

```
Assuming that  $p_1$  is smaller than  $p_2$ 
if both  $s_1$  and  $s_2$  can be aligned in the reference genome
  for each match position  $p_1$  of  $s_1$ 
    for each match position  $p_2$  of  $s_2$ 
      if the  $|p_2 - p_1 - D| \leq 3d$ 
        output the pair and break
else if no match is found
  if  $s_1$  has matches
    for each match position  $p_1$  of  $s_1$ 
      conduct SW( $s_2$ ,  $ref$ ) using reference segment of position  $p_1 + D - d$ 
      if the alignment score  $\leq$  threshold
        output the pair and break
else if no match is found
  if  $s_2$  has matches
    for each match position  $p_2$  of  $s_2$ 
      conduct SW( $s_1$ ,  $ref$ ) using ref segment of position  $p_2 - D - d$ 
      if the alignment score  $\leq$  threshold
        output the pair and break
```