Result of Leave-One-Out cross validation

In[•]:=
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BuildModel[]
```

Building functions with Symbolic regression

◆ BuildModel version 2.6.4 made on July 12th, 2020

Phase 1 Reading in data

Starting time: date 2020.7.13 time 20.49.33

Patient data name: ardata7, its dimensions: {51, 212}

Phase 2 Data Definition

The origianl colum labels:

```
{{1, RMale}, {2, Rage}, {3, InfectionCount}, {4, FeverOnly},
 {5, Pyrexia}, {6, Inflammation}, {7, VirusInfection}, {8, CMV}, {9, anemia},
 {10, HeartDisease}, {11, RespiratoryInfection}, {12, UpperRespiratoryInfection},
 {13, UpperDigestivetract}, {14, Diarrhea}, {15, UTI}, {16, WBCinUrine},
 {17, WBCpeakover10}, {18, urology}, {19, Skin}, {20, WoundInfection},
 {21, HerpesZoster}, {22, Orthopedics}, {23, Ascites}, {24, Surgery},
 {25, AerobicGPC}, {26, AerobicGNR}, {27, candida}, {28, staphylococcusaureus},
 {29, streptococcusaureus}, {30, enterobacteraerogenes}, {31, enterobactereclacue},
 {32, enterococcusfaecalis}, {33, citobacterdiversus}, {34, pseudomonas},
 {35, inflammationdatefirst}, {36, infectiondatelast}, {37, asthma},
 {38, pastanemia}, {39, infarctionhemohorrage}, {40, calcification},
 {41, digestiveorgan}, {42, appendicitis}, {43, polyp}, {44, ulcer}, {45, GERD},
 {46, pastheart}, {47, kidney}, {48, pastliverbilialy}, {49, HBV}, {50, HCV},
 {51, stone}, {52, hypothyroidism}, {53, gynecology}, {54, ocular}, {55, allergy},
 {56, hypertention}, {57, type2DM}, {58, BTF}, {59, timeoftransplantation},
 {60, Regraft}, {61, ABOI}, {62, HLAABmm}, {63, HLADRmm}, {64, HLAmm},
 {65, PRAclass1pre}, {66, PRAclass2pre}, {67, PRAclass1after}, {68, PRAclass2after},
 {69, MFImax}, {70, twinpeak}, {71, DSAclass1}, {72, DSAclass1number}, {73, DSAclass2},
 {74, DSAclass2number}, {75, preDSA}, {76, denovoDSA}, {77, antiHLAclass1},
 {78, HSAclass1number}, {79, antiHLAclass2}, {80, HSAclass2number},
 {81, DSAandHSAclass2}, {82, DSAandHSAclass1}, {83, DSAandHLAclass2pre},
 {84, DSAandHLAclass1pre}, {85, A23}, {86, A25}, {87, A26}, {88, A32}, {89, A34},
 {90, A66}, {91, B13}, {92, B18}, {93, B27}, {94, B35}, {95, B37}, {96, B38},
 {97, B42}, {98, B44}, {99, B45}, {100, B47}, {101, B49}, {102, B50}, {103, B51},
 {104, B52}, {105, B53}, {106, B54}, {107, B55}, {108, B56}, {109, B57}, {110, B58},
 {111, B59}, {112, B61}, {113, B62}, {114, B63}, {115, B7}, {116, B71}, {117, B73},
 {118, B75}, {119, B77}, {120, B78}, {121, B8}, {122, B82}, {123, Cw17}, {124, Cw6},
 {125, Cw9}, {126, DP10}, {127, DP11}, {128, DP13}, {129, DP14}, {130, DP15},
 {131, DP17}, {132, DP18}, {133, DP19}, {134, DP20}, {135, DP3}, {136, DP4},
 {137, DP5}, {138, DP6}, {139, DP9}, {140, DQ11}, {141, DQ2}, {142, DQ4}, {143, DQ5},
 {144, DQ6}, {145, DQ7}, {146, DQ8}, {147, DQ9}, {148, DR1}, {149, DR10}, {150, DR103},
 {151, DR11}, {152, DR12}, {153, DR13}, {154, DR14}, {155, DR15}, {156, DR16},
 {157, DR17}, {158, DR18}, {159, DR4}, {160, DR51}, {161, DR52}, {162, DR53},
 {163, DR7}, {164, DR8}, {165, DR9}, {166, pregnancyhistory}, {167, birthhistory},
 {168, NaturalAbortion}, {169, ArtificialAbortion}, {170, HDperiod}, {171, CGN},
 {172, IgA}, {173, NS}, {174, hypoplastickidney}, {175, MalignantHypertention},
 {176, Banfi}, {177, Banf t }, {178, Banf g }, {179, Banf v }, {180, Banfci},
 {181, Banfct}, {182, Banfcv}, {183, Banfcg}, {184, Banfptc}, {185, Banfptcbm},
 {186, Banfah}, {187, Banfaah}, {188, InterstitialHemorrhage}, {189, CellInvasion},
 {190, lymphinvasion}, {191, thrombusformation}, {192, coaglationnecrosis},
 {193, IgA}, {194, IgM}, {195, IgG}, {196, SABC1q}, {197, C3}, {198, C4d}, {199, C5b},
 {200, bulbarsclerosis}, {201, CRPpreRej}, {202, CRPpostRej}, {203, WBCpeakover5},
 {204, MaxCRP}, {205, WBCpreRej}, {206, WBCpostKTx}, {207, WBCpeakover9postRej},
 {208, MaxWBC}, {209, MMFpostRej}, {210, MMFatRej}, {211, CNIpostRej}, {212, GraftLoss}}
```

◆ **allNames (The last variable GraftLoss is a target response)**

```
{RMale, Rage, InfectionCount, FeverOnly, Pyrexia, Inflammation, VirusInfection,
 CMV, anemia, HeartDisease, RespiratoryInfection, UpperRespiratoryInfection,
 UpperDigestivetract, Diarrhea, UTI, WBCinUrine, WBCpeakover10, urology, Skin,
 WoundInfection, HerpesZoster, Orthopedics, Ascites, Surgery, AerobicGPC, AerobicGNR,
 candida, staphylococcusaureus, streptococcusaureus, enterobacteraerogenes,
 enterobactereclacue, enterococcusfaecalis, citobacterdiversus, pseudomonas,
 inflammationdatefirst, infectiondatelast, asthma, pastanemia, infarctionhemohorrage,
 calcification, digestiveorgan, appendicitis, polyp, ulcer, GERD, pastheart,
 kidney, pastliverbilialy, HBV, HCV, stone, hypothyroidism, gynecology, ocular,
 allergy, hypertention, type2DM, BTF, timeoftransplantation, Regraft, ABOI, HLAABmm,
 HLADRmm, HLAmm, PRAclass1pre, PRAclass2pre, PRAclass1after, PRAclass2after,
 MFImax, twinpeak, DSAclass1, DSAclass1number, DSAclass2, DSAclass2number, preDSA,
 denovoDSA, antiHLAclass1, HSAclass1number, antiHLAclass2, HSAclass2number,
 DSAandHSAclass2, DSAandHSAclass1, DSAandHLAclass2pre, DSAandHLAclass1pre, A23,
 A25, A26, A32, A34, A66, B13, B18, B27, B35, B37, B38, B42, B44, B45, B47, B49,
 B50, B51, B52, B53, B54, B55, B56, B57, B58, B59, B61, B62, B63, B7, B71, B73, B75,
 B77, B78, B8, B82, Cw17, Cw6, Cw9, DP10, DP11, DP13, DP14, DP15, DP17, DP18, DP19,
 DP20, DP3, DP4, DP5, DP6, DP9, DQ11, DQ2, DQ4, DQ5, DQ6, DQ7, DQ8, DQ9, DR1, DR10,
 DR103, DR11, DR12, DR13, DR14, DR15, DR16, DR17, DR18, DR4, DR51, DR52, DR53, DR7,
 DR8, DR9, pregnancyhistory, birthhistory, NaturalAbortion, ArtificialAbortion,
 HDperiod, CGN, IgA, NS, hypoplastickidney, MalignantHypertention, Banfi, Banf t ,
 Banf g , Banf v , Banfci, Banfct, Banfcv, Banfcg, Banfptc, Banfptcbm, Banfah,
 Banfaah, InterstitialHemorrhage, CellInvasion, lymphinvasion, thrombusformation,
 coaglationnecrosis, IgA, IgM, IgG, SABC1q, C3, C4d, C5b, bulbarsclerosis,
 CRPpreRej, CRPpostRej, WBCpeakover5, MaxCRP, WBCpreRej, WBCpostKTx,
 WBCpeakover9postRej, MaxWBC, MMFpostRej, MMFatRej, CNIpostRej, GraftLoss}
```

- **allTrainingData (The last column is a response variable, the others are explanatory variables)**

```
{{0, 37, 4, 1, 1, 1, 1, 1, 0, 0, 0, 0, 0, 1, 0, 6.052, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
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 0, 1, 1, 0, 0, 1, 0, 0, 1, 1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 1, 1, 1, 1, 0, 0, 1, 1, 1, 0, 0,
 1, 1, 0, 1, 0, 1, 1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 2, 0, 0, 0, 0.353183,
 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0,
 0, 1.406, 0.1668, 1, 10.53, 1.969, 6.078, 4, 25.38, 2.54667, 0.56, 0.115666, 0}}
```

(The above output is suppressed below 100 lines.)

Phase 3 Interpolation of Empty Cells

◆ Data Completeness Check

◇ **Non-numeric cells were replaced with median values of the row.**

◆ 1. New Data Completeness Check

■ N of columns = 51, n of rows = 212

■ Selected variables (the last one is the response varialbe:

```
{{1, RMale}, {2, Rage}, {3, InfectionCount}, {4, FeverOnly}, {5,
   Pyrexia}, {6, Inflammation}, {7, VirusInfection}, {8, CMV}, {9,
   anemia}, {10, HeartDisease}, {11, RespiratoryInfection}, {12,
   UpperRespiratoryInfection}, {13, UpperDigestivetract}, {14,
   Diarrhea}, {15, UTI}, {16, WBCinUrine}, {17, WBCpeakover10}, {18,
   urology}, {19, Skin}, {20, WoundInfection}, {21,
   HerpesZoster}, {22, Orthopedics}, {23, Ascites}, {24,
   Surgery}, {25, AerobicGPC}, {26, AerobicGNR}, {27, candida}, {28,
   staphylococcusaureus}, {29, streptococcusaureus}, {30,
   enterobacteraerogenes}, {31, enterobactereclacue}, {32,
   enterococcusfaecalis}, {33, citobacterdiversus}, {34,
   pseudomonas}, {35, inflammationdatefirst}, {36,
   infectiondatelast}, {37, asthma}, {38, pastanemia}, {39,
   infarctionhemohorrage}, {40, calcification}, {41,
   digestiveorgan}, {42, appendicitis}, {43, polyp}, {44, ulcer}, {45,
   GERD}, {46, pastheart}, {47, kidney}, {48, pastliverbilialy}, {49,
   HBV}, {50, HCV}, {51, stone}, {52, hypothyroidism}, {53,
   gynecology}, {54, ocular}, {55, allergy}, {56, hypertention}, {57,
   type2DM}, {58, BTF}, {59, timeoftransplantation}, {60,
   Regraft}, {61, ABOI}, {62, HLAABmm}, {63, HLADRmm}, {64,
   HLAmm}, {65, PRAclass1pre}, {66, PRAclass2pre}, {67,
   PRAclass1after}, {68, PRAclass2after}, {69, MFImax}, {70,
   twinpeak}, {71, DSAclass1}, {72, DSAclass1number}, {73,
   DSAclass2}, {74, DSAclass2number}, {75, preDSA}, {76,
   denovoDSA}, {77, antiHLAclass1}, {78, HSAclass1number}, {79,
   antiHLAclass2}, {80, HSAclass2number}, {81, DSAandHSAclass2}, {82,
```

```
DSAandHSAclass1}, {83, DSAandHLAclass2pre}, {84,
DSAandHLAclass1pre}, {85, A23}, {86, A25}, {87, A26}, {88,
A32}, {89, A34}, {90, A66}, {91, B13}, {92, B18}, {93, B27}, {94,
B35}, {95, B37}, {96, B38}, {97, B42}, {98, B44}, {99, B45}, {100,
B47}, {101, B49}, {102, B50}, {103, B51}, {104, B52}, {105,
B53}, {106, B54}, {107, B55}, {108, B56}, {109, B57}, {110,
B58}, {111, B59}, {112, B61}, {113, B62}, {114, B63}, {115,
B7}, {116, B71}, {117, B73}, {118, B75}, {119, B77}, {120,
B78}, {121, B8}, {122, B82}, {123, Cw17}, {124, Cw6}, {125,
Cw9}, {126, DP10}, {127, DP11}, {128, DP13}, {129, DP14}, {130,
DP15}, {131, DP17}, {132, DP18}, {133, DP19}, {134, DP20}, {135,
DP3}, {136, DP4}, {137, DP5}, {138, DP6}, {139, DP9}, {140,
DQ11}, {141, DQ2}, {142, DQ4}, {143, DQ5}, {144, DQ6}, {145,
DQ7}, {146, DQ8}, {147, DQ9}, {148, DR1}, {149, DR10}, {150,
DR103}, {151, DR11}, {152, DR12}, {153, DR13}, {154, DR14}, {155,
DR15}, {156, DR16}, {157, DR17}, {158, DR18}, {159, DR4}, {160,
DR51}, {161, DR52}, {162, DR53}, {163, DR7}, {164, DR8}, {165,
DR9}, {166, pregnancyhistory}, {167, birthhistory}, {168,
NaturalAbortion}, {169, ArtificialAbortion}, {170,
HDperiod}, {171, CGN}, {172, IgA}, {173, NS}, {174,
hypoplastickidney}, {175, MalignantHypertention}, {176,
Banfi}, {177, Banft}, {178, Banfg}, {179, Banfv}, {180,
Banfci}, {181, Banfct}, {182, Banfcv}, {183, Banfcg}, {184,
Banfptc}, {185, Banfptcbm}, {186, Banfah}, {187, Banfaah}, {188,
InterstitialHemorrhage}, {189, CellInvasion}, {190,
lymphinvasion}, {191, thrombusformation}, {192,
coaglationnecrosis}, {193, IgA}, {194, IgM}, {195,
IgG}, {196, SABC1q}, {197, C3}, {198, C4d}, {199, C5b}, {200,
bulbarsclerosis}, {201, CRPpreRej}, {202, CRPpostRej}, {203,
WBCpeakover5}, {204, MaxCRP}, {205, WBCpreRej}, {206,
WBCpostKTx}, {207, WBCpeakover9postRej}, {208, MaxWBC}, {209,
MMFpostRej}, {210, MMFatRej}, {211, CNIpostRej}, {212, GraftLoss}}
```

Phase 4 Validation Method

◆ **Selection of Validation Method**

◇ Validataion method: Leave-One-Out
Cross Validation method was selected.

Phase 12 Leave-One-Out cross validation

■ The LEAVE-ONE-OUT Cross-Validation method was chosen.

◇ This method is the same as K-fold
cross-validation when the K is equal to the sample size.
The number of test data is one, and the
rest is used as the training data.
Then the validation is repeated K times.
The accuracy is figured out with the K results.

■ Preliminary Analysis: Correlation Coefficient
between Explanatory Vairables and Target Variable

◆ 1. Correlation Chart of Data in the original order
(BLUE: Positive correlation, RED: Negative correlation)

◆ **2. Correlation Chart of**

Data in the correlation coefficient order

(BLUE: Positive correlation, RED: Negative correlation)

■ Setting HypterParameters in Leave-One-Out Cross Validation

◆ The project name is PredictGraftLoss.

□ Leave-One-Out cross validation starts.

■ The Setting for Symbolic Regression

◇ The time constraint is 3 min for one validation.

◇ A number of independent evolutions per validation is 8.

◇ Fitting index is 0.75`.

(Fitting index sets the initial QualityBox level,
changing the tendency for overfitting or underfitting)

◇ A total time of calculation per validation is {0, 24, 0}.

◇ A total time of calculation with 2 cores PC is {20, 24, 0}.

◆ Present Time : 2020年 7月 13日 20時 49分 46秒
◆ Finish Time with 8 cores PC : 2020年 7月 14日 1時 55分 46秒
◇ A total time of calculation
using the PRESENT 8 cores PC is {5, 6, 0}.

◇ The DataSubsetSize: 100.%

■ The 1st cross-validation out of 51 turns

□ The 1st Genetic Programming has started.
◆ Present Time: 2020年 7月 13日 20時 49分 48秒

□ The 1st Genetic Programming has ended.
◆ Present Time: 2020年 7月 13日 20時 56分 31秒

◆ Monitors Plot

ModelAccuracy
ModelAge

Pareto Fronts
Error = 1 − R²
Model Complexity

Pareto Fronts
R²

◆ **ParetoFront Plot**

◆ **A total of 893 models were created with Symbolic Regression though machien learning**

◆ **Setting Quality Box values**

◇ **Quatiliy Box values are {43., 0.1761} in the first turn.**

◇ **Limits of percents for narrowing down models: Min 8%, Max 20%**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 893 Selected models: 1 (0.112%)

◆ Inning 0. Complexity: 43. Error: 0.1761 Number of Selected models: 1 (0.112%)

◆ Inning 1. Complexity: 44. Error: 0.1861 Number of Selected models: 1 (0.112%)

◆ Inning 2. Complexity: 45. Error: 0.1961 Number of Selected models: 1 (0.112%)

◆ Inning 3. Complexity: 46. Error: 0.2061 Number of Selected models: 1 (0.112%)

◆ Inning 4. Complexity: 47. Error: 0.2161 Number of Selected models: 5 (0.5599%)

◆ Inning 5. Complexity: 48. Error: 0.2261 Number of Selected models: 6 (0.6719%)

◆ Inning 6. Complexity: 49. Error: 0.2361 Number of Selected models: 8 (0.8959%)

◆ Inning 7. Complexity: 50. Error: 0.2461 Number of Selected models: 15 (1.68%)

◆ Inning 8. Complexity: 51. Error: 0.2561 Number of Selected models: 34 (3.807%)

◆ Inning 9. Complexity: 52. Error: 0.2661 Number of Selected models: 36 (4.031%)

◆ Inning 10. Complexity: 53. Error: 0.2761 Number of Selected models: 43 (4.815%)

◆ Inning 11. Complexity: 54. Error: 0.2861 Number of Selected models: 46 (5.151%)

◆ Inning 12. Complexity: 55. Error: 0.2961 Number of Selected models: 59 (6.607%)

◆ Inning 13. Complexity: 56. Error: 0.3061 Number of Selected models: 72 (8.063%)

◆ **72 interesting models were selected**

◇ Quatiliy Box values are {56., 0.306062}.

