

iRecSpot-EF: Effective Sequence Based Features for Recombination Hotspot Prediction

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1 Supplementary Information (Sp3): How does our web service work?

1.1 Step #1:

Access the service by clicking the link at <http://irecspot.pythonanywhere.com/>. We will see the home-page.

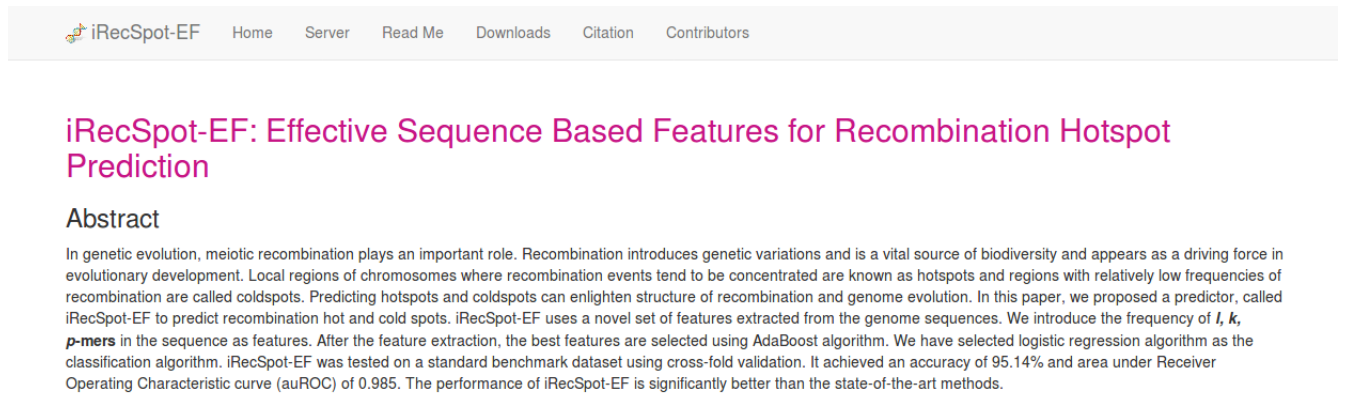



Figure 1: Home Page

1.2 Step #2:

Click on the 'Server' button on the top menu or go to this link <http://irecspot.pythonanywhere.com/server>. We will see the server page.

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 **iRecSpot-EF**
Effective Sequence Based Features for Recombination Hotspot Prediction

Enter the query sequences in **FASTA** format :

Recommended browser : Google Chrome or Mozilla Firefox

Enter Step Size:
(Recommended step size >= 200)


Figure 2: Server Page


1.3 Step #3:

Once in the server page, either type or copy and paste the query DNA sequence into the input box. The input sequence should be in the FASTA format. A sequence in FASTA format consists of a single initial line beginning with the symbol ‘>’ in the first column, followed by lines of sequence data in which nucleotides are represented using single-letter codes. Except for the mandatory symbol ‘>’, all the other characters in the single initial line are optional and only used for the purpose of identification and description. The sequence ends if another line starting with the symbol ‘>’ appears; this indicates the start of another sequence. Example sequences in FASTA format can be seen by clicking on the Example button right above the input box.

1.4 Step #4:

Users are able to set the step size which denotes length of the sub-sequences of interest. The predictor predicts the type (hotspot, coldspot or none) for each sub-sequence according to the selected step size. Example: if sequence length is 519 and step size is 200, then the model will predict the types of three sub-sequences. First one ranging from position 1 to 200 of the input sequence, the second one from position 201 to 400 and the third one from 401 to 519.


