MiRduplexSVM - Help file

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MiRduplexSVM – miRNA: miRNA* duplex prediction.

This tool predicts the most likely miRNA duplex on a given miRNA hairpin and offers two modes of operation.

1. You can upload a text file (.txt) containing your sequences in fasta format, including the fasta file header.
2. You can paste your sequences (including the fasta file header) directly into the provided textbox, which is the default operation.

The output is presented as a three-column tab-delimited table. The first column lists the sequence IDs as specified by the user, while the second and third columns display the most probable matures from the 5' and the 3' strands 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 for the respective lines.

If you wish to receive your results via email, you can provide your email address. Thank you for using *MiRduplexSVM duplex prediction*.

Input Example:

```
>MI0000060
UGGGAUGAGGUAGUAGGUUGUAUAGUUUUAGGGUCACACCCACCACUGGGAGAUAACUAUACAAUCUACUGUCUUUCCUA
>MI0000061
AGGUUGAGGUAGUAGGUUGUAUAGUUUAGAAUUACAUCAAGGGAGAUAACUGUACAGCCUCCUAGCUUUCCU
>MI0000065
CCUAGGAAGAGGUAGUAGGUUGCAUAGUUUUAGGGCAGGGAUUUUGCCCACAAGGAGGUAACUAUACGACCUGCUGCCUUUC
UUAGG
>MI0003603
UCUUAUCAAUGAGGUAGACCAUGGGUUCUCAUUGUAAUAGUGUAGAAUGUUGGUUAACUGUGGACUCCCUGGCUCUGUCUCA
AAUCUACUGAUUC
>MI0000070
GUCAGCAGUGCCUUAGCAGCACGUAAAUAUUGGCGUUAAGAUUCUAAAAUUAUCUCCAGUAUUAACUGUGCUGCUGAAGUAA
GGUUGAC
>MI0003681
GUGUAGUAGAGCUAGGAGGAGAGGGUCCUGGAGAAGCGUGGACCGGUCCGGGUGGGUUCCGGCAGGUUCUCACCCUCUCUAG
GCCCCAUUCUCCUCUG
>MI0000071
GUCAGAAUAAUGUCAAAGUGCUUACAGUGCAGGUAGUGAUAUGUGCAUCUACUGCAGUGAAGGCACUUGUAGCAUUAUGGUG
AC
```

Output example:

```
sequenceID     5strandMature           3strandMature
MI0000060      UGAGGUAGUAGGUUGUAUAGUU   CUAUACAAUCUACUGUCUUUC
MI0000061      UGAGGUAGUAGGUUGUAUAGUU   CUGUACAGCCUCCUAGCUUUCC
MI0000065      AGAGGUAGUAGGUUGCAUAGUU   CUAUACGACCUGCUGCCUUUC
MI0003603      Multibranch - No prediction
MI0000070      UAGCAGCACGUAAAUAUUGGCG   CCAGUAUUAACUGUGCUGCUGA
MI0003681      UGGAGAAGCGUGGACCGGUCC    CAGGUUCUCACCCUCUCUAGG
MI0000071      CAAAGUGCUUACAGUGCAGGUAG  ACUGCAGUGAAGGCACUUGUAG
```

MiRduplexSVM: miRNA Evaluator - Missing duplex finder.

This tool evaluates a mature miRNA using MiRduplexSVM's score and predicts the mature molecule located on the opposite strand. It has two modes of operation.

You can either upload two text files (.txt) with your sequences in fasta format, including the fasta file header. One file should contain the miRNA precursor sequences; the other should contain the respective mature miRNA sequences. Alternatively, you can paste your sequences in fasta format (include fasta file header) in the appropriate text boxes in the online form.

The output is a four-column tab-delimited table. The first column specifies the sequences' IDs as provided by the user. The second and third columns show the matures from the 5' and 3' strands of the hairpin. One mature corresponds to the one 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 for the respective line.

If you wish to receive your results via email, you can provide your email address. Thank you for using *MiRduplexSVM: Evaluator – Missing duplex finder*.

Input Example - precursors sequences:
```
>MI0000064
GCAUCCGGGUUGAGGUAGUAGGUUGUAUGGUUUAGAGUUACACCCUGGGAGUUAACUGUACAACCUUCUAGCUUUCCUUGGA
GC
>MI0000238
GUGAAUUAGGUAGUUUCAUGUUGUUGGGCCUGGGUUUCUGAACACAACAACAUUAAACCACCCGAUUCAC
>MI0003603
UCUUAUCAAUGAGGUAGACCAUGGGUUCUCAUUGUAAUAGUGUAGAAUGUUGGUUAACUGUGGACUCCCUGGCUCUGUCUCA
AAUCUACUGAUUC
>MI0000240
UCAUUGGUCCAGAGGGGAGAUAGGUUCCUGUGAUUUUUCCUUCUUCUCUAUAGAAUAAAUGA
>MI0003681
GUGUAGUAGAGCUAGGAGGAGAGGGUCCUGGAGAAGCGUGGACCGGUCCGGGUGGGUUCCGGCAGGUUCUCACCCUCUCUAG
GCCCCAUUCUCCUCUG
>MI0000265
AGAUUAGAGUGGCUGUGGUCUAGUGCUGUGUGGAAGACUAGUGAUUUUGUUGUUCUGAUGUACUACGACAACAAGUCACAGC
CGGCCUCAUAGCGCAGACUCCCUUCGAC
>MI0000291
```

```
AUCAUUCAGAAAUGGUAUACAGGAAAAUGACCUAUGAAUUGACAGACAAUAUAGCUGAGUUUGUCUGUCAUUUCUUUAGGCC
AAUAUUCUGUAUGACUGUGCUACUUCAA
```