◆ Variable Presence (Popularity of each variable) FOCUSED on important variables

◆ TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, pyrexia, gynecology, cNIpostRej, b45}

◆ Defining Ensembles

graftLoss

	Complexity	$1-R^2$	Function
1	35	0.305	$-(3.03\times10^{-2})+0.15\,\text{cRPpostRej}+0.66\,\text{igG}-0.39\,\text{pyrexia}+0.66\,\text{respiratoryInfection}$
2	38	0.222	$3.22\times10^{-2}+0.12\,\text{cNIpostRej}+0.84\,\text{respiratoryInfection}-0.55\,\text{pyrexia upperRespiratoryInfection}+1.07\,b_{45}$
3	38	0.267	$3.39\times10^{-2}+0.11\,\text{cNIpostRej}+0.36\,\text{respiratoryInfection}+0.60\,\text{respiratoryInfection antiHLAclass}_2+1.06\,b_{45}$
4	43	0.176	$4.75\times10^{-2}+0.11\,\text{cNIpostRej}-0.83\,\text{gynecology}-0.51\,\text{pyrexia}+0.88\,\text{respiratoryInfection}+1.05\,b_{45}$
5	43	0.199	$3.38\times10^{-2}+0.11\,\text{cNIpostRej}+0.42\,\text{igG}-0.43\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+0.85\,b_{45}$
6	43	0.270	$6.95\times10^{-2}+(8.39\times10^{-2})\,\text{cNIpostRej}-0.77\,\text{gynecology}+0.66\,\text{igG}-0.47\,\text{pyrexia}+0.77\,\text{respiratoryInfection}$
7	46	0.244	$4.47\times10^{-2}+0.12\,\text{cNIpostRej}-0.44\,\text{pyrexia}+$ $0.76\,\text{respiratoryInfection}+(9.11\times10^{-3})\,\text{pRAclass1pre respiratoryInfection}+1.05\,b_{45}$
8	47	0.171	$5.04\times10^{-2}+0.11\,\text{cNIpostRej}-0.84\,\text{gynecology}-0.62\,\sqrt{\text{pyrexia}}+0.89\,\text{respiratoryInfection}+1.04\,b_{45}$
9	47	0.204	$1.98\times10^{-2}+(1.55\times10^{-2})\,\text{cNIpostRej}^2+0.49\,\text{igG}-0.43\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.73\,b_{45}$
10	47	0.232	$5.86\times10^{-2}-0.86\,\text{gynecology}+0.43\,\text{igG}-0.60\,\sqrt{\text{pyrexia}}+0.80\,\text{respiratoryInfection}+0.73\,b_{45}$
11	47	0.257	$2.88\times10^{-2}+0.41\,\text{candida}^2+0.51\,\text{igG}-0.40\,\text{pyrexia}+0.67\,\text{respiratoryInfection}+0.72\,b_{45}$
12	55	0.129	$2.24\times10^{-2}+(1.55\times10^{-2})\,\text{cNIpostRej}^2-0.86\,\text{gynecology}+$ $0.44\,\text{igG}-0.49\,\text{pyrexia}+0.83\,\text{respiratoryInfection}+0.74\,b_{45}$
13	55	0.160	$1.26\times10^{-2}+(1.57\times10^{-2})\,\text{cNIpostRej}^2-0.86\,\text{gynecology}-$ $0.49\,\text{pyrexia}+0.84\,\text{respiratoryInfection}+0.98\,b_{45}+0.20\,dR_{15}$
14	55	0.204	$4.97\times10^{-2}+0.11\,\text{cNIpostRej}+0.68\,\text{igG}-0.40\,\text{pyrexia}+0.71\,\text{respiratoryInfection}-$ $(8.49\times10^{-4})\,\text{wBCpeakover9postRej}+(6.64\times10^{-2})\,\text{dSAandHSAclass}_1{}^2$

◆ Ensembles in ParetoFront

■ The 1st Validation with Leave-One-Out Method out of 51 turns

```
The Estimated value: -0.7735, The Observed value: 0, Error: -0.7735
```

The Prediction: Right

Accuracy so far: 100.% (1.961% completed)

◇ Estimated Remaining time: `` hour `` min `` sec hr 4 min 59 sec

◆ **Accuracies until the 1st trun in the Leave-One-Out Cross Validation out of 51 turns**

◆ **Error(= Predicted value - Observed value) in the 1st Cross Validation**

◇ **Average Error is 0.7735± 0. until the 1st turn in the LOO method.**

- The start time: Date: 2020, 7, 13, Hour: 20, 56, 33.64
- The required total time for 1200 times calculations: 50 min
- The expected end time: Date: 2020, 7, 14, Hour: 17, 20, 33.64

■ The 2nd cross-validation out of 51 turns

□ **The 2nd Genetic Programming has started.**

◆ **Present Time: 2020年 7月 13日 20時 56分 34秒**

□ **The 2th Genetic Programming has ended.**

◆ **Present Time: 2020年 7月 13日 21時 3分 12秒**

◆ Monitors Plot

Error = 1 − R²
0.10
0.05
0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
100
80
60
40
20
0
−20

Pareto Fronts
Error = 1 − R²
1
0.50
0.10
0.05

◆ **1025 models were created**

◇ **Quatiliy Box values are {49., 0.1488} in the 2nd turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1025 Selected models: 1 (0.09756%)

◆ Inning 0. Complexity: 49. Error: 0.1488 Number of Selected models: 1 (0.09756%)

◆ Inning 1. Complexity: 50. Error: 0.1588 Number of Selected models: 1 (0.09756%)

◆ Inning 2. Complexity: 51. Error: 0.1688 Number of Selected models: 1 (0.09756%)

◆ Inning 3. Complexity: 52. Error: 0.1788 Number of Selected models: 1 (0.09756%)

◆ Inning 4. Complexity: 53. Error: 0.1888 Number of Selected models: 6 (0.5854%)

◆ Inning 5. Complexity: 54. Error: 0.1988 Number of Selected models: 11 (1.073%)

- Inning 6. Complexity: 55. Error: 0.2088 Number of Selected models: 11 (1.073%)
- Inning 7. Complexity: 56. Error: 0.2188 Number of Selected models: 16 (1.561%)
- Inning 8. Complexity: 57. Error: 0.2288 Number of Selected models: 20 (1.951%)
- Inning 9. Complexity: 58. Error: 0.2388 Number of Selected models: 27 (2.634%)
- Inning 10. Complexity: 59. Error: 0.2488 Number of Selected models: 37 (3.61%)
- Inning 11. Complexity: 60. Error: 0.2588 Number of Selected models: 39 (3.805%)
- Inning 12. Complexity: 61. Error: 0.2688 Number of Selected models: 43 (4.195%)
- Inning 13. Complexity: 62. Error: 0.2788 Number of Selected models: 49 (4.78%)
- Inning 14. Complexity: 63. Error: 0.2888 Number of Selected models: 56 (5.463%)
- Inning 15. Complexity: 64. Error: 0.2988 Number of Selected models: 72 (7.024%)
- Inning 16. Complexity: 65. Error: 0.3088 Number of Selected models: 84 (8.195%)

- **84 interesting models were selected**
  - **Quatiliy Box values are {65., 0.308839}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, pyrexia, b45, igG, wBCpeakover5}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.280	$5.30\times10^{-2}+0.12\,\text{cNIpostRej}-0.37\,\text{pyrexia}+0.73\,\text{respiratoryInfection}+1.04\,b_{45}$
2	38	0.282	$3.38\times10^{-2}+0.11\,\text{cNIpostRej}+0.87\,\text{respiratoryInfection}-0.34\,\text{feverOnly respiratoryInfection}+1.06\,b_{45}$
3	41	0.299	$-(1.90\times10^{-2})+0.64\,\text{igG}+0.53\,\text{respiratoryInfection}+(7.50\times10^{-2})\,\text{cRPpostRej wBCpreRej}+0.40\,\text{cRPpostRej}\,b_{13}$
4	43	0.271	$4.65\times10^{-2}+0.12\,\text{cNIpostRej}+0.19\,\text{coaglationnecrosis}-0.36\,\text{pyrexia}+0.71\,\text{respiratoryInfection}+1.05\,b_{45}$
5	43	0.275	$7.83\times10^{-2}-\frac{1.89\times10^{-3}}{\text{hDperiod}}+0.45\,\text{igG}-0.41\,\text{pyrexia}+0.71\,\text{respiratoryInfection}+0.70\,b_{45}$
6	46	0.180	$2.27\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}+0.76\,\text{respiratoryInfection}-0.49\,\text{pyrexia respiratoryInfection}+0.86\,b_{45}$
7	46	0.185	$1.38\times10^{-2}-\frac{2.01\times10^{-3}}{\text{hDperiod}}+0.86\,\text{respiratoryInfection}-0.63\,\text{pyrexia respiratoryInfection}+0.95\,b_{45}+(1.96\times10^{-2})\,\text{wBCpeakover}_5$
8	46	0.242	$6.76\times10^{-3}-0.16\,\text{artificialAbortion}+0.81\,\text{respiratoryInfection}-0.60\,\text{pyrexia respiratoryInfection}+1.03\,b_{45}+(2.07\times10^{-2})\,\text{wBCpeakover}_5$
9	49	0.149	$-(2.99\times10^{-2})+0.80\,\text{respiratoryInfection}-0.57\,\text{pyrexia respiratoryInfection}+0.99\,b_{45}+0.95\,\text{igG}\,dR_{15}+(2.03\times10^{-2})\,\text{wBCpeakover}_5$
10	49	0.178	$-(2.05\times10^{-2})+0.71\,\text{respiratoryInfection}-0.51\,\text{pyrexia respiratoryInfection}+0.98\,b_{45}+0.59\,\text{igG}\,dQ_6+(2.02\times10^{-2})\,\text{wBCpeakover}_5$
11	51	0.186	$2.51\times10^{-2}-\frac{1.72\times10^{-3}}{\text{hDperiod}}+0.44\,\text{igG}-0.41\,\text{pyrexia}+0.71\,\text{respiratoryInfection}+0.72\,b_{45}+(1.83\times10^{-2})\,\text{wBCpeakover}_5$
12	51	0.202	$4.13\times10^{-2}-\frac{1.95\times10^{-3}}{\text{hDperiod}}-0.44\,\text{polyp}-0.41\,\text{pyrexia}+0.78\,\text{respiratoryInfection}+0.92\,b_{45}+(2.15\times10^{-2})\,\text{wBCpeakover}_5$
13	52	0.200	$-0.10+(9.57\times10^{-3})\,\text{hDperiod}+0.63\,\text{igG}+(6.38\times10^{-2})\,\text{cRPpostRej mMFatRej}+0.70\,\text{respiratoryInfection}-1.64\,\text{cRPpostRej pyrexia respiratoryInfection}$
14	53	0.146	$-(2.90\times10^{-2})+(1.32\times10^{-2})\,\text{hDperiod}^2\,\text{igG}+0.76\,\text{respiratoryInfection}-0.54\,\text{pyrexia respiratoryInfection}+0.99\,b_{45}+(2.02\times10^{-2})\,\text{wBCpeakover}_5$
15	54	0.171	$-(1.46\times10^{-2})+(9.25\times10^{-2})\,\text{cNIpostRej}+(6.91\times10^{-3})\,\text{hDperiod}+0.43\,\text{igG}+0.77\,\text{respiratoryInfection}-0.50\,\text{pyrexia respiratoryInfection}+0.87\,b_{45}$

◆ Ensembles in ParetoFront

■ **The 2nd Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.768, The Observed value: 1

The Prediction: Right

Accuracy so far: 100.% (3.922% completed)

◆ **Accuracies until the 2nd turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 4 min 52 sec

◆ **Error(= Predicted value - Observed value) in the 2nd Cross Validation**

◇ **Average Error is 0.5027± 0.3829 until the 2nd turn in the LOO method.**

■ The 3rd cross-validation out of 51 turns

□ The 3rd Genetic Programming has started.

◆ Present Time: 2020年 7月 13日⧆21時 3分 15秒

□ The 3th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日⧆21時 9分 28秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
100
200
300
400
500
Model Complexity

,

◆ **956 models were created**

◇ **Quatiliy Box values are {46., 0.1976} in the 3rd turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 956 Selected models: 1 (0.1046%)

◆ Inning 0. Complexity: 46. Error: 0.1976 Number of Selected models: 1 (0.1046%)

◆ Inning 1. Complexity: 47. Error: 0.2076 Number of Selected models: 1 (0.1046%)

◆ Inning 2. Complexity: 48. Error: 0.2176 Number of Selected models: 1 (0.1046%)

◆ Inning 3. Complexity: 49. Error: 0.2276 Number of Selected models: 4 (0.4184%)

◆ Inning 4. Complexity: 50. Error: 0.2376 Number of Selected models: 5 (0.523%)

◆ Inning 5. Complexity: 51. Error: 0.2476 Number of Selected models: 6 (0.6276%)

◆ Inning 6. Complexity: 52. Error: 0.2576 Number of Selected models: 6 (0.6276%)

◆ Inning 7. Complexity: 53. Error: 0.2676 Number of Selected models: 10 (1.046%)

◆ Inning 8. Complexity: 54. Error: 0.2776 Number of Selected models: 18 (1.883%)

◆ Inning 9. Complexity: 55. Error: 0.2876 Number of Selected models: 21 (2.197%)

◆ Inning 10. Complexity: 56. Error: 0.2976 Number of Selected models: 26 (2.72%)

◆ Inning 11. Complexity: 57. Error: 0.3076 Number of Selected models: 42 (4.393%)

◆ Inning 12. Complexity: 58. Error: 0.3176 Number of Selected models: 54 (5.649%)

◆ Inning 13. Complexity: 59. Error: 0.3276 Number of Selected models: 75 (7.845%)

◆ Inning 14. Complexity: 60. Error: 0.3376 Number of Selected models: 85 (8.891%)

- 85 interesting models were selected
  - Quatiliy Box values are {60., 0.337565}.

- Variable Presence (Popularity of each variable) FOCUSED on important variables
- TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, igG, dQ8}

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.326	$6.16\times10^{-2}+0.48\,\text{igG}-0.38\,\text{pyrexia}+0.67\,\text{respiratoryInfection}+0.70\,b_{45}$
2	38	0.267	$3.32\times10^{-2}+0.11\,\text{cNIpostRej}+0.36\,\text{respiratoryInfection}+1.06\,b_{45}+0.60\,\text{respiratoryInfection}\,dQ_8$
3	38	0.270	$-(3.29\times10^{-2})+0.13\,\text{cRPpostRej}+1.09\,\text{respiratoryInfection}-0.49\,\text{banfi}\,\text{respiratoryInfection}+0.80\,b_{45}$
4	38	0.277	$-(4.23\times10^{-3})+0.28\,\text{respiratoryInfection}+$ $0.69\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.96\,b_{45}+(2.00\times10^{-2})\,\text{wBCpeakover}_5$
5	39	0.299	$4.13\times10^{-2}+(7.79\times10^{-3})\,\text{cRPpostRej}^3-0.40\,\text{pyrexia}+0.73\,\text{respiratoryInfection}+0.92\,b_{45}$
6	40	0.307	$3.73\times10^{-2}+0.30\,\text{respiratoryInfection}+$ $0.59\,\text{respiratoryInfection}\,dQ_7{}^2+0.13\,\text{dSAclass1number}\,\text{dSAclass}_2\,\text{wBCpeakover}_5$
7	41	0.243	$-(2.75\times10^{-2})+0.12\,\text{cRPpostRej}-0.35\,\text{pyrexia}+$ $0.69\,\text{respiratoryInfection}+0.12\,\text{dSAclass1number}\,\text{dSAclass}_2\,\text{wBCpeakover}_5$
8	41	0.299	$-(6.53\times10^{-2})+0.53\,\text{respiratoryInfection}+$ $0.85\,b_{45}+0.11\,\text{hLAABmm}\,dQ_7+(3.62\times10^{-4})\,\text{rage}\,\text{wBCpeakover}_5$
9	41	0.317	$-(5.24\times10^{-2})+0.54\,\text{igG}+0.58\,\text{respiratoryInfection}+(3.62\times10^{-4})\,\text{cRPpostRej}\,\text{rage}\,\text{wBCinUrine}+0.54\,b_{45}$
10	42	0.222	$5.98\times10^{-2}+0.11\,\text{cNIpostRej}+1.03\,\text{coaglationnecrosis}+1.03\,b_{45}+0.94\,\text{respiratoryInfection}\,dQ_8{}^2$
11	42	0.308	$7.70\times10^{-2}+(8.82\times10^{-2})\,\text{cNIpostRej}+0.36\,\text{igG}+0.82\,b_{45}+0.85\,\text{respiratoryInfection}\,dQ_8{}^2$
12	42	0.314	$5.41\times10^{-2}+0.80\,\text{coaglationnecrosis}+0.15\,\text{respiratoryInfection}+0.95\,b_{45}+0.80\,\text{respiratoryInfection}\,dQ_8{}^2$
13	43	0.274	$-(2.86\times10^{-2})+0.12\,\text{cNIpostRej}+0.50\,\text{igG}+0.57\,\text{respiratoryInfection}+0.79\,b_{45}+0.19\,dQ_8$
14	45	0.289	$-(1.49\times10^{-2})+0.66\,\text{igG}-0.38\,\sqrt{\text{pyrexia}}+$ $0.65\,\text{respiratoryInfection}+(3.76\times10^{-4})\,\text{cRPpostRej}\,\text{rage}\,\text{wBCinUrine}$
15	46	0.198	$3.25\times10^{-2}+0.11\,\text{cNIpostRej}+0.84\,\text{coaglationnecrosis}+$ $0.22\,\text{respiratoryInfection}+1.06\,b_{45}+0.74\,\text{respiratoryInfection}\,dQ_8$

◆ Ensembles in ParetoFront

■ **The 3rd Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: -0.01205, The Observed value: 0

The Prediction: Right

Accuracy so far: 100.% (5.882% completed)

◆ **Accuracies until the 3rd turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 4 min 46 sec

◆ **Error(= Predicted value - Observed value) in the 3rd Cross Validation**

◇ **Average Error is 0.3392± 0.3919 until the 3rd turn in the LOO method.**

■ The 4th cross-validation out of 51 turns

□ The 4th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日⁞21時 9分 32秒

□ The 4th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日⁞21時 15分 59秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
100
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
50
100
150
200
250
300
Model Complexity

,

◆ **996 models were created**

◇ **Quatiliy Box values are {55., 0.1567} in the 4th turn.**

- Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.
- Generated models: 996 Selected models: 1 (0.1004%)
- Inning 0. Complexity: 55. Error: 0.1567 Number of Selected models: 1 (0.1004%)
- Inning 1. Complexity: 56. Error: 0.1667 Number of Selected models: 1 (0.1004%)
- Inning 2. Complexity: 57. Error: 0.1767 Number of Selected models: 2 (0.2008%)
- Inning 3. Complexity: 58. Error: 0.1867 Number of Selected models: 4 (0.4016%)
- Inning 4. Complexity: 59. Error: 0.1967 Number of Selected models: 9 (0.9036%)
- Inning 5. Complexity: 60. Error: 0.2067 Number of Selected models: 15 (1.506%)
- Inning 6. Complexity: 61. Error: 0.2167 Number of Selected models: 17 (1.707%)
- Inning 7. Complexity: 62. Error: 0.2267 Number of Selected models: 26 (2.61%)
- Inning 8. Complexity: 63. Error: 0.2367 Number of Selected models: 38 (3.815%)
- Inning 9. Complexity: 64. Error: 0.2467 Number of Selected models: 44 (4.418%)
- Inning 10. Complexity: 65. Error: 0.2567 Number of Selected models: 60 (6.024%)
- Inning 11. Complexity: 66. Error: 0.2667 Number of Selected models: 69 (6.928%)
- Inning 12. Complexity: 67. Error: 0.2767 Number of Selected models: 94 (9.438%)

- **94 interesting models were selected**
  - **Quatiliy Box values are {67., 0.276687}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, cNIpostRej, b45, igG, pyrexia}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.251	$5.19\times10^{-2}+0.11\,\text{cNIpostRej}-0.35\,\text{pyrexia}+0.78\,\text{respiratoryInfection}+1.04\,b_{45}$
2	43	0.203	$4.06\times10^{-2}+0.11\,\text{cNIpostRej}+0.42\,\text{igG}-0.32\,\text{pyrexia}+0.74\,\text{respiratoryInfection}+0.84\,b_{45}$
3	47	0.216	$5.80\times10^{-3}+0.12\,\text{cNIpostRej}-0.18\,\text{pyrexia}^2+0.74\,\text{respiratoryInfection}+1.09\,b_{45}+0.20\,dR_{53}$
4	47	0.251	$7.91\times10^{-2}-(7.05\times10^{-2})\,\text{banfct}^2+0.50\,\text{igG}-0.37\,\text{pyrexia}+0.79\,\text{respiratoryInfection}+0.81\,b_{45}$
5	47	0.254	$1.26\times10^{-3}-(4.30\times10^{-2})\,\text{banfct}^2+0.12\,\text{cNIpostRej}+0.70\,\text{respiratoryInfection}+1.19\,b_{45}+0.24\,dR_{53}$
6	47	0.263	$2.37\times10^{-2}+0.10\,\text{cNIpostRej}+0.35\,\text{gERD}+0.73\,\text{igG}-0.47\,\sqrt{\text{pyrexia}}+0.71\,\text{respiratoryInfection}$
7	48	0.251	$1.11+0.10\,\text{cNIpostRej}-0.29\,\text{respiratoryInfection}-\frac{0.11}{\frac{1}{10}+\text{igG}+\text{respiratoryInfection}+b_{45}}$
8	51	0.173	$6.64\times10^{-2}-0.11\,\text{banfct}+0.10\,\text{cNIpostRej}+0.47\,\text{igG}-0.32\,\text{pyrexia}+0.80\,\text{respiratoryInfection}+0.90\,b_{45}$
9	51	0.221	$4.41\times10^{-2}-0.15\,\text{artificialAbortion}+0.12\,\text{cNIpostRej}+$ $0.17\,\text{gERD}-0.41\,\text{pyrexia}+0.82\,\text{respiratoryInfection}+1.05\,b_{45}$
10	51	0.233	$8.23\times10^{-3}+0.43\,\text{candida}+0.19\,\text{gERD}+0.56\,\text{igG}-0.35\,\text{pyrexia}+0.68\,\text{respiratoryInfection}+0.61\,b_{45}$
11	54	0.189	$-(1.88\times10^{-2})-0.73\,\text{enterobacteraerogenes}+0.78\,\text{igG}+1.09\,\text{respiratoryInfection}-$ $(9.10\times10^{-2})\,\text{respiratoryInfection uTI}+0.85\,b_{62}+(1.98\times10^{-2})\,\text{wBCpeakover}_5$
12	54	0.211	$-(5.60\times10^{-2})+0.15\,\text{cRPpostRej}-0.49\,\text{enterobacteraerogenes}+$ $0.57\,\text{igG}+1.13\,\text{respiratoryInfection}-0.10\,\text{respiratoryInfection uTI}+0.52\,b_{63}$
13	54	0.236	$-(1.34\times10^{-2})+0.20\,\text{heartDisease}+0.53\,\text{igG}+0.33\,b_{45}+$ $(8.16\times10^{-2})\,\text{inflammationdatefirst}\,(\text{respiratoryInfection}+b_{45})+0.26\,dR_7$
14	55	0.200	$3.72\times10^{-2}+0.11\,\text{cNIpostRej}+0.42\,\text{igG}-0.15\,\text{pyrexia}-0.11\,\text{pyrexia}^2+0.75\,\text{respiratoryInfection}+0.84\,b_{45}$
15	57	0.193	$-(9.92\times10^{-3})+0.13\,\text{cNIpostRej}-0.23\,\text{respiratoryInfection}+$ $0.40\,\sqrt{\text{inflammationdatefirst respiratoryInfection}}+0.98\,b_{45}+0.26\,dR_7$

◆ Ensembles in ParetoFront

■ **The 4th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.5101, The Observed value: 0

The Prediction: Wrong

Accuracy so far: 75.% (7.843% completed)

◆ **Accuracies until the 4th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 4 min 39 sec

◆ **Error(= Predicted value - Observed value) in the 4th Cross Validation**

◇ **Average Error is 0.3819± 0.3312 until the 4th turn in the LOO method.**

■ The 5th cross-validation out of 51 turns

□ The 5th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日⁞21時 16分 3秒

□ The 5th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日⁞21時 22分 42秒

◆ Monitors Plot

0.01
0
200
400
600
800
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
ModelAge
100
80
60
40
20
0
−20

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1− R2
0
100
200
300
400
Model Complexity

,

◆ **870 models were created**

◇ **Quatiliy Box values are {51., 0.1912} in the 5th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 870 Selected models: 1 (0.1149%)

◆ Inning 0. Complexity: 51. Error: 0.1912 Number of Selected models: 1 (0.1149%)

◆ Inning 1. Complexity: 52. Error: 0.2012 Number of Selected models: 1 (0.1149%)

◆ Inning 2. Complexity: 53. Error: 0.2112 Number of Selected models: 2 (0.2299%)

◆ Inning 3. Complexity: 54. Error: 0.2212 Number of Selected models: 10 (1.149%)

◆ Inning 4. Complexity: 55. Error: 0.2312 Number of Selected models: 16 (1.839%)

◆ Inning 5. Complexity: 56. Error: 0.2412 Number of Selected models: 16 (1.839%)

◆ Inning 6. Complexity: 57. Error: 0.2512 Number of Selected models: 16 (1.839%)

◆ Inning 7. Complexity: 58. Error: 0.2612 Number of Selected models: 22 (2.529%)

◆ Inning 8. Complexity: 59. Error: 0.2712 Number of Selected models: 33 (3.793%)

◆ Inning 9. Complexity: 60. Error: 0.2812 Number of Selected models: 33 (3.793%)

◆ Inning 10. Complexity: 61. Error: 0.2912 Number of Selected models: 38 (4.368%)

◆ Inning 11. Complexity: 62. Error: 0.3012 Number of Selected models: 47 (5.402%)

◆ Inning 12. Complexity: 63. Error: 0.3112 Number of Selected models: 55 (6.322%)

◆ Inning 13. Complexity: 64. Error: 0.3212 Number of Selected models: 68 (7.816%)

◆ Inning 14. Complexity: 65. Error: 0.3312 Number of Selected models: 81 (9.31%)

- 81 interesting models were selected
  - Quatiliy Box values are {65., 0.331244}.

