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

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Supporting Information (#1):

Details description of (l, k, p)-mers Composition:

Here, \boldsymbol{l} represents length of sequence, \boldsymbol{k} represents k-gap / total number of gap in a sequence, and \boldsymbol{p} represents positions of gap or where gap occurs. Gap represents don't care or any element of X. Nucleotides, $X = \{A, C, G, T\}$

Table 1: Description of $(\boldsymbol{l},\,\boldsymbol{k},\,\boldsymbol{p})$ -mers

Feature Structure	Values of (l, k, p) -mers
XX	l=2, k=0, p=None (because k is zero)
X _ X	l=3, k=1, p=2
X X	l=4, k=2, p=2, 3
X X	l=5, k=3, p=2, 3, 4
X X	l=6, k=4, p=2, 3, 4, 5
X X	l=7, k=5, p=2, 3, 4, 5, 6
XX _ X	l=4, k=1, p=3
XX X	l=5, k=2, p=3, 4
XX X	l=6, k=3, p=3, 4, 5
XX X	l=7, k=4, p=3, 4, 5, 6
XX X	l=8, k=5, p=3, 4, 5, 6, 7
XX X	l=9, k=6, p=3, 4, 5, 6, 7, 8
X _ XX	l=4, k=1, p=2
X XX	l=5, k=2, p=2, 3
X XX	l=6, k=3, p=2, 3, 4
X XX	l=7, k=4, p=2, 3, 4, 5
X XX	l=8, k=5, p=2, 3, 4, 5, 6
XX ₋ XX	l=5, k=1, p=3
XX XX	l=6, k=2, p=3, 4
XX XX	l=7, k=3, p=3, 4, 5
XX XX	l=8, k=4, p=3, 4, 5, 6
XX XX	l=9, k=5, p=3, 4, 5, 6, 7
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Table 1 Continued from previous page

Feature Structure	Values of (l, k, p) -mers
X _ XXX	l=5, k=1, p=2
X _ XXX	l=6, k=2, p=2, 3
X XXX	l=7, k=3, p=2, 3, 4
X XXX	l=8, k=4, p=2, 3, 4, 5
X XXX	l=9, k=5, p=2, 3, 4, 5, 6
XXX _ X	l=5, k=1, p=4
XXX X	l=6, k=2, p=4, 5
XXX X	l=7, k=3, p=4, 5, 6
XXX X	l=8, k=4, p=4, 5, 6, 7
XXX X	l=9, k=5, p=4, 5, 6, 7, 8
XXX _ XX	l=6, k=1, p=4
XXX XX	l=7, k=2, p=4, 5
XXX XX	l=8, k=3, p=4, 5, 6
XXX XX	l=9, k=4, p=4, 5, 6, 7
XXX XX	l=10, k=5, p=4, 5, 6, 7, 8
XX _ XXX	l=6, k=1, p=3
XX XXX	l=7, k=2, p=3, 4
XX XXX	l=8, k=3, p=3, 4, 5
XX XXX	l=9, k=4, p=3, 4, 5, 6
XX XXX	l=10, k=5, p=3, 4, 5, 6, 7

Table 1 shows, feature structure, and values of $(\boldsymbol{l},\,\boldsymbol{k},\,\boldsymbol{p})$ -mers.