	3strandMature
MI0000060	UGAGGUAGUAGGUUGUAUAGUU	CUAUACAAUCUACUGUCUUUC
MI0000061	UGAGGUAGUAGGUUGUAUAGUU	CUGUACAGCCUCCUAGCUUUCC
MI0000065	AGAGGUAGUAGGUUGCAUAGUU	CUAUACGACCUGCUGCCUUUC
MI0003603	Multibranch - No prediction	
MI0000070	UAGCAGCACGUAUUUUGGCG	CCAGUAUUUACUGUGCUGCUGA
MI0003681	Multibranch - No prediction	
MI0000071	CAAAGUGCUUACAGUGCAGGUAG	ACUGCAGUGAAGGCACUUGUAG

MiRduplexSVM: miRNA Evaluator - Missing duplex finder.

It evaluates a miRNA mature by assigning MiRduplexSVM's score and predicts the mature molecule that lies on the opposite strand. It has two modes of operation.

- You can upload two txt files with your sequences in fasta format, (include fasta file header). The one file should have the miRNA precursor sequences and the other should include the respective mature miRNA sequences.
- You can paste your sequences in fasta format (include fasta file header) in the appropriate textboxes in the online form.

Output is a four columns tab delimited table. The first column specifies the sequences' IDs as they were specified by the user, the second and the third columns show the matures from the 5' and the 3' strand of the hairpin respectively, the fourth column represents MiRduplexSVM's score. One mature correspond to the one has been provided by the user and the other one is the program's prediction. Entries for which the RNAfold output is not a hairpin or consists of multiple stems are filtered out and "Multibranch - No prediction" is returned as an output at the respective line.

An e-mail could be provided in order to receive your results.

Thank you for using MiRduplexSVM: Evaluator - Missing duplex finder

Input example - precursors sequences:

```
>MI0000064
GCAUCCGGGUUGAGGUAGUAGGUUGUAUGGUUUAGAGUUACACCCUGGGAG
UUAACUGUACAACCUUCUAGCUUCCUUGGAGC
>MI0000238
GUGAAUUAGGUAGUUUCAUGUUGUUGGGCCUGGGUUUCUGAACACAACAAC
AUUAAACCACCCGAUUCAC
>MI0003603
UCUUAUCAAUAGAGGUAGACCAUGGGUUCUCAUUGUAAUAGUGUAGAAUGUUG
GUUAACUGUGGACUCCUGGCUCUGUCUCAAUUCUACUGAUUC
>MI0000240
UCAUUGGUCCAGAGGGGAGAUAGGUUCCUGUGAUUUUUCCUUCUUCUCUAUA
GAAUAAAUGA
>MI0003681
GUGUAGUAGAGCUAGGAGGAGAGGGUCCUGGAGAAGCGUGGACCGGUCCGG
GUGGGUUCGGCAGGUUCUCACCCUCUCUAGGCCCAUUCUCCUCUG
>MI0000265
AGAUUAGAGUGGCUGUGGUCUAGUGCUGUGUGGAAGACUAGUGAUUUUGUU
GUUCUGAUGUACUACGACAACAAGUCACAGCCGGCCUCAUAGCGCAGACUCC
CUUCGAC
>MI0000291
AUCAUUCAGAAAUGGUUAUACAGGAAAAUGACCUAUGAAUUGACAGACAAUUAU
AGCUGAGUUUGUCUGUCAUUUCUUUAGGCCAAUAUUCUGUAUGACUGUGCUA
CUUCAA
```

Input example - mature sequences:

```
>MI0000064
UGAGGUAGUAGGUUGUAUGGUU
>MI0000238
UAGGUAGUUUCAUGUUGUUGG
>MI0003603
```

```

AGACCAUGGGUUCUCAUUGU
>MI0000240
GGUCCAGAGGGGAGAUAGGUUC
>MI0003681
GGCAGGUUCUCACCCUCUCUAGG
>MI0000265
UGGAAGACUAGUGAUUUUGUUGU
>MI0000291
AUGACCUAUGAAUUGACAGAC

```

Output example:

sequenceID	5strandMature	3strandMature	MiRduplexSVM-score
MI0000064	UGAGGUAGUAGGUUGUAUGGUU	CUGUACAACCUUCUAGCUUUC	1.258655e+00
MI0000238	UAGGUAGUUUCAUGUUGUUGG	CAACAACAUUAAACCACCCGAU	6.887440e-01
MI0003603	Multibranch - No prediction		
MI0000240	GGUCCAGAGGGGAGAUAGGUUC	UCCUUCUUCUCUAUAGAAUAAA	-8.162919e-01
MI0003681	Multibranch - No prediction		
MI0000265	UGGAAGACUAGUGAUUUUGUUGU	CAACAAGUCACAGCCGCCUCA	1.256639e+00
MI0000291	AUGACCUAUGAAUUGACAGAC	UCUGUCAUUUCUUUAGGCCAAU	7.194692e-01

MiRduplexSVM – miRNA:miRNA* Duplex Evaluator.