- Variable Presence (Popularity of each variable) FOCUSED on important variables
- TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, pyrexia, cNIpostRej, igG}

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.308	$3.63\times10^{-2}+0.92\,b_{45}+0.92\,\text{respiratoryInfection}\,dQ_8+(2.24\times10^{-2})\,\text{wBCpeakover}_5$
2	34	0.308	$3.63\times10^{-2}+0.92\,b_{45}+0.92\,\text{respiratoryInfection}^3\,dQ_8+(2.24\times10^{-2})\,\text{wBCpeakover}_5$
3	38	0.326	$6.16\times10^{-2}+0.48\,\text{igG}-0.38\,\text{pyrexia}+0.67\,\text{respiratoryInfection}+0.70\,a_{25}\,b_{45}$
4	43	0.218	$4.38\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.83\,b_{45}$
5	43	0.229	$-(2.34\times10^{-3})+0.12\,\text{cNIpostRej}+\frac{1.92\times10^{-2}}{\text{maxCRP}}-0.45\,\text{pyrexia}+0.80\,\text{respiratoryInfection}+1.09\,b_{45}$
6	43	0.259	$3.04\times10^{-2}+0.12\,\text{cNIpostRej}-0.35\,\text{pyrexia}+0.73\,\text{respiratoryInfection}+1.02\,b_{45}+(9.34\times10^{-2})\,dQ_8$
7	43	0.310	$3.97\times10^{-4}+0.12\,\text{cNIpostRej}+0.47\,\text{igG}+\frac{6.79\times10^{-3}}{\text{maxCRP}}+0.61\,\text{respiratoryInfection}+0.86\,b_{45}$
8	46	0.206	$4.12\times10^{-2}+0.11\,\text{cNIpostRej}+0.63\,\text{igG}-$ $0.35\,\text{pyrexia}+0.70\,\text{respiratoryInfection}+0.27\,b_{45}\,\text{dSAandHSAclass}_1$
9	46	0.220	$3.78\times10^{-2}+0.12\,\text{cNIpostRej}+0.83\,\text{respiratoryInfection}-$ $0.55\,\text{pyrexia respiratoryInfection}+1.10\,b_{45}-(6.84\times10^{-2})\,b_{58}$
10	46	0.237	$-(2.32\times10^{-2})+0.29\,\text{respiratoryInfection}+0.84\,b_{45}+$ $0.27\,c_3+0.69\,\text{respiratoryInfection}\,dQ_8+(2.23\times10^{-2})\,\text{wBCpeakover}_5$
11	50	0.301	$1.81-\frac{3.48}{1.92+\text{candida}+2\,\text{igG}-\text{polyp}+\text{respiratoryInfection}+b_{45}}$
12	51	0.191	$-(3.55\times10^{-3})+0.11\,\text{cNIpostRej}+0.38\,\text{igG}+\frac{1.61\times10^{-2}}{\text{maxCRP}}-0.42\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+0.90\,b_{45}$
13	54	0.178	$4.58\times10^{-3}+0.38\,\text{igG}-0.27\,\text{pyrexia}+0.45\,\text{respiratoryInfection}+$ $0.76\,b_{45}+0.43\,\text{respiratoryInfection}\,dQ_8+(2.17\times10^{-2})\,\text{wBCpeakover}_5$
14	54	0.253	$6.60\times10^{-2}-(1.60\times10^{-2})\,\text{banf t}+0.10\,\text{cNIpostRej}+0.63\,\text{igG}-$ $0.33\,\text{pyrexia}+0.66\,\text{respiratoryInfection}+(1.61\times10^{-2})\,\text{maxCRP}\,\text{dSAandHSAclass}_1$
15	54	0.270	$1.57\times10^{-3}+0.41\,\text{candida}+0.42\,\text{igG}+$ $0.33\,\text{respiratoryInfection}+0.79\,b_{45}+0.43\,\text{respiratoryInfection}\,dQ_8+0.17\,dR_{15}$

◆ Ensembles in ParetoFront

■ **The 5th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.0954, The Observed value: 0

The Prediction: Right

Accuracy so far: 80.% (9.804% completed)

◆ **Accuracies until the 5th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 4 min 33 sec

◆ **Error(= Predicted value - Observed value) in the 5th Cross Validation**

◇ **Average Error is 0.3246± 0.3141 until the 5th turn in the LOO method.**

■ The 6th cross-validation out of 51 turns

□ The 6th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日 21時 22分 46秒

□ The 6th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日 21時 28分 57秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
120
100
80
60
40
20
0
−20

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1− R2
0
100
200
300
400
500
600
Model Complexity

,

◆ **993 models were created**

◇ **Quatiliy Box values are {50., 0.133} in the 6th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 993 Selected models: 1 (0.1007%)

◆ Inning 0. Complexity: 50. Error: 0.133 Number of Selected models: 1 (0.1007%)

◆ Inning 1. Complexity: 51. Error: 0.143 Number of Selected models: 1 (0.1007%)

◆ Inning 2. Complexity: 52. Error: 0.153 Number of Selected models: 2 (0.2014%)

◆ Inning 3. Complexity: 53. Error: 0.163 Number of Selected models: 3 (0.3021%)

◆ Inning 4. Complexity: 54. Error: 0.173 Number of Selected models: 4 (0.4028%)

◆ Inning 5. Complexity: 55. Error: 0.183 Number of Selected models: 9 (0.9063%)

◆ Inning 6. Complexity: 56. Error: 0.193 Number of Selected models: 12 (1.208%)

◆ Inning 7. Complexity: 57. Error: 0.203 Number of Selected models: 12 (1.208%)

◆ Inning 8. Complexity: 58. Error: 0.213 Number of Selected models: 22 (2.216%)

◆ Inning 9. Complexity: 59. Error: 0.223 Number of Selected models: 27 (2.719%)

◆ Inning 10. Complexity: 60. Error: 0.233 Number of Selected models: 34 (3.424%)

◆ Inning 11. Complexity: 61. Error: 0.243 Number of Selected models: 36 (3.625%)

◆ Inning 12. Complexity: 62. Error: 0.253 Number of Selected models: 47 (4.733%)

◆ Inning 13. Complexity: 63. Error: 0.263 Number of Selected models: 65 (6.546%)

◆ Inning 14. Complexity: 64. Error: 0.273 Number of Selected models: 73 (7.351%)

- Inning 15. Complexity: 65. Error: 0.283 Number of Selected models: 89 (8.963%)

- **89 interesting models were selected**
  - **Quatiliy Box values are {65., 0.283026}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, cNIpostRej, igG, banfi, b45}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.282	$4.30\times10^{-2}+0.12\,\text{cNIpostRej}+(9.22\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.06\,b_{45}$
2	39	0.260	$-(1.50\times10^{-2})+0.12\,\text{cNIpostRej}+(4.71\times10^{-2})\,\text{denovoDSA}^2+0.90\,\text{igG}+0.57\,\text{respiratoryInfection}$
3	42	0.248	$2.05\times10^{-2}+(1.56\times10^{-2})\,\text{cNIpostRej}^2+$ $1.16\,\text{respiratoryInfection}-0.53\,\text{banfi}\,\text{respiratoryInfection}+0.97\,b_{45}$
4	42	0.261	$3.57\times10^{-2}+0.64\,\text{igG}+1.00\,\text{respiratoryInfection}-0.26\,\text{banfi}^2\,\text{respiratoryInfection}+0.64\,b_{45}$
5	42	0.277	$3.74\times10^{-2}+0.12\,\text{cNIpostRej}+(1.09\times10^{-2})\,\text{denovoDSA}^2+$ $(9.02\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.91\,b_{45}$
6	43	0.205	$-(2.62\times10^{-2})+0.12\,\text{cNIpostRej}+0.16\,\text{denovoDSA}+0.85\,\text{igG}-0.32\,\text{pyrexia}+0.66\,\text{respiratoryInfection}$
7	43	0.252	$1.06\times10^{-2}+0.10\,\text{cNIpostRej}+0.34\,\text{gERD}+0.97\,\text{igG}-0.45\,\text{pyrexia}+0.77\,\text{respiratoryInfection}$
8	43	0.254	$-(3.91\times10^{-2})+0.13\,\text{cRPpostRej}+0.83\,\text{igG}-$ $0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.17\,\text{dSAandHSAclass}_1$
9	43	0.267	$7.20\times10^{-2}-(7.72\times10^{-2})\,\text{banfct}+0.11\,\text{cNIpostRej}-0.38\,\text{pyrexia}+0.77\,\text{respiratoryInfection}+1.10\,b_{45}$
10	46	0.181	$-(6.85\times10^{-2})+0.14\,\text{cRPpostRej}+0.84\,\text{igG}+$ $1.18\,\text{respiratoryInfection}-0.53\,\text{banfi}\,\text{respiratoryInfection}+0.17\,\text{dSAandHSAclass}_1$
11	46	0.257	$1.01\times10^{-3}+0.94\,\text{igG}+1.21\,\text{respiratoryInfection}-$ $0.59\,\text{banfi}\,\text{respiratoryInfection}-0.13\,dQ_{11}+(1.97\times10^{-2})\,\text{wBCpeakover}_5$
12	47	0.175	$7.25\times10^{-3}+0.11\,\text{cNIpostRej}+(4.36\times10^{-2})\,\text{denovoDSA}^2+$ $0.88\,\text{igG}-0.33\,\text{pyrexia}+0.69\,\text{respiratoryInfection}$
13	49	0.150	$3.37\times10^{-2}+0.11\,\text{cNIpostRej}+0.69\,\text{respiratoryInfection}-$ $0.46\,\text{banfi}\,\text{respiratoryInfection}+(6.86\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.06\,b_{45}$
14	49	0.258	$7.30\times10^{-2}-(8.61\times10^{-2})\,\text{banfct}+0.70\,\text{respiratoryInfection}-$ $0.48\,\text{banfi}\,\text{respiratoryInfection}+(6.90\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.01\,b_{45}$
15	50	0.138	$-(9.07\times10^{-3})+0.11\,\text{cNIpostRej}+(4.29\times10^{-2})\,\text{denovoDSA}^2+$ $0.90\,\text{igG}+1.07\,\text{respiratoryInfection}-0.45\,\text{banfi}\,\text{respiratoryInfection}$

◆ Ensembles in ParetoFront

■ **The 6th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 1.81, The Observed value: 1

The Prediction: Right

Accuracy so far: 83.33% (11.76% completed)

◆ **Accuracies until the 6th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 4 min 26 sec

◆ **Error(= Predicted value - Observed value) in the 6th Cross Validation**

◇ **Average Error is 0.4055± 0.3438 until the 6th turn in the LOO method.**

■ The 7th cross-validation out of 51 turns

□ The 7th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日⧆21時 29分 0秒

□ The 7th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日⧆21時 35分 11秒

◆ Monitors Plot

0.01
0
200
400
600
800
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
100
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 – R2
0
100
200
300
400
500
Model Complexity

,

◆ **938 models were created**

◇ **Quatiliy Box values are {49., 0.1378} in the 7th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 938 Selected models: 1 (0.1066%)

◆ Inning 0. Complexity: 49. Error: 0.1378 Number of Selected models: 1 (0.1066%)

◆ Inning 1. Complexity: 50. Error: 0.1478 Number of Selected models: 1 (0.1066%)

◆ Inning 2. Complexity: 51. Error: 0.1578 Number of Selected models: 1 (0.1066%)

◆ Inning 3. Complexity: 52. Error: 0.1678 Number of Selected models: 1 (0.1066%)

◆ Inning 4. Complexity: 53. Error: 0.1778 Number of Selected models: 1 (0.1066%)

◆ Inning 5. Complexity: 54. Error: 0.1878 Number of Selected models: 3 (0.3198%)

◆ Inning 6. Complexity: 55. Error: 0.1978 Number of Selected models: 4 (0.4264%)

◆ Inning 7. Complexity: 56. Error: 0.2078 Number of Selected models: 6 (0.6397%)

◆ Inning 8. Complexity: 57. Error: 0.2178 Number of Selected models: 8 (0.8529%)

◆ Inning 9. Complexity: 58. Error: 0.2278 Number of Selected models: 17 (1.812%)

◆ Inning 10. Complexity: 59. Error: 0.2378 Number of Selected models: 26 (2.772%)

◆ Inning 11. Complexity: 60. Error: 0.2478 Number of Selected models: 26 (2.772%)

◆ Inning 12. Complexity: 61. Error: 0.2578 Number of Selected models: 27 (2.878%)

◆ Inning 13. Complexity: 62. Error: 0.2678 Number of Selected models: 34 (3.625%)

◆ Inning 14. Complexity: 63. Error: 0.2778 Number of Selected models: 42 (4.478%)

- Inning 15. Complexity: 64. Error: 0.2878 Number of Selected models: 43 (4.584%)
- Inning 16. Complexity: 65. Error: 0.2978 Number of Selected models: 43 (4.584%)
- Inning 17. Complexity: 66. Error: 0.3078 Number of Selected models: 46 (4.904%)
- Inning 18. Complexity: 67. Error: 0.3178 Number of Selected models: 58 (6.183%)
- Inning 19. Complexity: 68. Error: 0.3278 Number of Selected models: 60 (6.397%)
- Inning 20. Complexity: 69. Error: 0.3378 Number of Selected models: 71 (7.569%)
- Inning 21. Complexity: 70. Error: 0.3478 Number of Selected models: 76 (8.102%)

- **76 interesting models were selected**
  - **Quatiliy Box values are {70., 0.347837}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, pyrexia, cNIpostRej, c3}**

- **Defining Ensembles**

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.335	$-(2.13\times10^{-2})+0.13\,\text{cNIpostRej}+(1.04\times10^{-2})\,\text{hSAclass2number}+0.62\,\text{respiratoryInfection}+1.09\,b_{45}$
2	35	0.345	$7.43\times10^{-2}+(8.75\times10^{-2})\,\text{cNIpostRej}+0.70\,\text{igG}-0.36\,\text{pyrexia}+0.65\,\text{respiratoryInfection}$
3	38	0.222	$3.31\times10^{-2}+0.12\,\text{cNIpostRej}+0.84\,\text{respiratoryInfection}-0.55\,\text{pyrexia respiratoryInfection}+1.07\,b_{45}$
4	38	0.223	$4.50\times10^{-2}-0.42\,\text{pyrexia}+0.77\,\text{respiratoryInfection}+0.15\,\text{cNIpostRej surgery}+0.96\,b_{45}$
5	38	0.330	$4.28\times10^{-2}+0.42\,\text{igG}+0.29\,\text{respiratoryInfection}+0.75\,b_{45}+0.58\,\text{respiratoryInfection}\,dQ_7$
6	41	0.233	$-(2.20\times10^{-16})+0.33\,\text{respiratoryInfection}+0.67\,\text{surgery}\cdot\text{igA}+1.00\,b_{45}+0.67\,\text{respiratoryInfection}\,dQ_7$
7	41	0.344	$1.78-\frac{3.55}{2+\text{candida}+2\,\text{igG}+\text{respiratoryInfection}+b_{45}}$
8	42	0.333	$7.96\times10^{-2}-0.42\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.92\,b_{45}+0.44\,\text{cNIpostRej}\,\sqrt{dR_1}$
9	43	0.265	$4.85\times10^{-2}+0.12\,\text{cNIpostRej}-0.38\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+1.05\,b_{45}+(9.96\times10^{-2})\,dP_{11}$
10	46	0.188	$3.34\times10^{-2}+0.10\,\text{cNIpostRej}-0.38\,\text{pyrexia}+0.77\,\text{respiratoryInfection}+1.05\,b_{45}+0.85\,c_3\,dR_{52}$
11	49	0.138	$1.16\times10^{-2}+0.11\,\text{cNIpostRej}+0.85\,\text{respiratoryInfection}-$ $0.55\,\text{pyrexia respiratoryInfection}+1.08\,b_{45}+0.87\,c_3\,dQ_6$
12	51	0.203	$1.28\times10^{-2}+0.11\,\text{cNIpostRej}+0.35\,\text{igG}-0.33\,\text{pyrexia}+0.69\,\text{respiratoryInfection}+0.91\,b_{45}+0.13\,dQ_6$
13	51	0.218	$4.01\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}+$ $(5.39\times10^{-4})\,\text{pRAclass1after}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.82\,b_{45}$
14	53	0.207	$5.30\times10^{-2}-0.45\,\text{pyrexia}+0.83\,\text{respiratoryInfection}-$ $0.88\,\text{gynecology}^2\,\text{respiratoryInfection}+0.95\,b_{45}+0.95\,c_3\,dR_{52}$
15	57	0.138	$1.05\times10^{-2}+0.11\,\text{cNIpostRej}+(1.99\times10^{-2})\,\text{pyrexia}+$ $0.86\,\text{respiratoryInfection}-0.57\,\text{pyrexia respiratoryInfection}+1.08\,b_{45}+0.87\,c_3\,dR_{52}$

◆ Ensembles in ParetoFront

■ The 7th Cross Validation with Leave-One-Out Method out of 51 turns

The Estimated value: 0.01102, The Observed value: 0

The Prediction: Right

Accuracy so far: 85.71% (13.73% completed)

◆ **Accuracies until the 7th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 4 min 20 sec

◆ **Error(= Predicted value - Observed value) in the 7th Cross Validation**

◇ **Average Error is 0.3491± 0.3474 until the 7th turn in the LOO method.**

■ The 8th cross-validation out of 51 turns

□ The 8th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日 21時 35分 14秒

□ The 8th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日 21時 41分 57秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
50
100
150
Model Complexity

,

◆ **992 models were created**

◇ **Quatiliy Box values are {54., 0.1634} in the 8th turn.**

- Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.