Input Example - mature sequences:
```
>MI0000064
UGAGGUAGUAGGUUGUAUGGUU
>MI0000238
UAGGUAGUUUCAUGUUGUUGGG
>MI0003603
AGACCAUGGGUUCUCAUUGU
>MI0000240
GGUCCAGAGGGGAGAUAGGUUC
>MI0003681
GGCAGGUUCUCACCCUCUCUAGG
>MI0000265
UGGAAGACUAGUGAUUUUGUUGU
>MI0000291
AUGACCUAUGAAUUGACAGAC
```

Output example:
```
equenceID      5strandMature              3strandMature
MI0000064      UGAGGUAGUAGGUUGUAUGGUU      CUGUACAACCUUCUAGCUUUCC
MI0000238      UAGGUAGUUUCAUGUUGUUGGG      CAACAACAUUAAACCACCCGAU
MI0003603      Multibranch - No prediction
MI0000240      GGUCCAGAGGGGAGAUAGGUUC      UCCUUCUUCUCUAUAGAAUAAA
MI0003681      UGGAGAAGCGUGGACCGGUCCG      GGCAGGUUCUCACCCUCUCUAGG
MI0000265      UGGAAGACUAGUGAUUUUGUUGU     CAACAAGUCACAGCCGGCCUCA
MI0000291      AUGACCUAUGAAUUGACAGAC       UCUGUCAUUUCUUUAGGCCAAU
```

MiRduplexSVM – miRNA:miRNA* Duplex Evaluator.

This tool evaluates a miRNA:miRNA* duplex by assigning MiRduplexSVM's score. It has two modes of operation.

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

The output is a four-column tab-delimited table. The first column specifies the sequences' IDs as provided by the user. The second and third columns show the matures from the 5' and 3' strands of the hairpin, and 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 for the respective line.

If you wish to receive your results via email, you can provide your email address. Thank you for using **MiRduplexSVM – miRNA:miRNA* Duplex Evaluator**.

Input Example - precursors sequences:

```
>MI0000063
CGGGGUGAGGUAGUAGGUUGUGUGGUUUCAGGGCAGUGAUGUUGCCCCUCGGAAGAUAACUAUACAACCUACUGCCUUCCCU
G
>MI0000286
ACCCGGCAGUGCCUCCAGGCGCAGGGCAGCCCCUGCCCACCGCACACUGCGCUGCCCCAGACCCACUGUGCGUGUGACAGCG
GCUGAUCUGUGCCUGGGCAGCGCGACCC
>MI0000447
UGAGCUGUUGGAUUCGGGGCCGUAGCACUGUCUGAGAGGUUUACAUUUCUCACAGUGAACCGGUCUCUUUUUCAGCUGCUUC
>MI0000450
ACAAUGCUUUGCUAGAGCUGGUAAAAUGGAACCAAAUCGCCUCUUCAAUGGAUUUGGUCCCCUUCAACCAGCUGUAGCUAUG
CAUUGA
>MI0000451
GGGAGCCAAAUGCUUUGCUAGAGCUGGUAAAAUGGAACCAAAUCGACUGUCCAAUGGAUUUGGUCCCCUUCAACCAGCUGUA
GCUGUGCAUUGAUGGCGCCG
>MI0000474
CAGGGUGUGUGACUGGUUGACCAGAGGGGCAUGCACUGUGUUCACCCUGUGGGCCACCUAGUCACCAACCCUC
```

Input Example - mature sequences from 3' strand:

```
>MI0000063
CUAUACAACCUACUGCCUUCCC
>MI0000286
CUGUGCGUGUGACAGCGGCUGA
>MI0000447
UCACAGUGAACCGGUCUCUUU
>MI0000450
UUUGGUCCCCUUCAACCAGCUG
>MI0000451
UUUGGUCCCCUUCAACCAGCUG
>MI0000474
CCUGUGGGCCACCUAGUCACCAA
```

Input Example - mature sequences from 5' strand:

```
>MI0000063
UGAGGUAGUAGGUUGUGUGGUU
>MI0000286
AGCCCCUGCCCACCGCACACUG
>MI0000447
CGGGGCCGUAGCACUGUCUGAGA
>MI0000450
AGCUGGUAAAAUGGAACCAAAU
>MI0000451
AGCUGGUAAAAUGGAACCAAAU
>MI0000474
UGUGACUGGUUGACCAGAGGGG
```

Output example:

sequenceID	5strandMature	3strandMature	MiRduplexSVM-score
MI0000063	UGAGGUAGUAGGUUGUGUGGUU	CUAUACAACCUACUGCCUUCCC	9.780586e-01
MI0000286	AGCCCCUGCCCACCGCACACUG	CUGUGCGUGUGACAGCGGCUGA	1.175949e+00
MI0000447	CGGGGCCGUAGCACUGUCUGAGA	UCACAGUGAACCGGUCUCUUU	1.003558e+00
MI0000450	AGCUGGUAAAAUGGAACCAAAU	UUUGGUCCCCUUCAACCAGCUG	1.380121e+00
MI0000451	AGCUGGUAAAAUGGAACCAAAU	UUUGGUCCCCUUCAACCAGCUG	1.121841e+00
MI0000474	UGUGACUGGUUGACCAGAGGGG	CCUGUGGGCCACCUAGUCACCAA	-6.557550e-02