It evaluates a miRNA:miRNA* duplex by assigning MiRduplexSVM's score.

- You can upload three txt files with your sequences in fasta format, (include fasta file header). The first file should have the miRNA precursor sequences, the second should include the mature miRNA sequences produced by the 5' strand and the third file the mature miRNA sequences produced by the 3' strand.
- Alternatively, you can paste your sequences in fasta format (include fasta file header) in the appropriate textboxes in the online form.

Output is a four columns tab delimited table. The first column specifies the sequences' IDs as they were specified by the user, the second and the third columns show the matures from the 5' and the 3' strand of the hairpin respectively, the fourth column represents MiRduplexSVM's score. Entries for which the RNAfold output is not a hairpin or consists of multiple stems are filtered out and "Multibranch - No prediction" is returned as an output at the respective line.

An e-mail could be provided in order to receive your results.

Thank you for using MiRduplexSVM – miRNA:miRNA* Duplex Evaluator

Input example – precursors sequences:

```

>MI0000063
CGGGGUGAGGUAGUAGGUUGUGUGGUUUCAGGGCAGUGAUUGCCCCUCG
GAAGAUAAUAUACAACCUACUGCCUUCCCUG
>MI0000286
ACCCGGCAGUGCCUCCAGGCGCAGGGCAGCCCCUGCCCACCGCACACUGCGC
UGCCCCAGACCCACUGUGCGUGUGACAGCGGCUGAUCUGUGCCUGGGCAGC
GCGACCC
>MI0000447
UGAGCUGUUGGAUUCGGGGCCGUAGCACUGUCUGAGAGGUUUACAUUUCUC
ACAGUGAACCGGUCUCUUUUUCAGCUGCUUC
>MI0000450
ACAAUGCUUUGCUAGAGCUGGUAAAAUGGAACCAAUCCGCCUCUCAAUGGA
UUUGGUCCCCUUAACCAGCUGUAGCUAUGCAUUGA
>MI0000451

```

```

GGGAGCCAAAUGCUUUGCUAGAGCUGGUAAAAUGGAACCAAUUCGACUGUCC
AAUGGAUUUGGUCCCCUUAACCAGCUGUAGCUGUGCAUUGAUGGCGCCG
>MI0000474
CAGGGUGUGUGACUGGUUGACCAGAGGGGCAUGCACUGUGUUCACCCUGUG
GGCCACCUAGUCACCAACCCUC

```

Input example - mature sequences from 5'strand :

```

>MI0000063
UGAGGUAGUAGGUUGUGUGGUU
>MI0000286
AGCCCCUGCCCACCGCACACUG
>MI0000447
CGGGGCCGUAGCACUGUCUGAGA
>MI0000450
AGCUGGUAAAAUGGAACCAAU
>MI0000451
AGCUGGUAAAAUGGAACCAAU
>MI0000474
UGUGACUGGUUGACCAGAGGGG

```

Input example - mature sequences from 3'strand :

```

>MI0000063
CUAUACAACCUACUGCCUCCCC
>MI0000286
CUGUGCGUGUGACAGCGGCUGA
>MI0000447
UCACAGUGAACCGGUCUCUUU
>MI0000450
UUUGGUCCCCUUAACCAGCUG
>MI0000451
UUUGGUCCCCUUAACCAGCUG
>MI0000474
CCUGUGGGCCACCUAGUCACCAA

```

Output example:

sequenceID	5strandMature	3strandMature	MiRduplexSVM-score
MI0000063	Multibranch - No prediction		
MI0000286	AGCCCCUGCCCACCGCACACUG	CUGUGCGUGUGACAGCGGCUGA	1.175949e+00
MI0000447	CGGGGCCGUAGCACUGUCUGAGA	UCACAGUGAACCGGUCUCUUU	1.003558e+00
MI0000450	AGCUGGUAAAAUGGAACCAAU	UUUGGUCCCCUUAACCAGCUG	1.380121e+00
MI0000451	AGCUGGUAAAAUGGAACCAAU	UUUGGUCCCCUUAACCAGCUG	1.121841e+00
MI0000474	UGUGACUGGUUGACCAGAGGGG	CCUGUGGGCCACCUAGUCACCAA	-6.557550e-02