- Generated models: 992 Selected models: 1 (0.1008%)
- Inning 0. Complexity: 54. Error: 0.1634 Number of Selected models: 1 (0.1008%)
- Inning 1. Complexity: 55. Error: 0.1734 Number of Selected models: 1 (0.1008%)
- Inning 2. Complexity: 56. Error: 0.1834 Number of Selected models: 2 (0.2016%)
- Inning 3. Complexity: 57. Error: 0.1934 Number of Selected models: 8 (0.8065%)
- Inning 4. Complexity: 58. Error: 0.2034 Number of Selected models: 13 (1.31%)
- Inning 5. Complexity: 59. Error: 0.2134 Number of Selected models: 19 (1.915%)
- Inning 6. Complexity: 60. Error: 0.2234 Number of Selected models: 28 (2.823%)
- Inning 7. Complexity: 61. Error: 0.2334 Number of Selected models: 41 (4.133%)
- Inning 8. Complexity: 62. Error: 0.2434 Number of Selected models: 53 (5.343%)
- Inning 9. Complexity: 63. Error: 0.2534 Number of Selected models: 66 (6.653%)
- Inning 10. Complexity: 64. Error: 0.2634 Number of Selected models: 67 (6.754%)
- Inning 11. Complexity: 65. Error: 0.2734 Number of Selected models: 83 (8.367%)

- **83 interesting models were selected**
  - **Quatiliy Box values are {65., 0.273351}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, dQ7, igG, cNIpostRej}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	34	0.270	$3.51\times10^{-2}+(3.15\times10^{-2})\,\text{cRPpostRej}^2+0.87\,b_{45}+0.93\,\text{respiratoryInfection}\,dQ_7$
2	38	0.251	$3.86\times10^{-2}+0.46\,\text{coaglationnecrosis}+0.42\,\text{igG}+0.75\,b_{45}+0.88\,\text{respiratoryInfection}\,dQ_7$
3	42	0.201	$2.98\times10^{-2}+(7.89\times10^{-3})\,\text{cRPpostRej}^3+0.43\,\text{igG}+0.71\,b_{45}+0.87\,\text{respiratoryInfection}\,dQ_7$
4	43	0.233	$6.69\times10^{-3}+0.12\,\text{cNIpostRej}-0.30\,\text{pyrexia}+0.66\,\text{respiratoryInfection}+1.10\,b_{45}+0.23\,dR_{53}$
5	46	0.184	$2.56\times10^{-2}+0.10\,\text{cNIpostRej}+0.37\,\text{igG}+$ $0.23\,\text{respiratoryInfection}+0.87\,b_{45}+0.66\,\text{respiratoryInfection}\,dQ_7$
6	46	0.217	$1.29-\frac{0.90}{0.71+\text{candida}+\text{igG}+b_{45}+2\,\text{respiratoryInfection}\,dQ_7}$
7	50	0.187	$-(3.76\times10^{-2})+0.52\,\text{coaglationnecrosis}^2+$ $0.12\,\text{cRPpostRej}+0.43\,\text{igG}+0.61\,b_{45}+0.86\,\text{respiratoryInfection}\,dQ_7$
8	50	0.204	$-(6.99\times10^{-2})+0.13\,\text{cNIpostRej}+0.46\,\text{coaglationnecrosis}+$ $0.18\,\text{denovoDSA}+0.86\,\text{anemia}^2\,\text{igG}+0.42\,\text{respiratoryInfection}$
9	54	0.163	$3.55\times10^{-2}+0.10\,\text{cNIpostRej}+0.37\,\text{igG}-0.19\,\text{pyrexia}+$ $0.37\,\text{respiratoryInfection}+0.87\,b_{45}+0.51\,\text{respiratoryInfection}\,dQ_7$
10	54	0.174	$9.30\times10^{-3}+(1.79\times10^{-3})\,\text{cRPpostRej}^4+0.44\,\text{igG}+$ $0.19\,\text{respiratoryInfection}+0.75\,b_{45}+0.71\,\text{respiratoryInfection}\,dQ_7$
11	54	0.186	$4.87\times10^{-2}-(5.43\times10^{-2})\,\text{banfct}+(1.72\times10^{-3})\,\text{cRPpostRej}^4+$ $0.45\,\text{igG}+0.76\,b_{45}+0.89\,\text{respiratoryInfection}\,dQ_7$
12	54	0.213	$-(2.08\times10^{-2})+0.11\,\text{cRPpostRej}+0.42\,\text{igG}-0.17\,\text{pyrexia}+$ $0.32\,\text{respiratoryInfection}+0.61\,b_{45}+0.54\,\text{respiratoryInfection}\,dQ_7$
13	65	0.110	$-(6.83\times10^{-3})+0.11\,\text{cNIpostRej}+0.50\,\text{coaglationnecrosis}+0.44\,\text{igG}+$ $0.18\,\text{respiratoryInfection}+0.88\,b_{45}+0.31\,\text{mMFatRej}\,\text{respiratoryInfection}\,dQ_7+0.15\,dR_{15}$
14	65	0.120	$-(8.51\times10^{-3})+0.11\,\text{cNIpostRej}+0.51\,\text{coaglationnecrosis}+0.43\,\text{igG}+$ $0.18\,\text{respiratoryInfection}+0.85\,b_{45}+(6.70\times10^{-2})\,dQ_7+0.30\,\text{mMFatRej}\,\text{respiratoryInfection}\,dQ_7$
15	65	0.158	$-(4.32\times10^{-2})+0.53\,\text{coaglationnecrosis}^2+0.12\,\text{cRPpostRej}+0.66\,\text{igG}+$ $0.50\,b_{45}+0.98\,\text{respiratoryInfection}\,dQ_7-(2.70\times10^{-2})\,\text{denovoDSA}^2\,dR_{51}$

◆ Ensembles in ParetoFront

■ **The 8th Cross Validation with Leave-One-Out Method out of 51 turns**

```
The Estimated value: 0.1554, The Observed value: 1
The Prediction: Wrong
Accuracy so far: 75.%   (15.69% completed)
```

◆ **Accuracies until the 8th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 4 min 13 sec

◆ **Error(= Predicted value - Observed value) in the 8th Cross Validation**

◇ **Average Error is 0.4111± 0.3663 until the 8th turn in the LOO method.**

■ The 9th cross-validation out of 51 turns

□ The 9th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日⧈21時 41分 60秒

□ The 9th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日⧈21時 48分 15秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0
−20

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1− R2
0
100
200
300
400
500
600
Model Complexity

,

◆ **1028 models were created**

◇ **Quatiliy Box values are {51., 0.1986} in the 9th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1028 Selected models: 1 (0.09728%)

◆ Inning 0. Complexity: 51. Error: 0.1986 Number of Selected models: 1 (0.09728%)

◆ Inning 1. Complexity: 52. Error: 0.2086 Number of Selected models: 1 (0.09728%)

◆ Inning 2. Complexity: 53. Error: 0.2186 Number of Selected models: 3 (0.2918%)

◆ Inning 3. Complexity: 54. Error: 0.2286 Number of Selected models: 6 (0.5837%)

◆ Inning 4. Complexity: 55. Error: 0.2386 Number of Selected models: 10 (0.9728%)

◆ Inning 5. Complexity: 56. Error: 0.2486 Number of Selected models: 10 (0.9728%)

◆ Inning 6. Complexity: 57. Error: 0.2586 Number of Selected models: 13 (1.265%)

◆ Inning 7. Complexity: 58. Error: 0.2686 Number of Selected models: 16 (1.556%)

◆ Inning 8. Complexity: 59. Error: 0.2786 Number of Selected models: 34 (3.307%)

◆ Inning 9. Complexity: 60. Error: 0.2886 Number of Selected models: 42 (4.086%)

◆ Inning 10. Complexity: 61. Error: 0.2986 Number of Selected models: 48 (4.669%)

◆ Inning 11. Complexity: 62. Error: 0.3086 Number of Selected models: 59 (5.739%)

◆ Inning 12. Complexity: 63. Error: 0.3186 Number of Selected models: 73 (7.101%)

◆ Inning 13. Complexity: 64. Error: 0.3286 Number of Selected models: 81 (7.879%)

◆ Inning 14. Complexity: 65. Error: 0.3386 Number of Selected models: 97 (9.436%)

- **97 interesting models were selected**
  - **Quatiliy Box values are {65., 0.338585}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, pyrexia, igG, wBCpeakover5}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.324	$3.60\times10^{-2}+0.93\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.92\,b_{45}+(1.99\times10^{-2})\,\text{wBCpeakover}_5$
2	35	0.326	$6.16\times10^{-2}+0.48\,\text{igG}-0.38\,\text{pyrexia}+0.67\,\text{respiratoryInfection}+0.70\,b_{45}$
3	35	0.333	$3.46\times10^{-2}+0.70\,\text{igG}-0.38\,\text{pyrexia}+0.63\,\text{respiratoryInfection}+(1.83\times10^{-2})\,\text{wBCpeakover}_5$
4	38	0.331	$3.41\times10^{-2}+0.12\,\text{cNIpostRej}+0.51\,\text{respiratoryInfection}+0.45\,\text{allergy}\,\text{respiratoryInfection}+1.06\,b_{45}$
5	38	0.337	$9.51\times10^{-2}+(9.25\times10^{-2})\,\text{cNIpostRej}-(9.51\times10^{-2})\,\text{regraft}+0.90\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.98\,b_{45}$
6	41	0.270	$-(5.93\times10^{-2})+0.14\,\text{cRPpostRej}\,\text{hLADRmm}^2+0.27\,\text{respiratoryInfection}+0.67\,\text{respiratoryInfection}\,dQ_7{}^2$
7	43	0.218	$4.33\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.83\,b_{45}$
8	43	0.259	$-(1.01\times10^{-2})-0.38\,\text{pyrexia}+0.69\,\text{respiratoryInfection}+0.97\,b_{45}+0.25\,dR_{15}+(2.02\times10^{-2})\,\text{wBCpeakover}_5$
9	43	0.273	$-(2.98\times10^{-2})+(9.09\times10^{-2})\,\text{banfah}-0.46\,\text{pyrexia}+0.74\,\text{respiratoryInfection}+0.94\,b_{45}+(2.17\times10^{-2})\,\text{wBCpeakover}_5$
10	45	0.287	$4.42\times10^{-2}+0.46\,\sqrt{\text{igG}+\text{respiratoryInfection}+b_{62}}\,(\text{coaglationnecrosis}+\text{cRPpostRej}+dQ_7)$
11	47	0.301	$-(4.68\times10^{-3})+0.64\,\text{igG}+0.55\,\text{respiratoryInfection}+0.53\,b_{45}+0.31\,b_{61}+(5.07\times10^{-4})\,\text{wBCpeakover}_5{}^2$
12	51	0.199	$-(5.99\times10^{-2})+0.12\,\text{banfah}+0.53\,\text{igG}-0.44\,\text{pyrexia}+0.70\,\text{respiratoryInfection}+0.69\,b_{45}+(2.19\times10^{-2})\,\text{wBCpeakover}_5$
13	51	0.211	$5.15\times10^{-2}+0.11\,\text{cNIpostRej}+0.46\,\text{igG}-0.36\,\text{pyrexia}+0.71\,\text{respiratoryInfection}+0.89\,b_{45}-0.17\,b_{51}$
14	51	0.214	$2.95\times10^{-2}+(8.11\times10^{-2})\,\text{cNIpostRej}+0.44\,\text{igG}-0.37\,\text{pyrexia}+0.71\,\text{respiratoryInfection}+0.81\,b_{45}+(6.52\times10^{-3})\,\text{wBCpeakover}_5$
15	51	0.250	$-(5.62\times10^{-2})+0.11\,\text{banfah}+0.77\,\text{igG}-0.43\,\text{pyrexia}+0.67\,\text{respiratoryInfection}+0.42\,a_{34}+(2.19\times10^{-2})\,\text{wBCpeakover}_5$

◆ Ensembles in ParetoFront

■ **The 9th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.07227, The Observed value: 0

The Prediction: Right

Accuracy so far: 77.78% (17.65% completed)

◆ **Accuracies until the 9th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 4 min 7 sec

◆ **Error(= Predicted value - Observed value) in the 9th Cross Validation**

◇ **Average Error is 0.3734± 0.3608 until the 9th turn in the LOO method.**

■ The 10th cross-validation out of 51 turns

□ The 10th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日⧆21時 48分 18秒

□ The 10th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日⧆21時 54分 58秒

◆ Monitors Plot

0.01
0
200
400
600
800
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
60
50
40
30
20
10
0
−10

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
100
200
300
400
500
Model Complexity

,

◆ **914 models were created**

◇ **Quatiliy Box values are {50., 0.1498} in the 10th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 914 Selected models: 1 (0.1094%)

◆ Inning 0. Complexity: 50. Error: 0.1498 Number of Selected models: 1 (0.1094%)

◆ Inning 1. Complexity: 51. Error: 0.1598 Number of Selected models: 1 (0.1094%)

◆ Inning 2. Complexity: 52. Error: 0.1698 Number of Selected models: 1 (0.1094%)

◆ Inning 3. Complexity: 53. Error: 0.1798 Number of Selected models: 1 (0.1094%)

◆ Inning 4. Complexity: 54. Error: 0.1898 Number of Selected models: 1 (0.1094%)

◆ Inning 5. Complexity: 55. Error: 0.1998 Number of Selected models: 2 (0.2188%)

◆ Inning 6. Complexity: 56. Error: 0.2098 Number of Selected models: 3 (0.3282%)

◆ Inning 7. Complexity: 57. Error: 0.2198 Number of Selected models: 7 (0.7659%)

◆ Inning 8. Complexity: 58. Error: 0.2298 Number of Selected models: 9 (0.9847%)

◆ Inning 9. Complexity: 59. Error: 0.2398 Number of Selected models: 9 (0.9847%)

◆ Inning 10. Complexity: 60. Error: 0.2498 Number of Selected models: 15 (1.641%)

◆ Inning 11. Complexity: 61. Error: 0.2598 Number of Selected models: 22 (2.407%)

◆ Inning 12. Complexity: 62. Error: 0.2698 Number of Selected models: 32 (3.501%)

◆ Inning 13. Complexity: 63. Error: 0.2798 Number of Selected models: 34 (3.72%)

◆ Inning 14. Complexity: 64. Error: 0.2898 Number of Selected models: 44 (4.814%)

- Inning 15. Complexity: 65. Error: 0.2998 Number of Selected models: 48 (5.252%)
- Inning 16. Complexity: 66. Error: 0.3098 Number of Selected models: 69 (7.549%)
- Inning 17. Complexity: 67. Error: 0.3198 Number of Selected models: 75 (8.206%)

- **75 interesting models were selected**
  - **Quatiliy Box values are {67., 0.319765}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, pyrexia, cNIpostRej, igG, b45}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	34	0.288	$2.62\times10^{-2}+0.48\,(c4d+type2DM)\,(heartDisease+respiratoryInfection+b_{45})$
2	34	0.309	$3.38\times10^{-2}+0.44\,(heartDisease+igG+respiratoryInfection)\,(c4d+type2DM)$
3	38	0.301	$1.21\times10^{-2}+0.49\,banfcv\,candida+0.58\,igG+0.53\,respiratoryInfection+0.70\,b_{45}$
4	38	0.308	$-(1.79\times10^{-2})+0.13\,cNIpostRej+0.59\,respiratoryInfection+1.12\,a_{25}\,b_{13}+0.28\,dR_{53}$
5	42	0.258	$6.36\times10^{-2}+0.65\,igG-0.40\,pyrexia+0.71\,respiratoryInfection+0.14\,cNIpostRej\,surgery^2$
6	43	0.217	$4.51\times10^{-2}+0.11\,cNIpostRej+0.43\,igG-0.36\,pyrexia+0.71\,respiratoryInfection+0.83\,b_{45}$
7	43	0.245	$3.99\times10^{-2}+0.10\,cNIpostRej+0.58\,igG-$ $0.34\,pyrexia+0.68\,respiratoryInfection+0.22\,dSAandHSAclass_1$
8	46	0.208	$4.63\times10^{-2}+0.11\,cNIpostRej+0.47\,igG-0.36\,pyrexia+0.71\,respiratoryInfection-0.98\,cNIpostRej\,b_{13}$
9	46	0.239	$3.03\times10^{-2}+(2.55\times10^{-2})\,cNIpostRej\,cRPpostRej+$ $0.62\,igG-0.35\,pyrexia+0.66\,respiratoryInfection+0.20\,dSAandHSAclass_1$
10	47	0.265	$-(6.70\times10^{-2})+0.16\,cRPpostRej+0.29\,gERD^3+0.69\,igG-0.39\,pyrexia+0.67\,respiratoryInfection$
11	49	0.195	$4.09\times10^{-2}-0.42\,pyrexia+0.78\,respiratoryInfection+$ $0.15\,cNIpostRej\,(igG+surgery)+0.51\,a_{25}\,wBCpeakover_5$
12	50	0.150	$3.62\times10^{-2}+0.41\,igG-0.41\,pyrexia+0.76\,respiratoryInfection+0.14\,cNIpostRej\,surgery^2+0.76\,b_{45}$
13	50	0.212	$3.26\times10^{-2}+(4.29\times10^{-2})\,candida\,cRPpostRej^2+$ $0.50\,igG-0.36\,pyrexia+0.67\,respiratoryInfection+0.72\,b_{45}$
14	54	0.265	$1.76\times10^{-2}+0.41\,coaglationnecrosis+0.28\,heartDisease+$ $0.38\,igG+0.15\,respiratoryInfection+0.79\,b_{45}+0.58\,respiratoryInfection\,dQ_8$
15	57	0.218	$4.03\times10^{-2}-0.44\,pyrexia+0.82\,respiratoryInfection+$ $0.15\,cNIpostRej\,(cGN+surgery)\,(surgery+type2DM)+0.63\,b_{13}$

◆ Ensembles in ParetoFront

■ **The 10th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.1028, The Observed value: 0

The Prediction: Right

Accuracy so far: 80.% (19.61% completed)

◆ **Accuracies until the 10th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 4 min 0 sec

◆ **Error (= Predicted value - Observed value) in the 10th Cross Validation**

◇ **Average Error is 0.3464±0.3507 until the 10th turn in the LOO method.**

■ The 11th cross-validation out of 51 turns

□ The 11th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日 21時 55分 1秒

□ The 11th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日 22時 1分 13秒

◆ Monitors Plot

0.01
0
200
400
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
60
50
40
30
20
10
0
−10

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1− R2
0
50
100
150
200
250
300
350
Model Complexity

,

◆ **999 models were created**

◇ **Quatiliy Box values are {46., 0.1632} in the 11th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 999 Selected models: 1 (0.1001%)

◆ Inning 0. Complexity: 46. Error: 0.1632 Number of Selected models: 1 (0.1001%)

◆ Inning 1. Complexity: 47. Error: 0.1732 Number of Selected models: 1 (0.1001%)

◆ Inning 2. Complexity: 48. Error: 0.1832 Number of Selected models: 2 (0.2002%)

◆ Inning 3. Complexity: 49. Error: 0.1932 Number of Selected models: 2 (0.2002%)

◆ Inning 4. Complexity: 50. Error: 0.2032 Number of Selected models: 4 (0.4004%)

◆ Inning 5. Complexity: 51. Error: 0.2132 Number of Selected models: 12 (1.201%)

◆ Inning 6. Complexity: 52. Error: 0.2232 Number of Selected models: 13 (1.301%)

◆ Inning 7. Complexity: 53. Error: 0.2332 Number of Selected models: 16 (1.602%)

◆ Inning 8. Complexity: 54. Error: 0.2432 Number of Selected models: 27 (2.703%)

◆ Inning 9. Complexity: 55. Error: 0.2532 Number of Selected models: 34 (3.403%)

◆ Inning 10. Complexity: 56. Error: 0.2632 Number of Selected models: 37 (3.704%)

◆ Inning 11. Complexity: 57. Error: 0.2732 Number of Selected models: 45 (4.505%)

◆ Inning 12. Complexity: 58. Error: 0.2832 Number of Selected models: 56 (5.606%)

◆ Inning 13. Complexity: 59. Error: 0.2932 Number of Selected models: 68 (6.807%)

◆ Inning 14. Complexity: 60. Error: 0.3032 Number of Selected models: 77 (7.708%)

- Inning 15. Complexity: 61. Error: 0.3132 Number of Selected models: 84 (8.408%)

- **84 interesting models were selected**
  - **Quatiliy Box values are {61., 0.313187}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, pyrexia, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.276	$1.68\times10^{-2}-0.37\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+0.94\,b_{45}+(1.95\times10^{-2})\,\text{wBCpeakover}_5$
2	35	0.308	$5.39\times10^{-2}-(8.95\times10^{-2})\,\text{banfci}+0.12\,\text{cNIpostRej}+0.75\,\text{respiratoryInfection}+1.14\,b_{45}$
3	38	0.209	$3.28\times10^{-2}+0.12\,\text{cNIpostRej}+0.85\,\text{respiratoryInfection}-$ $0.50\,\text{pyrexia upperRespiratoryInfection}+1.07\,b_{45}$
4	38	0.276	$4.86\times10^{-2}-0.36\,\text{pyrexia}+0.75\,\sqrt{\text{igG}+\text{respiratoryInfection}+b_{45}}$
5	38	0.301	$5.49\times10^{-2}+(9.12\times10^{-2})\,\text{cNIpostRej}+0.69\,\text{igG}+$ $0.74\,\text{respiratoryInfection}-0.45\,\text{pyrexia upperRespiratoryInfection}$
6	43	0.199	$4.00\times10^{-2}+0.11\,\text{cNIpostRej}+0.42\,\text{igG}-0.32\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+0.84\,b_{45}$
7	43	0.218	$4.45\times10^{-3}+0.46\,\text{igG}-0.35\,\text{pyrexia}+0.71\,\text{respiratoryInfection}+0.73\,b_{45}+(1.91\times10^{-2})\,\text{wBCpeakover}_5$
8	43	0.225	$6.51\times10^{-2}+0.12\,\text{cNIpostRej}-0.31\,\text{pyrexia}+0.82\,\text{respiratoryInfection}-0.20\,\text{urology}+1.03\,b_{45}$
9	43	0.242	$3.12\times10^{-2}+0.11\,\text{cNIpostRej}+0.45\,\text{igG}-0.35\,\text{polyp}+0.69\,\text{respiratoryInfection}+0.84\,b_{45}$
10	46	0.163	$4.02\times10^{-2}+0.10\,\text{cNIpostRej}+0.43\,\text{igG}+$ $0.86\,\text{respiratoryInfection}-1.00\,\text{upperRespiratoryInfection wBCpreRej}+0.93\,b_{45}$
11	46	0.178	$-(3.00\times10^{-2})+0.12\,\text{cNIpostRej}+0.89\,\text{respiratoryInfection}-$ $0.95\,\text{upperRespiratoryInfection wBCpreRej}+0.16\,\text{antiHLAclass}_2+1.06\,b_{45}$
12	46	0.185	$5.69\times10^{-2}-(9.98\times10^{-2})\,\text{banfci}+0.12\,\text{cNIpostRej}+$ $0.91\,\text{respiratoryInfection}-0.51\,\text{pyrexia upperRespiratoryInfection}+1.14\,b_{45}$
13	47	0.196	$3.33\times10^{-2}+0.11\,\text{cNIpostRej}+0.42\,\text{igG}-0.19\,\text{pyrexia}^2+0.75\,\text{respiratoryInfection}+0.85\,b_{45}$
14	51	0.242	$5.16\times10^{-2}+0.10\,\text{cNIpostRej}+0.52\,\text{igG}-0.29\,\text{pyrexia}+0.76\,\text{respiratoryInfection}-0.16\,\text{urology}+0.50\,b_{63}$
15	54	0.130	$5.13\times10^{-2}-0.12\,\text{banfci}+0.11\,\text{cNIpostRej}+0.46\,\text{igG}+$ $0.88\,\text{respiratoryInfection}-0.48\,\text{pyrexia upperRespiratoryInfection}+0.93\,b_{45}$

◆ Ensembles in ParetoFront

■ **The 11th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.4966, The Observed value: 0

The Prediction: Right

Accuracy so far: 81.82% (21.57% completed)

◆ **Accuracies until the 11th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 3 min 54 sec

◆ **Error(= Predicted value - Observed value) in the 11th Cross Validation**

◇ **Average Error is 0.36±0.3358 until the 11th turn in the LOO method.**

■ The 12th cross-validation out of 51 turns

□ The 12th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日22時 1分 16秒

□ The 12th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日22時 7分 28秒

◆ Monitors Plot

0.01
0
200
400
600
800
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0
−20

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1− R2
0
100
200
300
400
Model Complexity

,

◆ **954 models were created**

◇ **Quatiliy Box values are {44., 0.1845} in the 12th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 954 Selected models: 1 (0.1048%)

◆ Inning 0. Complexity: 44. Error: 0.1845 Number of Selected models: 1 (0.1048%)

◆ Inning 1. Complexity: 45. Error: 0.1945 Number of Selected models: 2 (0.2096%)

◆ Inning 2. Complexity: 46. Error: 0.2045 Number of Selected models: 2 (0.2096%)

◆ Inning 3. Complexity: 47. Error: 0.2145 Number of Selected models: 5 (0.5241%)

◆ Inning 4. Complexity: 48. Error: 0.2245 Number of Selected models: 5 (0.5241%)

◆ Inning 5. Complexity: 49. Error: 0.2345 Number of Selected models: 8 (0.8386%)

◆ Inning 6. Complexity: 50. Error: 0.2445 Number of Selected models: 8 (0.8386%)

◆ Inning 7. Complexity: 51. Error: 0.2545 Number of Selected models: 10 (1.048%)

◆ Inning 8. Complexity: 52. Error: 0.2645 Number of Selected models: 19 (1.992%)

◆ Inning 9. Complexity: 53. Error: 0.2745 Number of Selected models: 35 (3.669%)

