Correction to: Machine learning techniques for pathogenicity prediction of non-synonymous single nucleotide polymorphisms in human body

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In the original article the below Pseudocode 1 has been missed to be added and was unfortunately processed as ESM.

```
Input: number of generations(no_Gen), max number of attributes (max_Att_No), set of attributes that annotate each variant (Att_list), user defined accuracy (Threshold_Acc).  
For (j= 1: no_Gen)  
  ○ Select a random initial set of (n) distinct attributes  
  ○ Compute the classification accuracy of the initially selected attributes where each attribute represents a seti  
  For each set (i = 1: n)  
    While selected number of attributes not exceeded (max_Att_No) and accuracy can still be increased (<100%)  
      ○ Compute the fitness value of each attribute which can be selected from (Att_list)  
      ○ Select the candidate attribute for the set(i)  
      ○ Compute the accuracy of the set(i) after adding the new attribute  
      ○ If the computed accuracy is less than or equal the previous accuracy  
        Then discard this attribute and choose successive attribute with next fitness value  
    End while  
    Final set of attributes is obtained for the current set(i)  
  End for  
  ○ Find the attribute subsets that achieved the best accuracy in the current generation for various sets  
  ○ Upgrade the values of attributes that are part of the best set to increase the opportunity of their selection in next generations  
End for  
Obtain the global best sets of attributes from all different sets which achieved best possible accuracy in all generations.  
If the achieved accuracy < (Threshold_Acc)  
Then repeat all the process once after update (Att_list) to include the set of the tool's prediction scores then quit.
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Pseudocode 1 The different steps of attribute selection process based on MLT classification accuracy.

The original article can be found online at <https://doi.org/10.1007/s12652-021-03581-3>.

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