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iRecSpot-EF

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Enter the query sequences in **FASTA** format :

```

>YDL087C 1.67
ATGTCAACTATGTCAACGCCTGCCGCGAGAACAACGCAAACTCGTGAACAGCTGATGGGCAGGAC
TTCAGTTTCCGCCACAACAGGTATTGCGATCAAAAAGAGACCTCGGACTACACGATCCAAGATC
TGCAAGTCATACCTTGTGGCGAGTGCCCTACGACCTGTTTCAGGGCACCAAGAGCCTGGGA
AAATGCCCGCAGATGCATCTTACCAAGCATAAAATTCAGTACGAGAGAGGGTCAAGCAGGGCAAA
ACGTTTCCCGAATTCGAAAGAGAATATCTGGCCATTCTATCTCGGTTGTTAATGAGTGAATGGC
CAGATATCCGTAGCACTACAAAATCTAAAACACACCCGCTGAGAACGAATGAAGATTCAGCAGGTT
ACCGAAGAAGTATAGTGTCTTGGACGTGCGGATAGGCCAATGGGACAAGAGATTGATTCTTTAATT
CGTGCAGATGAAGTCAGTATGGGTATGCTACAGCAGTCAAATTACAAGAACTGATTAGTAAAAGG
AAAGAAGTTGCAAAACGTGTACGAACATACAGAAAACGTGGGCCAGAGCGCCAGCAAAAGTTA

```

Recommended browser : Google Chrome or Mozilla Firefox

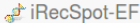
Enter Step Size:
(Recommended step size >= 200)

Submit
Reset
Example

Figure 3: Enter FASTA and step size

1.5 Step #5:

Click on the ‘Submit’ button for predictions. Please wait, the system will take some time to generate results.


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Results

FASTA: >YDL087C 1.67 Result Visualization			
Position	Predicted Type	Probability	Sequence Details
1 1 - 200	hotspot	0.957988204916	Sequence Details
2 201 - 400	None	0.525209029969	Sequence Details
3 401 - 600	hotspot	0.896245125194	Sequence Details
4 601 - 773	None	0.664904784768	Sequence Details

FASTA: >YDR163W 0.82 Result Visualization			
Position	Predicted Type	Probability	Sequence Details
1 1 - 200	coldspot	0.772002728263	Sequence Details
2 201 - 400	None	0.672076476888	Sequence Details
3 401 - 519	None	0.592098291188	Sequence Details

Figure 4.1: Predictions for respective sub-sequences

Note that each of the predictions is accompanied by the corresponding probability for the predicted class which can be interpreted as prediction-confidence.

1.5.1 Step #5.1:

Click 'Result visualization' to see the sequence details.

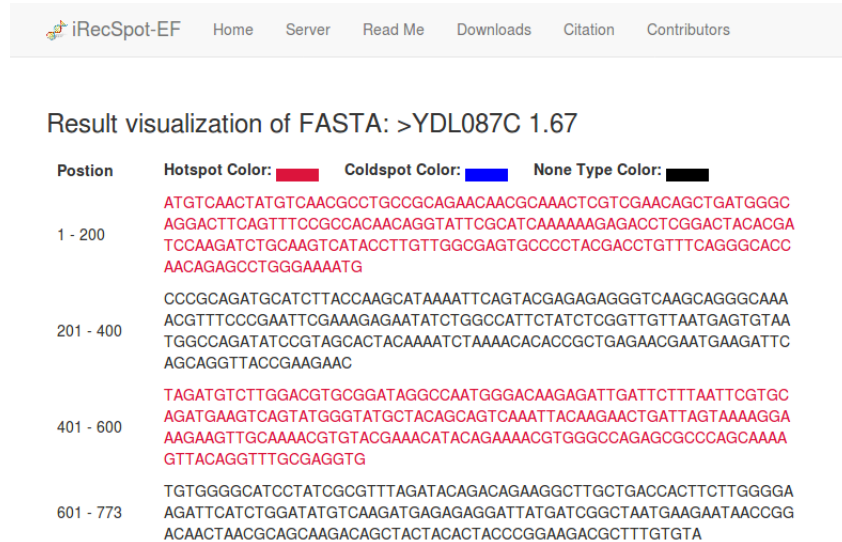


Figure 4.2: Results visualization