◆ Inning 10. Complexity: 54. Error: 0.2845 Number of Selected models: 38 (3.983%)

◆ Inning 11. Complexity: 55. Error: 0.2945 Number of Selected models: 53 (5.556%)

◆ Inning 12. Complexity: 56. Error: 0.3045 Number of Selected models: 63 (6.604%)

◆ Inning 13. Complexity: 57. Error: 0.3145 Number of Selected models: 80 (8.386%)

◆ **80 interesting models were selected**

  ◇ **Quatiliy Box values are {57., 0.31449}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, igG, hLAmm}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.299	$5.44\times10^{-2}+0.12\,\text{cNIpostRej}+(9.61\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.05\,b_{45}$
2	31	0.314	$1.39-\frac{1.39}{1+\text{candida}+\text{igG}+\text{respiratoryInfection}+b_{45}}$
3	34	0.277	$-(4.41\times10^{-2})+(2.34\times10^{-3})\,\text{cRPpostRej}\,\text{hLAmm}^3+0.59\,\text{igG}+0.61\,\text{respiratoryInfection}$
4	35	0.269	$5.43\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+1.04\,b_{45}$
5	38	0.194	$3.30\times10^{-2}+0.12\,\text{cNIpostRej}+0.87\,\text{respiratoryInfection}-0.86\,\text{pyrexia}\,\text{respiratoryInfection}+1.07\,b_{45}$
6	40	0.210	$-(3.17\times10^{-2})+(2.68\times10^{-3})\,\text{cRPpostRej}\,\text{hLAmm}^3+$ $1.13\,\text{respiratoryInfection}-(3.72\times10^{-2})\,\text{banfi}\,\text{maxWBC}\,\text{respiratoryInfection}$
7	41	0.226	$3.43\times10^{-2}+0.11\,\text{cNIpostRej}+1.09\,\text{respiratoryInfection}-0.44\,\text{banfi}\,\text{respiratoryInfection}+0.19\,\text{hLAmm}\,b_{45}$
8	42	0.194	$3.30\times10^{-2}+0.12\,\text{cNIpostRej}+0.87\,\text{respiratoryInfection}-0.86\,\text{pyrexia}\,\text{respiratoryInfection}^2+1.07\,b_{45}$
9	43	0.256	$6.27\times10^{-2}+0.11\,\text{cNIpostRej}+0.51\,\text{igG}-(6.88\times10^{-2})\,\text{lymphinvasion}+0.67\,\text{respiratoryInfection}+0.77\,b_{45}$
10	44	0.184	$3.50\times10^{-2}+0.11\,\text{cNIpostRej}+1.14\,\text{respiratoryInfection}-$ $(3.45\times10^{-2})\,\text{banfi}\,\text{maxWBC}\,\text{respiratoryInfection}+0.19\,\text{hLAmm}\,b_{45}$
11	46	0.261	$-(1.64\times10^{-3})+(9.71\times10^{-2})\,\text{cNIpostRej}+$ $(3.80\times10^{-2})\,\text{cRPpostRej}+0.50\,\text{igG}+0.66\,\text{respiratoryInfection}+0.14\,\text{hLAmm}\,b_{45}$
12	48	0.199	$3.83\times10^{-2}+0.11\,\text{cNIpostRej}+1.14\,\text{respiratoryInfection}-$ $(3.45\times10^{-2})\,\text{banfi}\,\text{maxWBC}\,\text{respiratoryInfection}+(5.78\times10^{-3})\,\text{hLAmm}^3\,b_{45}$
13	50	0.236	$-(1.52\times10^{-2})-(1.90\times10^{-2})\,\text{cRPpostRej}+$ $(2.37\times10^{-3})\,\text{cRPpostRej}\,\text{hLAmm}^3+0.56\,\text{igG}-0.32\,\text{pyrexia}+0.66\,\text{respiratoryInfection}$
14	51	0.178	$3.25\times10^{-2}+0.12\,\text{cNIpostRej}+1.05\,\text{respiratoryInfection}-$ $0.81\left(\frac{1}{\text{inflammationdatefirst}}+\text{pyrexia}\right)\text{respiratoryInfection}+1.07\,b_{45}$
15	52	0.214	$-(8.75\times10^{-2})+0.16\,\text{cRPpostRej}+0.24\,\text{twinpeak}+0.56\,(\text{c4d}+\text{type2DM})\,(-\text{respiratoryInfection}+c_3)^2$

◆ Ensembles in ParetoFront

■ **The 12th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: -0.2212, The Observed value: 0

The Prediction: Right

Accuracy so far: 83.33% (23.53% completed)

◆ **Accuracies until the 12th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 3 min 48 sec

◆ **Error(= Predicted value - Observed value) in the 12th Cross Validation**

◇ **Average Error is 0.3484±0.3227 until the 12th turn in the LOO method.**

■ The 13th cross-validation out of 51 turns

□ The 13th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日⧆22時 7分 31秒

□ The 13th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日⧆22時 14分 12秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
−200
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
100
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
200
400
600
800
Model Complexity

,

◆ **1044 models were created**

◇ **Quatiliy Box values are {46., 0.1753} in the 13th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1044 Selected models: 1 (0.09579%)

◆ Inning 0. Complexity: 46. Error: 0.1753 Number of Selected models: 1 (0.09579%)

◆ Inning 1. Complexity: 47. Error: 0.1853 Number of Selected models: 2 (0.1916%)

◆ Inning 2. Complexity: 48. Error: 0.1953 Number of Selected models: 4 (0.3831%)

◆ Inning 3. Complexity: 49. Error: 0.2053 Number of Selected models: 6 (0.5747%)

◆ Inning 4. Complexity: 50. Error: 0.2153 Number of Selected models: 10 (0.9579%)

◆ Inning 5. Complexity: 51. Error: 0.2253 Number of Selected models: 20 (1.916%)

◆ Inning 6. Complexity: 52. Error: 0.2353 Number of Selected models: 27 (2.586%)

◆ Inning 7. Complexity: 53. Error: 0.2453 Number of Selected models: 30 (2.874%)

◆ Inning 8. Complexity: 54. Error: 0.2553 Number of Selected models: 45 (4.31%)

◆ Inning 9. Complexity: 55. Error: 0.2653 Number of Selected models: 47 (4.502%)

◆ Inning 10. Complexity: 56. Error: 0.2753 Number of Selected models: 57 (5.46%)

◆ Inning 11. Complexity: 57. Error: 0.2853 Number of Selected models: 61 (5.843%)

◆ Inning 12. Complexity: 58. Error: 0.2953 Number of Selected models: 73 (6.992%)

◆ Inning 13. Complexity: 59. Error: 0.3053 Number of Selected models: 87 (8.333%)

◆ **87 interesting models were selected**

  ◇ **Quatiliy Box values are {59., 0.305254}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, pyrexia, cNIpostRej, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	34	0.295	$2.78\times10^{-2}+0.12\,\text{cNIpostRej}+\frac{8.94\,\text{respiratoryInfection}}{\text{maxWBC}}+1.07\,b_{45}$
2	35	0.305	$-(2.99\times10^{-2})+(1.61\times10^{-2})\,\text{hDperiod}-0.48\,\text{pyrexia}+0.78\,\text{respiratoryInfection}+1.01\,b_{45}$
3	38	0.221	$3.62\times10^{-2}+0.12\,\text{cNIpostRej}-1.95\,\text{cRPpostRej}\,\text{pyrexia}+0.84\,\text{respiratoryInfection}+1.06\,b_{45}$
4	38	0.242	$-(2.26\times10^{-3})-2.10\,\text{cRPpostRej}\,\text{pyrexia}+$ $0.81\,\text{respiratoryInfection}+0.96\,b_{45}+(2.05\times10^{-2})\,\text{wBCpeakover}_5$
5	38	0.286	$4.36\times10^{-2}+0.47\,\text{igG}-1.88\,\text{cRPpostRej}\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+0.72\,b_{45}$
6	38	0.293	$-(4.47\times10^{-2})+0.16\,\text{cRPpostRej}+0.72\,\text{igG}+$ $1.25\,\text{respiratoryInfection}-(4.70\times10^{-2})\,\text{maxWBC}\,\text{respiratoryInfection}$
7	42	0.245	$-(2.60\times10^{-2})+0.56\,\text{igG}+\frac{8.19\,\text{respiratoryInfection}}{\text{maxWBC}}+0.71\,b_{45}+(1.87\times10^{-2})\,\text{wBCpeakover}_5$
8	42	0.267	$3.51\times10^{-2}+0.11\,\text{cNIpostRej}+0.36\,\text{respiratoryInfection}+$ $0.60\,\text{respiratoryInfection}\,\text{antiHLAclass}_2{}^2+1.06\,b_{45}$
9	43	0.203	$3.51\times10^{-2}+0.11\,\text{cNIpostRej}+0.42\,\text{igG}-0.42\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+0.84\,b_{45}$
10	46	0.175	$2.60\times10^{-2}+0.11\,\text{cNIpostRej}+0.41\,\text{igG}-1.83\,\text{cRPpostRej}\,\text{pyrexia}+0.79\,\text{respiratoryInfection}+0.86\,b_{45}$
11	46	0.184	$3.04\times10^{-2}+0.11\,\text{cNIpostRej}+0.41\,\text{igG}-0.24\,\text{banfi}\,\text{pyrexia}+0.78\,\text{respiratoryInfection}+0.85\,b_{45}$
12	46	0.186	$2.89\times10^{-2}+0.11\,\text{cNIpostRej}+0.61\,\text{cNIpostRej}\,\text{igG}-0.45\,\text{pyrexia}+0.81\,\text{respiratoryInfection}+1.28\,b_{45}$
13	46	0.187	$3.00\times10^{-2}+0.12\,\text{cNIpostRej}\,\text{diarrhea}+0.45\,\text{igG}-0.42\,\text{pyrexia}+0.74\,\text{respiratoryInfection}+0.79\,b_{45}$
14	46	0.193	$-(4.30\times10^{-2})+0.13\,\text{cNIpostRej}+0.82\,\text{respiratoryInfection}-$ $0.49\,\text{pyrexia}\,\text{respiratoryInfection}+0.15\,\text{antiHLAclass}_2+1.00\,b_{45}$
15	46	0.203	$3.51\times10^{-2}+0.11\,\text{cNIpostRej}+0.42\,\text{diarrhea}\,\text{igG}-0.42\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+0.84\,b_{45}$

◆ Ensembles in ParetoFront

■ The 13th Cross Validation with Leave-One-Out Method out of 51 turns

The Estimated value: -0.2977, The Observed value: 0

The Prediction: Right

Accuracy so far: 84.62% (25.49% completed)

◆ **Accuracies until the 13th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 3 min 41 sec

◆ **Error(= Predicted value - Observed value) in the 13th Cross Validation**

◇ **Average Error is 0.3445±0.3093 until the 13th turn in the LOO method.**

■ The 14th cross-validation out of 51 turns

□ The 14th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日 22時 14分 16秒

□ The 14th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日 22時 20分 31秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1− R2
0
100
200
300
400
Model Complexity

,

◆ **1013 models were created**

◇ **Quatiliy Box values are {46., 0.1549} in the 14th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1013 Selected models: 1 (0.09872%)

◆ Inning 0. Complexity: 46. Error: 0.1549 Number of Selected models: 1 (0.09872%)

◆ Inning 1. Complexity: 47. Error: 0.1649 Number of Selected models: 1 (0.09872%)

◆ Inning 2. Complexity: 48. Error: 0.1749 Number of Selected models: 1 (0.09872%)

◆ Inning 3. Complexity: 49. Error: 0.1849 Number of Selected models: 2 (0.1974%)

◆ Inning 4. Complexity: 50. Error: 0.1949 Number of Selected models: 6 (0.5923%)

◆ Inning 5. Complexity: 51. Error: 0.2049 Number of Selected models: 6 (0.5923%)

◆ Inning 6. Complexity: 52. Error: 0.2149 Number of Selected models: 10 (0.9872%)

◆ Inning 7. Complexity: 53. Error: 0.2249 Number of Selected models: 15 (1.481%)

◆ Inning 8. Complexity: 54. Error: 0.2349 Number of Selected models: 37 (3.653%)

◆ Inning 9. Complexity: 55. Error: 0.2449 Number of Selected models: 44 (4.344%)

◆ Inning 10. Complexity: 56. Error: 0.2549 Number of Selected models: 50 (4.936%)

◆ Inning 11. Complexity: 57. Error: 0.2649 Number of Selected models: 63 (6.219%)

◆ Inning 12. Complexity: 58. Error: 0.2749 Number of Selected models: 76 (7.502%)

◆ Inning 13. Complexity: 59. Error: 0.2849 Number of Selected models: 91 (8.983%)

◆ **91 interesting models were selected**

  ◇ **Quatiliy Box values are {59., 0.28487}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, igG, pyrexia}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.284	$5.35\times10^{-2}+0.11\,\text{cNIpostRej}-0.38\,\text{pyrexia}+0.73\,\text{respiratoryInfection}+1.04\,b_{45}$
2	38	0.216	$-(2.30\times10^{-3})+0.12\,\text{cNIpostRej}+0.10\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.11\,b_{45}+0.40\,dR_{15}$
3	38	0.236	$4.34\times10^{-2}-0.41\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+0.15\,\text{cNIpostRej}\,\text{surgery}+0.96\,b_{45}$
4	38	0.279	$-(4.08\times10^{-2})+0.12\,\text{cNIpostRej}+0.15\,\text{denovoDSA}+0.50\,\text{respiratoryInfection}+0.86\,\text{igG}\,c_3$
5	41	0.195	$3.12\times10^{-2}+0.11\,\text{cNIpostRej}+$ $(7.11\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.06\,b_{45}+0.60\,\text{respiratoryInfection}\,dR_{53}$
6	43	0.278	$-(1.91\times10^{-2})+0.32\,\text{gERD}+0.75\,\text{igG}-0.43\,\text{pyrexia}+$ $0.64\,\text{respiratoryInfection}+(1.99\times10^{-2})\,\text{wBCpeakover}_5$
7	46	0.155	$-(9.50\times10^{-3})+0.12\,\text{cNIpostRej}+0.46\,\text{igG}+$ $(9.74\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.88\,b_{45}+0.34\,dR_{15}$
8	46	0.188	$-(5.01\times10^{-2})+0.50\,\text{igG}+(9.04\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+$ $0.76\,b_{45}+0.35\,dR_{15}+(1.95\times10^{-2})\,\text{wBCpeakover}_5$
9	46	0.210	$3.79\times10^{-2}+0.11\,\text{cNIpostRej}+0.58\,\text{igG}-0.34\,\text{pyrexia}+0.67\,\text{respiratoryInfection}+0.21\,\text{denovoDSA}\,b_{45}$
10	46	0.219	$3.57\times10^{-2}+0.11\,\text{cNIpostRej}+0.44\,\text{igG}+$ $0.70\,\text{respiratoryInfection}-(1.37\times10^{-2})\,\text{pyrexia}\,\text{wBCpeakover9postRej}+0.84\,b_{45}$
11	47	0.231	$3.92\times10^{-2}+0.10\,\text{cNIpostRej}+0.69\,\text{igG}-0.33\,\text{pyrexia}+$ $0.65\,\text{respiratoryInfection}+(6.49\times10^{-2})\,\text{dSAandHSAclass}_1{}^2$
12	49	0.146	$2.02\times10^{-2}+0.11\,\text{cNIpostRej}+0.42\,\text{igG}+$ $(7.36\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.86\,b_{45}+0.49\,\text{respiratoryInfection}\,dR_{53}$
13	49	0.183	$3.05\times10^{-2}-0.40\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+0.14\,\text{cNIpostRej}\,\text{surgery}+0.70\,b_{45}+0.54\,\text{igG}\,c_3$
14	49	0.195	$1.75\times10^{-2}+0.11\,\text{cNIpostRej}-0.31\,\text{pyrexia}+$ $0.65\,\text{respiratoryInfection}+1.08\,b_{45}+(4.97\times10^{-2})\,\text{diarrhea}\,\text{wBCinUrine}\,dR_{53}$
15	49	0.212	$3.39\times10^{-2}+0.11\,\text{cNIpostRej}+0.64\,\text{respiratoryInfection}-$ $0.42\,\text{pyrexia}\,\text{respiratoryInfection}+1.06\,b_{45}+0.32\,\text{respiratoryInfection}\,dR_{53}$

◆ Ensembles in ParetoFront

■ The 14th Cross Validation with Leave-One-Out Method out of 51 turns

The Estimated value: 0.8114, The Observed value: 1

The Prediction: Right

Accuracy so far: 85.71% (27.45% completed)

◆ Accuracies until the 14th turn in the Leave-One-Out Cross Validation out of 51 turns

◇ Estimated Remaining time: `` hour `` min `` sec hr 3 min 35 sec

◆ Error(= Predicted value - Observed value) in the 14th Cross Validation

◇ Average Error is 0.3334± 0.3 until the 14th turn in the LOO method.

■ The 15th cross-validation out of 51 turns

□ The 15th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日22時 20分 35秒

□ The 15th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日22時 26分 47秒

◆ Monitors Plot

0.01
0
200
400
600
800
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
100
80
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
50
100
150
200
250
Model Complexity

,

◆ **925 models were created**

◇ **Quatiliy Box values are {46., 0.1753} in the 15th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 925 Selected models: 1 (0.1081%)

◆ Inning 0. Complexity: 46. Error: 0.1753 Number of Selected models: 1 (0.1081%)

◆ Inning 1. Complexity: 47. Error: 0.1853 Number of Selected models: 1 (0.1081%)

◆ Inning 2. Complexity: 48. Error: 0.1953 Number of Selected models: 1 (0.1081%)

◆ Inning 3. Complexity: 49. Error: 0.2053 Number of Selected models: 2 (0.2162%)

◆ Inning 4. Complexity: 50. Error: 0.2153 Number of Selected models: 3 (0.3243%)

◆ Inning 5. Complexity: 51. Error: 0.2253 Number of Selected models: 11 (1.189%)

◆ Inning 6. Complexity: 52. Error: 0.2353 Number of Selected models: 14 (1.514%)

◆ Inning 7. Complexity: 53. Error: 0.2453 Number of Selected models: 14 (1.514%)

◆ Inning 8. Complexity: 54. Error: 0.2553 Number of Selected models: 26 (2.811%)

◆ Inning 9. Complexity: 55. Error: 0.2653 Number of Selected models: 33 (3.568%)

◆ Inning 10. Complexity: 56. Error: 0.2753 Number of Selected models: 40 (4.324%)

◆ Inning 11. Complexity: 57. Error: 0.2853 Number of Selected models: 40 (4.324%)

◆ Inning 12. Complexity: 58. Error: 0.2953 Number of Selected models: 46 (4.973%)

◆ Inning 13. Complexity: 59. Error: 0.3053 Number of Selected models: 57 (6.162%)

◆ Inning 14. Complexity: 60. Error: 0.3153 Number of Selected models: 61 (6.595%)

- Inning 15. Complexity: 61. Error: 0.3253 Number of Selected models: 70 (7.568%)
- Inning 16. Complexity: 62. Error: 0.3353 Number of Selected models: 83 (8.973%)

- **83 interesting models were selected**
  - **Quatiliy Box values are {62., 0.335333}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, pyrexia, cNIpostRej, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.324	$3.56\times10^{-2}+0.92\,b_{45}+0.93\,\text{respiratoryInfection}\,dQ_8+(1.99\times10^{-2})\,\text{wBCpeakover}_5$
2	35	0.307	$-(3.06\times10^{-2})+0.13\,\text{cNIpostRej}+0.59\,\text{respiratoryInfection}+1.01\,b_{45}+0.25\,dQ_7$
3	38	0.222	$3.20\times10^{-2}+0.12\,\text{cNIpostRej}+0.84\,\text{respiratoryInfection}-0.55\,\text{pyrexia respiratoryInfection}+1.07\,b_{45}$
4	38	0.290	$4.14\times10^{-2}+0.47\,\text{igG}+0.74\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.72\,b_{45}$
5	38	0.311	$5.49\times10^{-2}+(9.05\times10^{-2})\,\text{cNIpostRej}+0.69\,\text{igG}+$ $0.72\,\text{respiratoryInfection}-0.50\,\text{pyrexia respiratoryInfection}$
6	43	0.218	$4.18\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.83\,b_{45}$
7	43	0.246	$7.09\times10^{-2}+0.14\,\text{cNIpostRej}-0.25\,\text{enterococcusfaecalis}-$ $0.40\,\text{pyrexia}+0.77\,\text{respiratoryInfection}+1.04\,b_{45}$
8	46	0.175	$2.21\times10^{-2}+0.11\,\text{cNIpostRej}+0.41\,\text{igG}+$ $0.80\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.87\,b_{45}$
9	46	0.204	$3.29\times10^{-2}+0.11\,\text{cNIpostRej}+1.03\,\text{respiratoryInfection}-$ $0.29\,(\text{banfi}+\text{pyrexia})\,\text{respiratoryInfection}+1.06\,b_{45}$
10	46	0.250	$-(9.13\times10^{-2})+0.13\,\text{cNIpostRej}+$ $0.56\,\text{coaglationnecrosis}+0.27\,(\text{respiratoryInfection}+\text{antiHLAclass}_2+b_{44})^2$
11	46	0.264	$-(2.16\times10^{-3})+0.29\,\text{diarrhea gERD}-0.48\,\text{pyrexia}+$ $0.74\,\text{respiratoryInfection}+0.96\,b_{45}+(2.04\times10^{-2})\,\text{wBCpeakover}_5$
12	50	0.180	$7.99\times10^{-3}+(1.57\times10^{-2})\,\text{cNIpostRej}^2+0.48\,\text{igG}+$ $0.77\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.74\,b_{45}$
13	51	0.214	$-(1.56\times10^{-2})+0.41\,\text{igG}-0.36\,\text{pyrexia}+$ $0.66\,\text{respiratoryInfection}+0.77\,b_{45}+0.20\,dR_{15}+(1.97\times10^{-2})\,\text{wBCpeakover}_5$
14	61	0.130	$-(6.94\times10^{-4})+(4.33\times10^{-2})\,\text{cNIpostRej}+(1.01\times10^{-2})\,\text{cNIpostRej}^2+$ $0.85\,\text{respiratoryInfection}-0.55\,\text{pyrexia respiratoryInfection}+1.03\,b_{45}+0.94\,\text{igG}\,dR_{103}$
15	62	0.175	$-(7.48\times10^{-3})+0.11\,\text{cNIpostRej}+0.38\,\text{igG}+1.28\,\text{respiratoryInfection}-$ $(4.31\times10^{-2})\,(\text{banfi}+\text{maxWBC})\,\text{respiratoryInfection}+0.91\,b_{45}+0.16\,dQ_6$

◆ Ensembles in ParetoFront

■ **The 15th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.01534, The Observed value: 0

The Prediction: Right

Accuracy so far: 86.67% (29.41% completed)

◆ **Accuracies until the 15th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 3 min 28 sec

◆ **Error(= Predicted value - Observed value) in the 15th Cross Validation**

◇ **Average Error is 0.3122±0.3006 until the 15th turn in the LOO method.**

■ The 16th cross-validation out of 51 turns

□ The 16th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日22時 26分 51秒

□ The 16th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日22時 33分 5秒

◆ Monitors Plot

0.01
0
200
400
600
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
60
40
20
0

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Pareto Fronts
Error = 1 − R²
1
0.50
0.10
0.05
0.01
0
50
100
150
200
250
300
350
Model Complexity

,

◆ **1022 models were created**

◇ **Quatiliy Box values are {46., 0.1521} in the 16th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1022 Selected models: 1 (0.09785%)

◆ Inning 0. Complexity: 46. Error: 0.1521 Number of Selected models: 1 (0.09785%)

◆ Inning 1. Complexity: 47. Error: 0.1621 Number of Selected models: 1 (0.09785%)

◆ Inning 2. Complexity: 48. Error: 0.1721 Number of Selected models: 1 (0.09785%)

◆ Inning 3. Complexity: 49. Error: 0.1821 Number of Selected models: 2 (0.1957%)

◆ Inning 4. Complexity: 50. Error: 0.1921 Number of Selected models: 7 (0.6849%)

◆ Inning 5. Complexity: 51. Error: 0.2021 Number of Selected models: 7 (0.6849%)

◆ Inning 6. Complexity: 52. Error: 0.2121 Number of Selected models: 11 (1.076%)

◆ Inning 7. Complexity: 53. Error: 0.2221 Number of Selected models: 12 (1.174%)

◆ Inning 8. Complexity: 54. Error: 0.2321 Number of Selected models: 22 (2.153%)

◆ Inning 9. Complexity: 55. Error: 0.2421 Number of Selected models: 27 (2.642%)

◆ Inning 10. Complexity: 56. Error: 0.2521 Number of Selected models: 32 (3.131%)

◆ Inning 11. Complexity: 57. Error: 0.2621 Number of Selected models: 44 (4.305%)

◆ Inning 12. Complexity: 58. Error: 0.2721 Number of Selected models: 51 (4.99%)

◆ Inning 13. Complexity: 59. Error: 0.2821 Number of Selected models: 69 (6.751%)

◆ Inning 14. Complexity: 60. Error: 0.2921 Number of Selected models: 84 (8.219%)

- 84 interesting models were selected
  - Quatiliy Box values are {60., 0.292144}.

