**Supplementary File-7: Pseudo codes of the algorithms for the computation of best ShAP score for 824 genes and 28 genomic features at a sample level**

Table-2: (A) Pseudo-codes of algorithm A for estimating the best ShAP score of 824 genes and (B) Algorithm B for estimating the best ShAP score of 28 genomic features at a sample level. Here, both algorithms (Algorithms A and B) process one sample at a time and require the sample feature matrix as input. Thus, the output obtained from algorithms A and B have the best ShAP score of 824 genes and 28 genomic features, respectively at a sample level.

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| **Algorithm A:** Estimate the Best ShAP Score (BSS) for each gene at a sample level | **Algorithm B:** Estimate the Best ShAP Score (BSS) for each genomic feature (GF) at a sample level |
| 1. Fivefold classifiers := [List of five classifiers trained on each fold of test dataset] 2. CPC := [List of correct prediction classifiers i.e. classifiers that correctly predicted the sample’s class] 3. SFM := Sample feature matrix 4. Genes := [List of 824 genes] 5. := [List of genomic features having positive   ShAP score for a gene “g” and classifier “c”]   1. := [List of genomic features having negative ShAP score for a gene “g” and classifier “c”] 2. := Best ShAP score of gene “g” and classifier “c” 3. := [List of best ShAP scores of gene “g” for all the classifiers that correctly predicted the sample] 4. := Best ShAP score of gene “g” among all classifiers. 5. := List of the best ShAP score of all the genes among all the classifiers 6. **function** BSS gene (SFM) 7. **for** classifier in (Fivefold classifiers) **do** 8. Predict the sample’s class with the help of classifier. 9. **if** classifier predict the sample class correctly **then**    * + 1. Append classifier in CPC list.        2. Apply ShAP algorithm on the classifier.        3. Collect the ShAP score for all 824 genes on their respective 28 GF for that classifier. 10. **for** gene in Genes **do** 11. **for** classifier in CPC **do** 12. Collect features having positive ShAP score. 13. Collect features having negative ShAP score 14. **If**  **then** 16. **else**   14. **Output**: | 1. Fivefold classifiers := [List of five classifiers trained on each fold of test dataset] 2. CPC := [List of correct prediction classifiers i.e. classifiers that correctly predicted the sample’s class] 3. SFM := Sample feature matrix 4. Genomic Features := [List of 28 GFs] 5. := [List of genes having positive ShAP score for a genomic feature and classifier] 6. := [List of genes having negative ShAP score for a genomic feature and classifier] 7. := Best ShAP score of GF “gf” and classifier “c” 8. := [List of best ShAP scores of gene “gf” for all the classifiers that correctly predicted the sample] 9. := Best ShAP score of GF “gf” among all classifiers. 10. := List of the best ShAP score of all GF among all classifiers 11. **function** BSS genomic feature (SFM) 12. **for** classifier in (Fivefold classifiers) **do** 13. Predict the sample’s class with the help of classifier. 14. **if** classifier predict the sample class correctly **then** 15. Append classifier in CPC list. 16. Apply ShAP algorithm on the classifier. 17. Collect the ShAP score for all 824 genes on their respective 28 GF for that classifier. 18. **for** feature in Genomic features **do** 19. **for** classifier in CPC **do** 20. Collect genes having positive ShAP score. 21. Collect genes having negative ShAP score 22. **if** **then** 24. **else**   14. **Output**: |