Naive RNA Splicing Checker

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We first determine that whether $\mathbb{S}(x) = \emptyset$ for a given string x.

```
Procedure NaiveMatchFinder(X, start, end)
Input: A string X of length n, start and end for search range on X
Output: Y/N
x = x_1...x_{start}...x_{end}...x_n
/* Finding corresponding match string(\theta(u)) to the factor string(u)
                                                                                        */
/* P1 indicates subset of factor string end points on X
/* S2,M2, and P2 each indicate matched string, subset of matched strings
    and subset of matched string start points on \boldsymbol{X}
for i \leftarrow start \ to \ end/2 \ do
    /* start point of factor string
    for j \leftarrow start \ to \ end/2 \ do
       /* end point of factor string
       for k \leftarrow end to start do
          /* length of string X.
                                                                                        */
          t = i
          p = 0
          while l \neq j do
              if x_k = \theta(x_t) then
                  S2[p] = X_k
                                                            // save matched character
                  if p=0 then
                                          // save match start(backward-end) point
                   P2 \leftarrow k
                  t++
                 p++
              if X[n] \neq \theta(X[T]) then
                  p=0
               ∟ break
          M2 \leftarrow S2
                                                               // save matched string
          P1 \leftarrow j
                                                             // save factor end point
return M2,P1,P2
```



Figure 1: NaiveMatchFinder

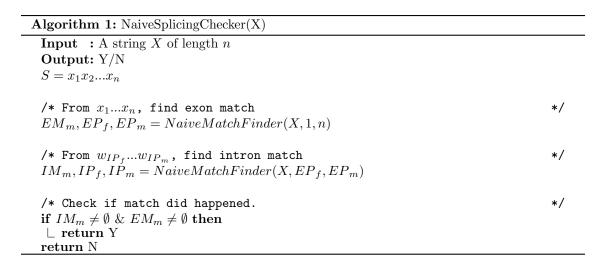
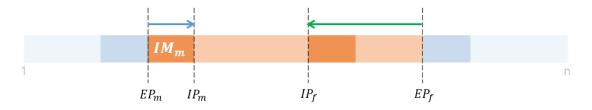




Figure 2: NaiveMatchFinder for exon match



 $Figure \ 3: \ Naive Match Finder \ for \ intron \ match$

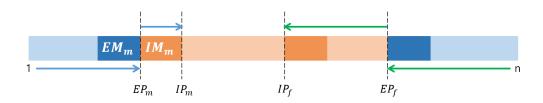


Figure 4: FullNaiveSplicingChecker(X)