- Variable Presence (Popularity of each variable) FOCUSED on important variables
- TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, inflammationdatefirst, igG}

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	38	0.204	$3.61\times10^{-2}+0.12\,\text{cNIpostRej}+0.57\,\text{igG}+(9.32\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.78\,b_{45}$
2	41	0.190	$4.19\times10^{-2}+0.12\,\text{cNIpostRej}+(6.42\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.06\,b_{45}+0.54\,\text{respiratoryInfection}\,dQ_7$
3	41	0.266	$6.67\times10^{-2}+0.11\,\text{cNIpostRej}+(9.47\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.11\,b_{45}+0.22\,\text{cNIpostRej}\,dQ_7$
4	41	0.280	$-(6.74\times10^{-2})+0.54\,\text{respiratoryInfection}+(1.94\times10^{-4})\,\text{hLAmm}^2\,\text{rage}\,(\text{cRPpostRej}+\text{igG}+dQ_7)$
5	42	0.186	$3.95\times10^{-2}+0.12\,\text{cNIpostRej}+1.01\,\text{respiratoryInfection}-0.25\,\text{banfi}^2\,\text{respiratoryInfection}+1.06\,b_{45}$
6	43	0.270	$3.65\times10^{-2}+0.42\,\text{candida}+0.51\,\text{igG}-0.35\,\text{pyrexia}+0.64\,\text{respiratoryInfection}+0.71\,b_{45}$
7	46	0.152	$5.64\times10^{-2}+0.11\,\text{cNIpostRej}-\frac{1.91\times10^{-3}}{\text{hDperiod}}+0.90\,\text{respiratoryInfection}-0.60\,\text{pyrexia}\,\text{respiratoryInfection}+1.04\,b_{45}$
8	46	0.199	$-(9.92\times10^{-3})+0.13\,\text{cNIpostRej}+(9.26\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.06\,b_{45}+0.11\,dQ_7+0.29\,dR_{51}$
9	46	0.208	$-(1.38\times10^{-2})+0.34\,\text{igG}+1.03\,\text{respiratoryInfection}-0.46\,\text{banfi}\,\text{respiratoryInfection}+0.80\,b_{45}+(2.01\times10^{-2})\,\text{wBCpeakover}_5$
10	46	0.233	$-(3.03\times10^{-3})+0.13\,\text{cNIpostRej}+(9.04\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}-(4.99\times10^{-2})\,\text{stone}+1.00\,b_{45}+0.22\,dQ_7$
11	46	0.245	$1.27\times10^{-2}+0.12\,\text{cNIpostRej}+0.39\,\text{respiratoryInfection}+1.09\,b_{45}+0.48\,\text{respiratoryInfection}\,dQ_7+0.14\,dR_{53}$
12	49	0.140	$2.87\times10^{-2}+0.11\,\text{cNIpostRej}+0.44\,\text{igG}+(6.84\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.85\,b_{45}+0.44\,\text{respiratoryInfection}\,dQ_7$
13	49	0.172	$9.54\times10^{-3}+(6.01\times10^{-2})\,\text{birthhistory}+0.12\,\text{cNIpostRej}+(6.81\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.03\,b_{45}+0.53\,\text{respiratoryInfection}\,dQ_7$
14	49	0.201	$6.96\times10^{-2}-(7.88\times10^{-2})\,\text{aerobicGPC}+0.13\,\text{cNIpostRej}+(8.77\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.04\,b_{45}+0.68\,\text{respiratoryInfection}\,dR_{52}$
15	49	0.233	$-(6.32\times10^{-2})+0.35\,\text{respiratoryInfection}+0.55\,\text{respiratoryInfection}\,dQ_7+(1.05\times10^{-2})\,\text{hLAmm}^2\,(\text{cRPpostRej}+\text{igG}+dR_7)$

◆ Ensembles in ParetoFront

■ **The 16th Cross Validation**
with Leave-One-Out Method out of 51 turns

The Estimated value: 0.1969, The Observed value: 0

The Prediction: Right

Accuracy so far: 87.5% (31.37% completed)

◆ **Accuracies until the 16th turn in the**
Leave-One-Out Cross Validation out of 51 turns

◇ Estimated Remaining time: `` hour `` min `` sec hr 3 min 22 sec

◆ **Error(= Predicted value - Observed value) in the 16th Cross Validation**

◇ **Average Error is 0.305±0.2918 until the 16th turn in the LOO method.**

■ The 17th cross-validation out of 51 turns

□ The 17th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日22時 33分 9秒

□ The 17th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日22時 39分 22秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
50
100
150
200
250
300
Model Complexity

,

◆ **984 models were created**

◇ **Quatiliy Box values are {38., 0.1434} in the 17th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 984 Selected models: 1 (0.1016%)

◆ Inning 0. Complexity: 38. Error: 0.1434 Number of Selected models: 1 (0.1016%)

◆ Inning 1. Complexity: 39. Error: 0.1534 Number of Selected models: 1 (0.1016%)

◆ Inning 2. Complexity: 40. Error: 0.1634 Number of Selected models: 1 (0.1016%)

◆ Inning 3. Complexity: 41. Error: 0.1734 Number of Selected models: 2 (0.2033%)

◆ Inning 4. Complexity: 42. Error: 0.1834 Number of Selected models: 3 (0.3049%)

◆ Inning 5. Complexity: 43. Error: 0.1934 Number of Selected models: 8 (0.813%)

◆ Inning 6. Complexity: 44. Error: 0.2034 Number of Selected models: 16 (1.626%)

◆ Inning 7. Complexity: 45. Error: 0.2134 Number of Selected models: 20 (2.033%)

◆ Inning 8. Complexity: 46. Error: 0.2234 Number of Selected models: 32 (3.252%)

◆ Inning 9. Complexity: 47. Error: 0.2334 Number of Selected models: 38 (3.862%)

◆ Inning 10. Complexity: 48. Error: 0.2434 Number of Selected models: 38 (3.862%)

◆ Inning 11. Complexity: 49. Error: 0.2534 Number of Selected models: 53 (5.386%)

◆ Inning 12. Complexity: 50. Error: 0.2634 Number of Selected models: 72 (7.317%)

◆ Inning 13. Complexity: 51. Error: 0.2734 Number of Selected models: 88 (8.943%)

◆ **88 interesting models were selected**

◇ **Quatiliy Box values are {51., 0.273351}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, pyrexia, b45, cNIpostRej, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.258	$5.26\times10^{-2}+0.90\,\text{respiratoryInfection}-0.64\,\text{pyrexia respiratoryInfection}+0.95\,b_{45}$
2	35	0.202	$5.75\times10^{-2}+0.11\,\text{cNIpostRej}-0.43\,\text{pyrexia}+0.84\,\text{respiratoryInfection}+1.03\,b_{45}$
3	38	0.143	$3.41\times10^{-2}+0.11\,\text{cNIpostRej}+0.94\,\text{respiratoryInfection}-0.62\,\text{pyrexia respiratoryInfection}+1.06\,b_{45}$
4	38	0.207	$5.15\times10^{-2}-0.45\,\text{pyrexia}+0.83\,\text{respiratoryInfection}+0.95\,\text{dSAandHLAclass1pre surgery}+0.95\,b_{45}$
5	38	0.209	$4.15\times10^{-2}+0.42\,\text{igG}+0.86\,\text{respiratoryInfection}-0.60\,\text{pyrexia respiratoryInfection}+0.75\,b_{45}$
6	38	0.253	$-(5.28\times10^{-3})+0.11\,\text{cRPpostRej hLADRmm}-0.42\,\text{pyrexia}+0.80\,\text{respiratoryInfection}+0.62\,b_{45}$
7	38	0.255	$6.89\times10^{-2}+(8.16\times10^{-2})\,\text{cNIpostRej}+0.42\,\text{hLADRmm igG}-0.42\,\text{pyrexia}+0.77\,\text{respiratoryInfection}$
8	39	0.220	$4.74\times10^{-2}+0.11\,\text{cNIpostRej}-0.25\,\text{pyrexia}^2+0.83\,\text{respiratoryInfection}+1.05\,b_{45}$
9	41	0.151	$5.27\times10^{-2}-0.45\,\text{pyrexia}+0.83\,\text{respiratoryInfection}+$ $0.14\,\text{cNIpostRej hLADRmm staphylococcusaureus}+0.95\,b_{45}$
10	41	0.170	$3.17\times10^{-2}+0.70\,\text{cNIpostRej igG}+0.93\,\text{respiratoryInfection}-0.64\,\text{pyrexia respiratoryInfection}+1.22\,b_{45}$
11	43	0.160	$4.66\times10^{-2}+0.10\,\text{cNIpostRej}+0.40\,\text{igG}-0.41\,\text{pyrexia}+0.80\,\text{respiratoryInfection}+0.84\,b_{45}$
12	43	0.180	$3.52\times10^{-2}+0.11\,\text{cNIpostRej}-0.40\,\text{pyrexia}+0.81\,\text{respiratoryInfection}+1.06\,b_{45}+0.19\,dR_{15}$
13	46	0.106	$2.51\times10^{-2}+0.11\,\text{cNIpostRej}+0.37\,\text{igG}+$ $0.90\,\text{respiratoryInfection}-0.59\,\text{pyrexia respiratoryInfection}+0.88\,b_{45}$
14	46	0.146	$2.25\times10^{-2}+0.10\,\text{cNIpostRej}+0.54\,\text{igG}+0.84\,\text{respiratoryInfection}-$ $0.55\,\text{pyrexia respiratoryInfection}+0.22\,\text{dSAandHSAclass}_1$
15	49	0.073	$1.65\times10^{-2}+0.10\,\text{cNIpostRej}+0.63\,\text{cNIpostRej igG}+$ $0.96\,\text{respiratoryInfection}-0.63\,\text{pyrexia respiratoryInfection}+1.30\,b_{45}$

◆ Ensembles in ParetoFront

■ The 17th Cross Validation with Leave-One-Out Method out of 51 turns

The Estimated value: 0.8054, The Observed value: 0

The Prediction: Wrong

Accuracy so far: 82.35% (33.33% completed)

◆ **Accuracies until the 17th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 3 min 16 sec

◆ **Error(= Predicted value - Observed value) in the 17th Cross Validation**

◇ **Average Error is 0.3344±0.3075 until the 17th turn in the LOO method.**

■ The 18th cross-validation out of 51 turns

□ The 18th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日22時 39分 25秒

□ The 18th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日22時 46分 7秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
60
40
20
0

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
50
100
150
Model Complexity

◆ **1046 models were created**

◇ **Quatiliy Box values are {49., 0.1668} in the 18th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1046 Selected models: 1 (0.0956%)

◆ Inning 0. Complexity: 49. Error: 0.1668 Number of Selected models: 1 (0.0956%)

◆ Inning 1. Complexity: 50. Error: 0.1768 Number of Selected models: 1 (0.0956%)

◆ Inning 2. Complexity: 51. Error: 0.1868 Number of Selected models: 1 (0.0956%)

◆ Inning 3. Complexity: 52. Error: 0.1968 Number of Selected models: 4 (0.3824%)

◆ Inning 4. Complexity: 53. Error: 0.2068 Number of Selected models: 4 (0.3824%)

◆ Inning 5. Complexity: 54. Error: 0.2168 Number of Selected models: 7 (0.6692%)

◆ Inning 6. Complexity: 55. Error: 0.2268 Number of Selected models: 11 (1.052%)

◆ Inning 7. Complexity: 56. Error: 0.2368 Number of Selected models: 12 (1.147%)

◆ Inning 8. Complexity: 57. Error: 0.2468 Number of Selected models: 20 (1.912%)

◆ Inning 9. Complexity: 58. Error: 0.2568 Number of Selected models: 25 (2.39%)

◆ Inning 10. Complexity: 59. Error: 0.2668 Number of Selected models: 47 (4.493%)

◆ Inning 11. Complexity: 60. Error: 0.2768 Number of Selected models: 54 (5.163%)

◆ Inning 12. Complexity: 61. Error: 0.2868 Number of Selected models: 57 (5.449%)

◆ Inning 13. Complexity: 62. Error: 0.2968 Number of Selected models: 74 (7.075%)

◆ Inning 14. Complexity: 63. Error: 0.3068 Number of Selected models: 81 (7.744%)

- Inning 15. Complexity: 64. Error: 0.3168 Number of Selected models: 88 (8.413%)

- **88 interesting models were selected**
  - **Quatiliy Box values are {64., 0.316841}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, igG, b45, antiHLAclass2, cRPpostRej}**

◆ Defining Ensembles

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	Complexity	$1-R^2$	Function
			graftLoss
1	26	0.238	$4.76\times10^{-2}+0.95\ \text{antiHLAclass}_2\ (\text{respiratoryInfection}+\bullet\text{igA}+b_{13})$
2	34	0.265	$3.34\times10^{-2}+(3.24\times10^{-2})\ \text{cRPpostRej}^2+0.91\ \text{antiHLAclass}_2\ (\text{respiratoryInfection}+b_{13})$
3	36	0.260	$5.21\times10^{-2}+0.73\ (\text{respiratoryInfection}+c_3)\ \sqrt{\text{type2DM}+dQ_7}$
4	36	0.302	$-0.13+0.20\ \text{hLADRmm}\ (\text{cRPpostRej}+2\ \text{respiratoryInfection}+dQ_7)$
5	38	0.241	$2.78\times10^{-2}+(3.39\times10^{-2})\ \text{cRPpostRej}^2+0.66\ \text{antiHLAclass}_2\ (\text{igG}+\text{respiratoryInfection}+b_{13})$
6	40	0.248	$2.68\times10^{-2}+(3.78\times10^{-2})\ \text{cRPpostRej}^2+0.86\ \sqrt{\text{igG}+\text{respiratoryInfection}}\ \text{antiHLAclass}_2$
7	41	0.194	$-(2.26\times10^{-2})+0.12\ \text{cRPpostRej}+0.80\ \text{antiHLAclass}_2\ \sqrt{\text{igG}+\text{respiratoryInfection}+b_{13}}$
8	41	0.289	$-0.40+0.17\ \text{cRPpostRej}+0.27\ \text{hLADRmm}+0.23\ (\text{respiratoryInfection}+dQ_7)^2$
9	42	0.239	$-(1.27\times10^{-2})+0.12\ \text{cRPpostRej}+0.37\ \text{igG}+0.78\ \text{antiHLAclass}_2{}^2\ (\text{respiratoryInfection}+b_{13})$
10	43	0.218	$4.01\times10^{-2}+0.11\ \text{cNIpostRej}+0.45\ \text{igG}-0.34\ \text{pyrexia}+0.68\ \text{respiratoryInfection}+0.83\ b_{45}$
11	43	0.235	$-0.29+0.14\ \text{cNIpostRej}+0.22\ \text{hLADRmm}+0.51\ \text{respiratoryInfection}+0.82\ b_{45}+0.29\ dQ_7$
12	43	0.248	$1.81\times10^{-2}+0.13\ \text{cNIpostRej}+(7.65\times10^{-2})\ \text{denovoDSA}-$ $0.32\ \text{pyrexia}+0.64\ \text{respiratoryInfection}+0.82\ b_{45}$
13	43	0.269	$-(1.49\times10^{-2})+0.13\ \text{cNIpostRej}+$ $(8.83\times10^{-2})\ \text{denovoDSA}+0.44\ \text{igG}+0.48\ \text{respiratoryInfection}+0.60\ b_{45}$
14	43	0.271	$9.01\times10^{-3}+0.11\ \text{cNIpostRej}+0.12\ \text{denovoDSA}+0.53\ \text{igG}-0.26\ \text{pyrexia}+0.52\ \text{respiratoryInfection}$
15	44	0.239	$-(4.37\times10^{-2})+0.13\ \text{hLADRmm}\ (\text{cNIpostRej}+\text{denovoDSA}+\text{igG}+2\ \text{respiratoryInfection}+dQ_7)$

◆ Ensembles in ParetoFront

■ The 18th Cross Validation with Leave-One-Out Method out of 51 turns

The Estimated value: 0.09838, The Observed value: 1

The Prediction: Wrong

Accuracy so far: 77.78% (35.29% completed)

◆ **Accuracies until the 18th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 3 min 9 sec

◆ **Error(= Predicted value - Observed value) in the 18th Cross Validation**

◇ **Average Error is 0.3659±0.3269 until the 18th turn in the LOO method.**

■ The 19th cross-validation out of 51 turns

□ The 19th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日22時 46分 11秒

□ The 19th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日22時 52分 25秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
ModelAge
60
50
40
30
20
10
0
−10

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
200
400
600
800
Model Complexity

,

◆ **883 models were created**

◇ **Quatiliy Box values are {46., 0.1755} in the 19th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 883 Selected models: 1 (0.1133%)

◆ Inning 0. Complexity: 46. Error: 0.1755 Number of Selected models: 1 (0.1133%)

◆ Inning 1. Complexity: 47. Error: 0.1855 Number of Selected models: 1 (0.1133%)

◆ Inning 2. Complexity: 48. Error: 0.1955 Number of Selected models: 1 (0.1133%)

◆ Inning 3. Complexity: 49. Error: 0.2055 Number of Selected models: 3 (0.3398%)

◆ Inning 4. Complexity: 50. Error: 0.2155 Number of Selected models: 3 (0.3398%)

◆ Inning 5. Complexity: 51. Error: 0.2255 Number of Selected models: 10 (1.133%)

◆ Inning 6. Complexity: 52. Error: 0.2355 Number of Selected models: 13 (1.472%)

◆ Inning 7. Complexity: 53. Error: 0.2455 Number of Selected models: 16 (1.812%)

◆ Inning 8. Complexity: 54. Error: 0.2555 Number of Selected models: 22 (2.492%)

◆ Inning 9. Complexity: 55. Error: 0.2655 Number of Selected models: 26 (2.945%)

◆ Inning 10. Complexity: 56. Error: 0.2755 Number of Selected models: 30 (3.398%)

◆ Inning 11. Complexity: 57. Error: 0.2855 Number of Selected models: 37 (4.19%)

◆ Inning 12. Complexity: 58. Error: 0.2955 Number of Selected models: 42 (4.757%)

◆ Inning 13. Complexity: 59. Error: 0.3055 Number of Selected models: 58 (6.569%)

◆ Inning 14. Complexity: 60. Error: 0.3155 Number of Selected models: 73 (8.267%)

- 73 interesting models were selected
  - Quatiliy Box values are {60., 0.3155}.

- Variable Presence (Popularity of each variable) FOCUSED on important variables
- TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, pyrexia, igG}

◆ Defining Ensembles

graftLoss

	Complexity	$1-R^2$	Function
1	35	0.301	$-(1.72\times10^{-2})+0.13\,\text{cNIpostRej}+0.58\,\text{respiratoryInfection}+1.12\,b_{45}+0.30\,dR_{53}$
2	38	0.230	$6.05\times10^{-2}+0.11\,\text{banfptc cNIpostRej}-0.37\,\text{pyrexia}+0.77\,\text{respiratoryInfection}+0.94\,b_{45}$
3	38	0.283	$2.87\times10^{-2}+0.11\,\text{banfptc cNIpostRej}+0.44\,\text{igG}+0.62\,\text{respiratoryInfection}+0.75\,b_{45}$
4	38	0.299	$7.68\times10^{-2}+(9.65\times10^{-2})\,\text{banfptc cNIpostRej}+0.63\,\text{igG}-0.35\,\text{pyrexia}+0.68\,\text{respiratoryInfection}$
5	43	0.218	$4.28\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.83\,b_{45}$
6	46	0.175	$2.31\times10^{-2}+0.11\,\text{cNIpostRej}+0.41\,\text{igG}+$ $0.80\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.86\,b_{45}$
7	47	0.242	$1.62\times10^{-2}+(1.56\times10^{-2})\,\text{cNIpostRej}^2-0.36\,\text{pyrexia}+0.69\,\text{respiratoryInfection}+0.97\,b_{45}+0.30\,dR_{51}$
8	49	0.177	$2.36\times10^{-2}+0.11\,\text{cNIpostRej}+(6.30\times10^{-3})\,\text{igG rage}+$ $0.79\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.87\,b_{45}$
9	49	0.222	$4.88\times10^{-2}+30.44\,\text{igG}-0.48\,\text{igG rage}+0.95\,b_{45}+0.95\,\text{respiratoryInfection}\,(\text{pastheart}+dQ_7)$
10	50	0.216	$7.29\times10^{-2}-(3.46\times10^{-2})\,\text{banfci}^2+$ $0.10\,\text{banfptc cNIpostRej}-0.40\,\text{pyrexia}+0.81\,\text{respiratoryInfection}+1.00\,b_{45}$
11	50	0.265	$8.80\times10^{-2}-0.13\,\text{banfci}+0.58\,\text{igG}-0.37\,\text{pyrexia}+\frac{4.63\,\text{respiratoryInfection}}{\text{wBCpostKTx}}+0.75\,b_{45}$
12	51	0.206	$1.43\times10^{-2}+0.11\,\text{cNIpostRej}+0.35\,\text{igG}-0.33\,\text{pyrexia}+0.69\,\text{respiratoryInfection}+0.85\,b_{45}+0.12\,dQ_7$
13	58	0.172	$6.40\times10^{-2}-(4.12\times10^{-2})\,\text{banfci}^2+(9.32\times10^{-2})\,\text{banfptc cNIpostRej}+$ $0.41\,\text{igG}-0.38\,\text{pyrexia}+0.78\,\text{respiratoryInfection}+0.81\,b_{45}$
14	58	0.183	$3.28\times10^{-2}+0.10\,\text{cNIpostRej}+0.30\,\text{igG}+$ $0.47\,\text{cNIpostRej igG}^2-0.37\,\text{pyrexia}+0.74\,\text{respiratoryInfection}+1.08\,b_{45}$
15	58	0.210	$-(1.92\times10^{-2})+0.12\,\text{cNIpostRej}+0.17\,\text{pyrexia}^2+(9.50\times10^{-4})\,\text{rage}+$ $0.85\,\text{respiratoryInfection}-0.83\,\text{pyrexia respiratoryInfection}+1.06\,b_{45}$

◆ Ensembles in ParetoFront

■ The 19th Cross Validation with Leave-One-Out Method out of 51 turns

The Estimated value: 0.04326, The Observed value: 0

The Prediction: Right

Accuracy so far: 78.95% (37.25% completed)

◆ **Accuracies until the 19th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 3 min 3 sec

◆ **Error(= Predicted value - Observed value) in the 19th Cross Validation**

◇ **Average Error is 0.349±0.3262 until the 19th turn in the LOO method.**

■ The 20th cross-validation out of 51 turns

□ The 20th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日 22時 52分 28秒

□ The 20th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日 22時 59分 38秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
50
40
30
20
10
0
−10

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
50
100
150
200
250
Model Complexity

,

◆ **956 models were created**

◇ **Quatiliy Box values are {50., 0.1682} in the 20th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 956 Selected models: 1 (0.1046%)

◆ Inning 0. Complexity: 50. Error: 0.1682 Number of Selected models: 1 (0.1046%)

◆ Inning 1. Complexity: 51. Error: 0.1782 Number of Selected models: 1 (0.1046%)

◆ Inning 2. Complexity: 52. Error: 0.1882 Number of Selected models: 1 (0.1046%)

◆ Inning 3. Complexity: 53. Error: 0.1982 Number of Selected models: 1 (0.1046%)

◆ Inning 4. Complexity: 54. Error: 0.2082 Number of Selected models: 7 (0.7322%)

◆ Inning 5. Complexity: 55. Error: 0.2182 Number of Selected models: 10 (1.046%)

◆ Inning 6. Complexity: 56. Error: 0.2282 Number of Selected models: 15 (1.569%)

◆ Inning 7. Complexity: 57. Error: 0.2382 Number of Selected models: 22 (2.301%)

◆ Inning 8. Complexity: 58. Error: 0.2482 Number of Selected models: 29 (3.033%)

◆ Inning 9. Complexity: 59. Error: 0.2582 Number of Selected models: 41 (4.289%)

◆ Inning 10. Complexity: 60. Error: 0.2682 Number of Selected models: 45 (4.707%)

◆ Inning 11. Complexity: 61. Error: 0.2782 Number of Selected models: 50 (5.23%)

◆ Inning 12. Complexity: 62. Error: 0.2882 Number of Selected models: 68 (7.113%)

◆ Inning 13. Complexity: 63. Error: 0.2982 Number of Selected models: 74 (7.741%)

◆ Inning 14. Complexity: 64. Error: 0.3082 Number of Selected models: 76 (7.95%)

- Inning 15. Complexity: 65. Error: 0.3182 Number of Selected models: 81 (8.473%)

- **81 interesting models were selected**
  - **Quatiliy Box values are {65., 0.318209}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, cNIpostRej, pyrexia, b45, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	38	0.253	$1.98\times10^{-2}+(9.87\times10^{-2})\,\text{cNIpostRej}+0.83\,\text{igG}+0.43\,\text{respiratoryInfection}+0.55\,\text{banfi}\,\text{antiHLAclass}_1$
2	38	0.285	$3.43\times10^{-2}+0.11\,\text{cNIpostRej}+0.36\,\text{respiratoryInfection}+0.62\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+1.06\,b_{45}$
3	42	0.216	$3.30\times10^{-2}+0.12\,\text{cNIpostRej}+0.86\,\text{respiratoryInfection}-0.72\sqrt{\text{pyrexia}}\,\text{respiratoryInfection}+1.07\,b_{45}$
4	42	0.298	$5.39\times10^{-2}+(1.51\times10^{-2})\,\text{cNIpostRej}^2+0.41\,\text{igG}+0.84\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.73\,b_{45}$
5	42	0.311	$1.20\times10^{-2}+0.11\,\text{cNIpostRej}+0.63\,\text{respiratoryInfection}+1.08\,b_{45}{}^2+0.87\,\text{surgery}\,dR_7$
6	43	0.231	$4.19\times10^{-2}+0.11\,\text{cNIpostRej}+0.44\,\text{igG}-0.35\,\text{pyrexia}+0.70\,\text{respiratoryInfection}+0.83\,b_{45}$
7	43	0.243	$5.24\times10^{-3}+0.48\,\text{igG}-0.37\,\text{pyrexia}+0.65\,\text{respiratoryInfection}+0.72\,b_{45}+(1.90\times10^{-2})\,\text{wBCpeakover}_5$
8	46	0.199	$3.85\times10^{-2}+(9.54\times10^{-2})\,\text{cNIpostRej}+0.78\,\text{igG}-0.27\,\text{pyrexia}+0.53\,\text{respiratoryInfection}+0.50\,\text{banfi}\,\text{antiHLAclass}_1$
9	46	0.200	$3.30\times10^{-2}+0.10\,\text{cNIpostRej}-0.38\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+0.85\,\text{igG}\,\text{staphylococcusaureus}+1.05\,b_{45}$
10	46	0.208	$3.46\times10^{-2}+0.10\,\text{cNIpostRej}-0.38\,\text{pyrexia}+0.76\sqrt{\text{igG}+\text{respiratoryInfection}+b_{45}}$
11	50	0.168	$2.35\times10^{-2}+0.11\,\text{cNIpostRej}+0.41\,\text{igG}+0.81\,\text{respiratoryInfection}-0.67\sqrt{\text{pyrexia}}\,\text{respiratoryInfection}+0.87\,b_{45}$
12	50	0.208	$1.52\times10^{-2}+0.12\,\text{cNIpostRej}+(3.91\times10^{-2})\,\text{preDSA}+0.88\,\text{respiratoryInfection}-0.72\sqrt{\text{pyrexia}}\,\text{respiratoryInfection}+1.03\,b_{45}$
13	50	0.256	$7.72\times10^{-3}+0.11\,\text{cNIpostRej}+(9.67\times10^{-2})\,\text{denovoDSA}+0.54\,\text{igG}+0.66\,\text{respiratoryInfection}-0.57\sqrt{\text{pyrexia}}\,\text{respiratoryInfection}$
14	54	0.216	$-(2.36\times10^{-2})+0.11\,\text{cNIpostRej}+0.16\,\text{denovoDSA}+1.06\,\text{igG}-0.27\,\text{denovoDSA}\,\text{igG}-0.31\,\text{pyrexia}+0.63\,\text{respiratoryInfection}$
15	57	0.162	$1.58\times10^{-2}+0.11\,\text{cNIpostRej}+0.72\,\text{igG}-0.13\,\text{denovoDSA}\,\text{igG}+0.84\,\text{respiratoryInfection}-0.54\,\text{pyrexia}\,\text{respiratoryInfection}+0.85\,b_{45}$

◆ Ensembles in ParetoFront

■ **The 20th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.8504, The Observed value: 1

The Prediction: Right

Accuracy so far: 80.% (39.22% completed)

◆ **Accuracies until the 20th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 2 min 56 sec

◆ **Error(= Predicted value - Observed value) in the 20th Cross Validation**

◇ **Average Error is 0.339±0.3206 until the 20th turn in the LOO method.**

■ The 21st cross-validation out of 51 turns

□ The 21st Genetic Programming has started.

◆ Present Time: 2020年 7月 13日22時 59分 42秒

□ The 21th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日23時 5分 59秒

◆ Monitors Plot

0.001
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1– R2
0
100
200
300
400
500
Model Complexity

,

◆ 977 models were created

◇ Quatiliy Box values are {38., 0.1478} in the 21st turn.

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 977 Selected models: 1 (0.1024%)

◆ Inning 0. Complexity: 38. Error: 0.1478 Number of Selected models: 1 (0.1024%)

◆ Inning 1. Complexity: 39. Error: 0.1578 Number of Selected models: 1 (0.1024%)

◆ Inning 2. Complexity: 40. Error: 0.1678 Number of Selected models: 1 (0.1024%)

◆ Inning 3. Complexity: 41. Error: 0.1778 Number of Selected models: 1 (0.1024%)

◆ Inning 4. Complexity: 42. Error: 0.1878 Number of Selected models: 4 (0.4094%)

◆ Inning 5. Complexity: 43. Error: 0.1978 Number of Selected models: 12 (1.228%)

◆ Inning 6. Complexity: 44. Error: 0.2078 Number of Selected models: 14 (1.433%)

◆ Inning 7. Complexity: 45. Error: 0.2178 Number of Selected models: 18 (1.842%)

◆ Inning 8. Complexity: 46. Error: 0.2278 Number of Selected models: 39 (3.992%)

◆ Inning 9. Complexity: 47. Error: 0.2378 Number of Selected models: 47 (4.811%)

◆ Inning 10. Complexity: 48. Error: 0.2478 Number of Selected models: 51 (5.22%)

◆ Inning 11. Complexity: 49. Error: 0.2578 Number of Selected models: 59 (6.039%)

◆ Inning 12. Complexity: 50. Error: 0.2678 Number of Selected models: 78 (7.984%)

◆ Inning 13. Complexity: 51. Error: 0.2778 Number of Selected models: 107 (10.95%)

◆ **107 interesting models were selected**

◇ **Quatiliy Box values are {51., 0.277846}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, pyrexia, antiHLAclass2}**

◆ Defining Ensembles

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	graftLoss		
	Complexity	$1-R^2$	Function
1	30	0.262	$2.70\times10^{-2}+0.81\,\text{respiratoryInfection}-0.56\,\text{pyrexia respiratoryInfection}+0.97\,b_{45}$
2	33	0.239	$4.83\times10^{-2}+(4.17\times10^{-2})\,\text{cNIpostRej cRPpreRej}+0.95\,b_{45}+0.95\,\text{respiratoryInfection}\,dQ_8$
3	34	0.212	$4.24\times10^{-2}+0.66\,\text{respiratoryInfection}\,(\text{allergy}+\text{coaglationnecrosis}+\text{antiHLAclass}_2)+0.96\,b_{45}$
4	34	0.238	$4.76\times10^{-2}+0.95\,b_{45}+0.95\,\text{respiratoryInfection}\,(\text{coaglationnecrosis}+b_{45}+dQ_8)$
5	35	0.270	$-(2.90\times10^{-2})+0.12\,\text{cNIpostRej}+(9.69\times10^{-2})\,\text{denovoDSA}+0.58\,\text{respiratoryInfection}+0.79\,b_{45}$
6	38	0.148	$1.19\times10^{-2}+0.11\,\text{cNIpostRej}+0.85\,\text{respiratoryInfection}-0.55\,\text{pyrexia respiratoryInfection}+1.08\,b_{45}$
7	38	0.154	$-(2.93\times10^{-2})+0.83\,\text{respiratoryInfection}-$ $0.58\,\text{pyrexia respiratoryInfection}+0.99\,b_{45}+(2.01\times10^{-2})\,\text{wBCpeakover}_5$
8	38	0.238	$4.19\times10^{-2}+(1.51\times10^{-2})\,\text{cNIpostRej}^2+0.95\,b_{45}+0.96\,\text{respiratoryInfection}\,dQ_8{}^2$
9	38	0.257	$-(1.71\times10^{-2})+0.11\,\text{cNIpostRej}+0.15\,\text{denovoDSA}+$ $0.67\,\text{respiratoryInfection}-0.46\,\text{pyrexia respiratoryInfection}$
10	38	0.277	$9.84\times10^{-3}+0.42\,\text{respiratoryInfection}$ $(8.31\times10^{-2}+\text{coaglationnecrosis}+\text{respiratoryInfection}+\text{antiHLAclass}_2)+0.99\,b_{45}$
11	41	0.233	$-(3.75\times10^{-2})+0.13\,\text{cRPpostRej}-$ $0.40\,\text{cNIpostRej respiratoryInfection}+0.82\,b_{45}+0.96\,\text{respiratoryInfection}\,dQ_8$
12	42	0.136	$3.10\times10^{-2}+(9.57\times10^{-2})\,\text{cNIpostRej}+$ $0.91\,\text{respiratoryInfection}\,(8.31\times10^{-2}+\text{coaglationnecrosis}+\text{antiHLAclass}_2)+1.05\,b_{45}$
13	42	0.152	$4.14\times10^{-2}+(9.30\times10^{-2})\,\text{cNIpostRej}+1.04\,b_{45}+0.97\,\text{respiratoryInfection}\,(\text{coaglationnecrosis}+b_{45}+dQ_8)$
14	42	0.167	$-(6.08\times10^{-3})+(1.59\times10^{-2})\,\text{cNIpostRej}^2+$ $0.33\,\text{respiratoryInfection}+0.99\,b_{45}+0.67\,\text{respiratoryInfection}\,dQ_8$
15	42	0.169	$6.06\times10^{-3}+0.28\,\text{heartDisease}+$ $0.79\,\text{respiratoryInfection}\,(8.31\times10^{-2}+\text{coaglationnecrosis}+\text{antiHLAclass}_2)+0.99\,b_{45}$

◆ Ensembles in ParetoFront

■ **The 21st Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.0725, The Observed value: 1

The Prediction: Wrong

Accuracy so far: 76.19% (41.18% completed)

◆ **Accuracies until the 21st turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 2 min 49 sec

◆ **Error(= Predicted value - Observed value) in the 21st Cross Validation**

◇ **Average Error is 0.367±0.3378 until the 21st turn in the LOO method.**

■ The 22nd cross-validation out of 51 turns

□ The 22nd Genetic Programming has started.

◆ Present Time: 2020年 7月 13日⧆23時 6分 3秒

□ The 22th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日⧆23時 12分 42秒

◆ Monitors Plot

0.01
0
200
400
600
800
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
−200
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
120
100
80
60
40
20
0
−20

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
100
200
300
400
500
Model Complexity

,

◆ **971 models were created**

◇ **Quatiliy Box values are {46., 0.2337} in the 22nd turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 971 Selected models: 1 (0.103%)

◆ Inning 0. Complexity: 46. Error: 0.2337 Number of Selected models: 1 (0.103%)

◆ Inning 1. Complexity: 47. Error: 0.2437 Number of Selected models: 1 (0.103%)

◆ Inning 2. Complexity: 48. Error: 0.2537 Number of Selected models: 2 (0.206%)

◆ Inning 3. Complexity: 49. Error: 0.2637 Number of Selected models: 2 (0.206%)

◆ Inning 4. Complexity: 50. Error: 0.2737 Number of Selected models: 6 (0.6179%)

◆ Inning 5. Complexity: 51. Error: 0.2837 Number of Selected models: 8 (0.8239%)

◆ Inning 6. Complexity: 52. Error: 0.2937 Number of Selected models: 8 (0.8239%)

◆ Inning 7. Complexity: 53. Error: 0.3037 Number of Selected models: 12 (1.236%)

◆ Inning 8. Complexity: 54. Error: 0.3137 Number of Selected models: 19 (1.957%)

◆ Inning 9. Complexity: 55. Error: 0.3237 Number of Selected models: 30 (3.09%)

◆ Inning 10. Complexity: 56. Error: 0.3337 Number of Selected models: 47 (4.84%)

◆ Inning 11. Complexity: 57. Error: 0.3437 Number of Selected models: 53 (5.458%)

◆ Inning 12. Complexity: 58. Error: 0.3537 Number of Selected models: 66 (6.797%)

◆ Inning 13. Complexity: 59. Error: 0.3637 Number of Selected models: 84 (8.651%)

◆ **84 interesting models were selected**

◇ **Quatiliy Box values are {59., 0.363696}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, igG, pyrexia, cRPpostRej}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.325	$3.52\times10^{-2}+0.93\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.93\,b_{45}+(1.99\times10^{-2})\,\text{wBCpeakover}_5$
2	31	0.359	$2.48-\frac{7.43}{3+\text{candida}+\text{igG}+\text{respiratoryInfection}+b_{45}}$
3	35	0.359	$1.26\times10^{-2}+0.48\,\text{candida}+0.58\,\text{igG}+0.53\,\text{respiratoryInfection}+0.70\,b_{45}$
4	38	0.277	$-(4.23\times10^{-3})+0.28\,\text{respiratoryInfection}+$ $0.69\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.96\,b_{45}+(2.00\times10^{-2})\,\text{wBCpeakover}_5$
5	38	0.278	$-(2.23\times10^{-2})+0.11\,\text{cRPpostRej}+0.63\,\text{igG}+$ $(8.56\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.52\,b_{45}$
6	38	0.341	$3.61\times10^{-2}+0.33\,\text{candida}+0.30\,\text{respiratoryInfection}+0.96\,b_{45}+0.60\,\text{respiratoryInfection}\,dQ_7$
7	38	0.345	$-(2.02\times10^{-3})+0.75\,\text{candida}\,\text{heartDisease}+0.51\,\text{respiratoryInfection}+1.00\,b_{45}+0.33\,dR_{15}$
8	39	0.309	$3.22\times10^{-2}+(3.81\times10^{-2})\,\text{cRPpostRej}^2+0.71\,\text{igG}-0.35\,\text{pyrexia}+0.64\,\text{respiratoryInfection}$
9	42	0.244	$5.92\times10^{-3}+(3.35\times10^{-2})\,\text{cRPpostRej}^2+0.65\,\text{igG}+$ $(8.79\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.56\,b_{45}$
10	42	0.283	$5.61\times10^{-2}+0.41\,\text{igG}+0.86\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.74\,b_{45}+(4.77\times10^{-4})\,\text{wBCpeakover}_5{}^2$
11	42	0.295	$2.93\times10^{-2}+0.93\,b_{45}+0.62\,\text{respiratoryInfection}\,(\text{type2DM}+b_{18}+dQ_9)+(1.96\times10^{-2})\,\text{wBCpeakover}_5$
12	42	0.303	$6.56\times10^{-2}+0.61\,\text{igG}-0.17\,\text{pyrexia}+(8.85\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.63\,\sqrt{b_{45}}$
13	42	0.303	$1.13\times10^{-2}+(3.55\times10^{-2})\,\text{ascites}+(3.71\times10^{-2})\,\text{cRPpostRej}^2+$ $0.84\,\text{igG}+(8.44\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}$
14	46	0.234	$1.97\times10^{-2}+0.11\,\text{cNIpostRej}+0.39\,\text{igG}+0.88\,b_{45}+0.43\,\text{respiratoryInfection}\,(1+dQ_7)$
15	47	0.305	$5.49\times10^{-2}+(3.57\times10^{-2})\,\text{cRPpostRej}^2-0.40\,\text{pyrexia}+$ $0.73\,\text{respiratoryInfection}-(6.43\times10^{-2})\,\text{staphylococcusaureus}+0.84\,b_{45}$

◆ Ensembles in ParetoFront

■ **The 22nd Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.02016, The Observed value: 0

The Prediction: Right

Accuracy so far: 77.27% (43.14% completed)

◆ **Accuracies until the 22nd turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 2 min 43 sec

◆ **Error(= Predicted value - Observed value) in the 22nd Cross Validation**

◇ **Average Error is 0.3512±0.3379 until the 22nd turn in the LOO method.**

■ The 23rd cross-validation out of 51 turns

□ The 23rd Genetic Programming has started.

◆ Present Time: 2020年 7月 13日23時 12分 45秒

□ The 23th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日23時 18分 60秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
60
50
40
30
20
10
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
50
100
150
200
Model Complexity

,

◆ **1003 models were created**

◇ **Quatiliy Box values are {41., 0.2226} in the 23rd turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1003 Selected models: 1 (0.0997%)

◆ Inning 0. Complexity: 41. Error: 0.2226 Number of Selected models: 1 (0.0997%)

◆ Inning 1. Complexity: 42. Error: 0.2326 Number of Selected models: 1 (0.0997%)

◆ Inning 2. Complexity: 43. Error: 0.2426 Number of Selected models: 2 (0.1994%)

◆ Inning 3. Complexity: 44. Error: 0.2526 Number of Selected models: 5 (0.4985%)

◆ Inning 4. Complexity: 45. Error: 0.2626 Number of Selected models: 6 (0.5982%)

◆ Inning 5. Complexity: 46. Error: 0.2726 Number of Selected models: 17 (1.695%)

◆ Inning 6. Complexity: 47. Error: 0.2826 Number of Selected models: 31 (3.091%)

◆ Inning 7. Complexity: 48. Error: 0.2926 Number of Selected models: 47 (4.686%)

◆ Inning 8. Complexity: 49. Error: 0.3026 Number of Selected models: 58 (5.783%)

◆ Inning 9. Complexity: 50. Error: 0.3126 Number of Selected models: 95 (9.472%)

◆ **95 interesting models were selected**

  ◇ **Quatiliy Box values are {50., 0.312628}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, cRPpostRej, igG, pyrexia, b45}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	34	0.284	$-0.13+0.52\,\text{respiratoryInfection}+(6.00\times10^{-2})\,\text{hLAmm}\,(\text{cRPpostRej}+\text{dQ}_7+\text{dR}_7)$
2	35	0.269	$5.41\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+1.04\,\text{b}_{45}$
3	38	0.243	$-(3.58\times10^{-2})+(5.31\times10^{-2})\,\text{cRPpostRej}\,\text{hLAmm}+0.59\,\text{igG}-0.31\,\text{pyrexia}+0.63\,\text{respiratoryInfection}$
4	38	0.273	$-(3.33\times10^{-2})+0.11\,\text{cNIpostRej}+0.16\,\text{denovoDSA}+0.40\,\text{respiratoryInfection}+0.64\,\text{aBOI}\,\text{dQ}_7$
5	39	0.305	$8.00\times10^{-2}+(6.67\times10^{-2})\,\text{cRPpostRej}^2-0.17\,\text{feverOnly}+0.71\,\text{igG}+0.58\,\text{respiratoryInfection}$
6	41	0.223	$2.68\times10^{-2}+0.90\,\text{igG}+0.22\,\text{respiratoryInfection}+$ $0.76\,\text{allergy}\,\text{respiratoryInfection}+0.58\,\text{banfi}\,\text{antiHLAclass}_1$
7	41	0.273	$-(3.39\times10^{-2})+0.22\,\text{cRPpostRej}+$ $1.00\,\text{coaglationnecrosis}\,\text{respiratoryInfection}+0.66\,\text{b}_{45}+0.95\,\text{respiratoryInfection}\,\text{dQ}_4$
8	42	0.243	$-(3.58\times10^{-2})+(5.31\times10^{-2})\,\text{cRPpostRej}\,\text{hLAmm}+0.59\,\sqrt{\text{igG}}-0.31\,\text{pyrexia}+0.63\,\text{respiratoryInfection}$
9	42	0.257	$-(5.13\times10^{-2})+0.19\,\text{cRPpostRej}+0.63\,\text{igG}+$ $0.69\,\text{respiratoryInfection}-0.46\,\text{pyrexia}\,\text{upperRespiratoryInfection}^2$
10	42	0.265	$-(8.12\times10^{-2})+0.23\,\text{cRPpostRej}+0.60\,\text{igG}+$ $0.40\,\text{respiratoryInfection}\,(\text{coaglationnecrosis}+\text{respiratoryInfection}+\text{dR}_{53})$
11	42	0.267	$3.41\times10^{-2}+0.11\,\text{cNIpostRej}+0.36\,\text{respiratoryInfection}+1.06\,\text{b}_{45}+0.60\,\text{respiratoryInfection}\,\text{dQ}_7{}^2$
12	42	0.279	$-0.14-(8.53\times10^{-2})\,\text{cRPpostRej}+0.55\,\text{respiratoryInfection}+$ $0.10\,\text{hLAABmm}\,(\text{cRPpostRej}+\text{igG}+\text{antiHLAclass}_2)$
13	43	0.218	$4.22\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.83\,\text{b}_{45}$
14	43	0.241	$6.59\times10^{-2}+0.35\,\text{cRPpostRej}-0.19\,\text{feverOnly}+0.58\,\text{igG}+0.73\,\text{respiratoryInfection}-(6.16\times10^{-2})\,\text{uTI}$
15	43	0.246	$3.71\times10^{-2}+0.10\,\text{cNIpostRej}+0.58\,\text{igG}-$ $0.34\,\text{pyrexia}+0.68\,\text{respiratoryInfection}+0.22\,\text{dSAandHSAclass}_1$

◆ Ensembles in ParetoFront

■ **The 23rd Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.3792, The Observed value: 0

The Prediction: Right

Accuracy so far: 78.26% (45.1% completed)

◆ **Accuracies until the 23rd turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 2 min 36 sec

◆ **Error(= Predicted value - Observed value) in the 23rd Cross Validation**

◇ **Average Error is 0.3525±0.3302 until the 23rd turn in the LOO method.**

■ The 24th cross-validation out of 51 turns

□ The 24th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日23時 19分 4秒

□ The 24th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日23時 25分 44秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 – R2
0
50
100
150
200
250
Model Complexity

,

◆ **979 models were created**

◇ **Quatiliy Box values are {46., 0.1754} in the 24th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 979 Selected models: 1 (0.1021%)

◆ Inning 0. Complexity: 46. Error: 0.1754 Number of Selected models: 1 (0.1021%)

◆ Inning 1. Complexity: 47. Error: 0.1854 Number of Selected models: 1 (0.1021%)

◆ Inning 2. Complexity: 48. Error: 0.1954 Number of Selected models: 1 (0.1021%)

◆ Inning 3. Complexity: 49. Error: 0.2054 Number of Selected models: 2 (0.2043%)

◆ Inning 4. Complexity: 50. Error: 0.2154 Number of Selected models: 6 (0.6129%)

◆ Inning 5. Complexity: 51. Error: 0.2254 Number of Selected models: 14 (1.43%)

◆ Inning 6. Complexity: 52. Error: 0.2354 Number of Selected models: 18 (1.839%)

◆ Inning 7. Complexity: 53. Error: 0.2454 Number of Selected models: 29 (2.962%)

◆ Inning 8. Complexity: 54. Error: 0.2554 Number of Selected models: 39 (3.984%)

◆ Inning 9. Complexity: 55. Error: 0.2654 Number of Selected models: 44 (4.494%)

◆ Inning 10. Complexity: 56. Error: 0.2754 Number of Selected models: 53 (5.414%)

◆ Inning 11. Complexity: 57. Error: 0.2854 Number of Selected models: 66 (6.742%)

◆ Inning 12. Complexity: 58. Error: 0.2954 Number of Selected models: 78 (7.967%)

◆ Inning 13. Complexity: 59. Error: 0.3054 Number of Selected models: 87 (8.887%)

◆ **87 interesting models were selected**

◇ **Quatiliy Box values are {59., 0.305381}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, pyrexia, cNIpostRej, igG, b45}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.268	$5.57\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+1.04\,b_{45}$
2	38	0.267	$3.56\times10^{-2}+0.11\,\text{cNIpostRej}+0.36\,\text{respiratoryInfection}+$ $0.60\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+1.06\,b_{45}$
3	38	0.275	$-(4.17\times10^{-2})+0.12\,\text{cNIpostRej}+0.15\,\text{denovoDSA}+0.43\,\text{igG}\,\text{preDSA}+0.53\,\text{respiratoryInfection}$
4	38	0.294	$-(2.70\times10^{-2})+0.15\,\text{cRPpostRej}+0.44\,\text{igG}\,\text{preDSA}-0.37\,\text{pyrexia}+0.71\,\text{respiratoryInfection}$
5	42	0.290	$4.14\times10^{-2}+0.47\,\text{igG}-0.52\,\text{pyrexia}\,\text{respiratoryInfection}+0.74\,\text{respiratoryInfection}^2+0.72\,b_{45}$
6	43	0.212	$7.53\times10^{-2}+0.11\,\text{cNIpostRej}-\frac{1.82\times10^{-3}}{\text{hDperiod}}-0.43\,\text{pyrexia}+0.81\,\text{respiratoryInfection}+1.02\,b_{45}$
7	43	0.255	$-(2.91\times10^{-2})-0.36\,\text{pyrexia}+0.67\,\text{respiratoryInfection}+$ $0.99\,b_{45}+0.22\,dR_{53}+(2.11\times10^{-2})\,\text{wBCpeakover}_5$
8	44	0.261	$4.73\times10^{-2}+(9.09\times10^{-2})\,\text{cNIpostRej}+0.43\,\text{hLADRmm}\,\text{igG}+$ $0.78\,\text{respiratoryInfection}-(8.28\times10^{-2})\,\text{pyrexia}\,\text{upperRespiratoryInfection}\,\text{wBCpostKTx}$
9	46	0.175	$2.40\times10^{-2}+0.11\,\text{cNIpostRej}+0.41\,\text{igG}+$ $0.79\,\text{respiratoryInfection}-0.52\,\text{pyrexia}\,\text{respiratoryInfection}+0.86\,b_{45}$
10	46	0.204	$-(1.22\times10^{-2})+0.11\,\text{cNIpostRej}+0.13\,\text{denovoDSA}+$ $0.43\,\text{igG}\,\text{preDSA}-0.31\,\text{pyrexia}+0.64\,\text{respiratoryInfection}$
11	46	0.209	$4.15\times10^{-2}+0.11\,\text{cNIpostRej}+0.47\,\text{igG}-0.36\,\text{pyrexia}+0.71\,\text{respiratoryInfection}-0.99\,\text{cNIpostRej}\,b_{45}$
12	46	0.210	$1.53\times10^{-2}+0.12\,\text{cNIpostRej}+(5.72\times10^{-2})\,\text{dSAclass1number}+$ $0.85\,\text{respiratoryInfection}-0.54\,\text{pyrexia}\,\text{respiratoryInfection}+0.91\,b_{45}$
13	49	0.203	$4.02\times10^{-2}+0.11\,\text{cNIpostRej}-0.35\,\text{pyrexia}+0.70\,\text{respiratoryInfection}+1.05\,\text{type2DM}\,b_{75}+0.55\,\text{igG}\,dR_{53}$
14	50	0.206	$1.30\times10^{-2}+(1.55\times10^{-2})\,\text{cNIpostRej}^2+0.40\,\text{hLADRmm}\,\text{igG}-$ $0.36\,\text{pyrexia}+0.70\,\text{respiratoryInfection}+0.20\,\text{dSAandHSAclass}_1$
15	57	0.161	$2.10\times10^{-2}+0.11\,\text{cNIpostRej}+0.53\,\text{igG}+0.78\,\text{respiratoryInfection}-$ $0.51\,\text{pyrexia}\,\text{respiratoryInfection}-1.35\,b_{45}-2.57\,\text{cNIpostRej}\,b_{45}$

◆ Ensembles in ParetoFront

■ **The 24th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.03634, The Observed value: 0

The Prediction: Right

Accuracy so far: 79.17% (47.06% completed)

◆ **Accuracies until the 24th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 2 min 29 sec

◆ **Error(= Predicted value - Observed value) in the 24th Cross Validation**

◇ **Average Error is 0.3393±0.3293 until the 24th turn in the LOO method.**

■ The 25th cross-validation out of 51 turns

□ The 25th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日⁚23時 25分 48秒

□ The 25th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日⁚23時 32分 28秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
500
400
300
200
100
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
50
40
30
20
10
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1− R2
50
100
150
200
Model Complexity

,

◆ **1049 models were created**

◇ **Quatiliy Box values are {33., 0.179} in the 25th turn.**

- Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.
- Generated models: 1049 Selected models: 1 (0.09533%)
- Inning 0. Complexity: 33. Error: 0.179 Number of Selected models: 1 (0.09533%)
- Inning 1. Complexity: 34. Error: 0.189 Number of Selected models: 1 (0.09533%)
- Inning 2. Complexity: 35. Error: 0.199 Number of Selected models: 1 (0.09533%)
- Inning 3. Complexity: 36. Error: 0.209 Number of Selected models: 2 (0.1907%)
- Inning 4. Complexity: 37. Error: 0.219 Number of Selected models: 2 (0.1907%)
- Inning 5. Complexity: 38. Error: 0.229 Number of Selected models: 7 (0.6673%)
- Inning 6. Complexity: 39. Error: 0.239 Number of Selected models: 9 (0.858%)
- Inning 7. Complexity: 40. Error: 0.249 Number of Selected models: 10 (0.9533%)
- Inning 8. Complexity: 41. Error: 0.259 Number of Selected models: 13 (1.239%)
- Inning 9. Complexity: 42. Error: 0.269 Number of Selected models: 18 (1.716%)
- Inning 10. Complexity: 43. Error: 0.279 Number of Selected models: 27 (2.574%)
- Inning 11. Complexity: 44. Error: 0.289 Number of Selected models: 33 (3.146%)
- Inning 12. Complexity: 45. Error: 0.299 Number of Selected models: 41 (3.908%)
- Inning 13. Complexity: 46. Error: 0.309 Number of Selected models: 55 (5.243%)
- Inning 14. Complexity: 47. Error: 0.319 Number of Selected models: 64 (6.101%)

- Inning 15. Complexity: 48. Error: 0.329 Number of Selected models: 86 (8.198%)

- **86 interesting models were selected**
  - **Quatiliy Box values are {48., 0.328968}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, igG, cNIpostRej, inflammationdatefirst, pyrexia}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	22	0.323	$3.86\times10^{-2}+0.85\,\text{igG}+(8.64\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}$
2	30	0.207	$2.65\times10^{-2}+0.11\,\text{cNIpostRej}+0.84\,\text{igG}+(9.19\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}$
3	30	0.289	$1.48\times10^{-2}+0.12\,\text{banf g cNIpostRej}+0.70\,\text{igG}+0.57\,\text{respiratoryInfection}$
4	30	0.299	$5.80\times10^{-2}+0.83\,\text{igG}-0.16\,\text{pyrexia}+(8.76\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}$
5	33	0.179	$9.34\times10^{-3}+0.38\,\text{cRPpreRej heartDisease}+$ $0.88\,\text{igG}+(8.61\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}$
6	33	0.225	$8.33\times10^{-6}+(8.27\times10^{-3})\,\text{cRPpreRej hDperiod}+$ $0.88\,\text{igG}+(9.04\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}$
7	35	0.318	$0.10+0.76\,\text{igG}-(7.48\times10^{-2})\,\text{lymphinvasion}-0.35\,\text{pyrexia}+0.65\,\text{respiratoryInfection}$
8	38	0.201	$-(1.52\times10^{-2})+0.71\,\text{igG}+0.73\,\text{respiratoryInfection}-$ $0.53\,\text{pyrexia respiratoryInfection}+(1.97\times10^{-2})\,\text{wBCpeakover}_5$
9	38	0.202	$1.89\times10^{-2}+0.11\,\text{cNIpostRej}+0.83\,\text{igG}+$ $0.10\,\text{respiratoryInfection}+(8.05\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}$
10	38	0.211	$5.01\times10^{-2}+(9.74\times10^{-2})\,\text{banfptc cNIpostRej}+0.65\,\text{igG}-0.34\,\text{pyrexia}+0.70\,\text{respiratoryInfection}$
11	38	0.239	$2.02\times10^{-2}+0.10\,\text{cNIpostRej}+0.82\,\text{igG}+0.95\,\text{respiratoryInfection}-0.24\,\text{banfptc respiratoryInfection}$
12	39	0.249	$3.50\times10^{-2}+0.10\,\text{cNIpostRej}+0.73\,\text{igG}-0.20\,\text{pyrexia}^2+0.67\,\text{respiratoryInfection}$
13	41	0.157	$2.23\times10^{-2}+0.10\,\text{cNIpostRej}+0.75\,\text{igG}+$ $(7.06\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+0.37\,\text{respiratoryInfection dQ}_7$
14	41	0.166	$4.55\times10^{-2}+0.41\,\text{cRPpreRej heartDisease}+0.88\,\text{igG}-$ $(9.65\times10^{-3})\,\text{maxCRP}+(8.90\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}$
15	44	0.174	$2.37\times10^{-2}+(8.36\times10^{-2})\,\text{banfptc cNIpostRej}+0.85\,\text{igG}+$ $0.80\,\text{respiratoryInfection}-0.30\,\text{aerobicGPC banfptc respiratoryInfection}$

◆ Ensembles in ParetoFront

■ **The 25th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: -0.009153, The Observed value: 1

The Prediction: Wrong

Accuracy so far: 76.% (49.02% completed)

◆ **Accuracies until the 25th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 2 min 23 sec

◆ **Error (= Predicted value - Observed value) in the 25th Cross Validation**

◇ **Average Error is 0.3661±0.3491 until the 25th turn in the LOO method.**

■ The 26th cross-validation out of 51 turns

□ The 26th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日⁚23時 32分 31秒

□ The 26th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日⁚23時 39分 7秒

◆ Monitors Plot

0.01
0
200
400
600
800
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
−200
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
ModelAge
80
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
50
100
150
200
250
Model Complexity

,

◆ **917 models were created**

◇ **Quatiliy Box values are {51., 0.2059} in the 26th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 917 Selected models: 1 (0.1091%)

◆ Inning 0. Complexity: 51. Error: 0.2059 Number of Selected models: 1 (0.1091%)

◆ Inning 1. Complexity: 52. Error: 0.2159 Number of Selected models: 2 (0.2181%)

◆ Inning 2. Complexity: 53. Error: 0.2259 Number of Selected models: 4 (0.4362%)

◆ Inning 3. Complexity: 54. Error: 0.2359 Number of Selected models: 4 (0.4362%)

◆ Inning 4. Complexity: 55. Error: 0.2459 Number of Selected models: 6 (0.6543%)

◆ Inning 5. Complexity: 56. Error: 0.2559 Number of Selected models: 6 (0.6543%)

◆ Inning 6. Complexity: 57. Error: 0.2659 Number of Selected models: 7 (0.7634%)

◆ Inning 7. Complexity: 58. Error: 0.2759 Number of Selected models: 10 (1.091%)

◆ Inning 8. Complexity: 59. Error: 0.2859 Number of Selected models: 23 (2.508%)

◆ Inning 9. Complexity: 60. Error: 0.2959 Number of Selected models: 30 (3.272%)

◆ Inning 10. Complexity: 61. Error: 0.3059 Number of Selected models: 34 (3.708%)

◆ Inning 11. Complexity: 62. Error: 0.3159 Number of Selected models: 48 (5.234%)

◆ Inning 12. Complexity: 63. Error: 0.3259 Number of Selected models: 64 (6.979%)

◆ Inning 13. Complexity: 64. Error: 0.3359 Number of Selected models: 79 (8.615%)

◆ **79 interesting models were selected**

  ◇ **Quatiliy Box values are {64., 0.335906}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, pyrexia, igG}**

◆ Defining Ensembles

graftLoss

	Complexity	$1-R^2$	Function
1	43	0.224	$4.10\times10^{-2}+0.11\,\text{cNIpostRej}+0.44\,\text{igG}-0.34\,\text{pyrexia}+0.68\,\text{respiratoryInfection}+0.83\,b_{45}$
2	43	0.273	$4.68\times10^{-2}+0.12\,\text{cNIpostRej}+0.19\,\text{coaglationnecrosis}-0.36\,\text{pyrexia}+0.71\,\text{respiratoryInfection}+1.05\,b_{45}$
3	43	0.301	$3.82\times10^{-2}-(7.66\times10^{-2})\,\text{banfci}+0.11\,\text{cNIpostRej}+0.54\,\text{igG}+0.60\,\text{respiratoryInfection}+0.86\,b_{45}$
4	43	0.315	$8.16\times10^{-2}-(9.97\times10^{-2})\,\text{banfci}+0.54\,\text{igG}-0.37\,\text{pyrexia}+0.69\,\text{respiratoryInfection}+0.75\,b_{45}$
5	51	0.206	$6.13\times10^{-2}-(8.58\times10^{-2})\,\text{banfci}+0.11\,\text{cNIpostRej}+$ $0.48\,\text{igG}-0.35\,\text{pyrexia}+0.73\,\text{respiratoryInfection}+0.87\,b_{45}$
6	51	0.256	$1.20\times10^{-2}+0.11\,\text{cNIpostRej}+0.64\,\text{igG}+0.48\,\text{respiratoryInfection}+0.38\,\text{antiHLAclass}_1+0.62\,b_{45}-0.48\,b_{51}$
7	51	0.268	$9.07\times10^{-2}+0.13\,\text{cNIpostRej}-0.37\,\text{pyrexia}+$ $0.78\,\text{respiratoryInfection}+(4.77\times10^{-2})\,\text{twinpeak}-(2.45\times10^{-2})\,\text{uTI}+1.00\,b_{45}$
8	54	0.192	$2.54\times10^{-2}+0.10\,\text{cNIpostRej}-0.36\,\text{pyrexia}+$ $0.73\,\text{respiratoryInfection}+(7.76\times10^{-2})\,\text{antiHLAclass}_1+0.98\,b_{45}+0.86\,\bullet\text{igA}\,dR_{51}$
9	57	0.219	$5.74\times10^{-4}+0.36\,\text{candida}+0.50\,\text{banfah}\,\text{citobacterdiversus}+$ $0.46\,\text{heartDisease}+0.62\,\text{igG}+1.00\,\text{coaglationnecrosis}\,\text{respiratoryInfection}+0.69\,b_{45}$
10	59	0.274	$-(6.19\times10^{-2})-0.19\,\text{aerobicGPC}+0.19\,\text{cRPpostRej}+0.57\,\text{igG}+$ $0.29\,\text{malignantHypertention}+0.50\,\text{respiratoryInfection}+0.12\,dQ_7+0.13\,\text{dSAandHSAclass}_1$
11	62	0.185	$2.83\times10^{-2}+0.11\,\text{cNIpostRej}-0.35\,\text{pyrexia}+$ $0.71\,\text{respiratoryInfection}+0.16\,\text{antiHLAclass}_1+0.99\,b_{45}-0.18\,b_{58}+0.85\,\bullet\text{igA}\,dR_{51}$
12	62	0.257	$-(2.54\times10^{-2})+0.41\,\text{candida}+0.36\,\text{banfah}\,\text{citobacterdiversus}+$ $0.26\,\text{heartDisease}+0.51\,\text{igG}+0.31\,\text{respiratoryInfection}+0.77\,b_{45}+0.21\,dR_{15}$
13	63	0.278	$0.21+0.40\,\text{coaglationnecrosis}+0.17\,\text{cRPpostRej}+0.70\,\text{igG}+$ $0.40\,\text{interstitialHemorrhage}+0.41\,\text{respiratoryInfection}-0.13\,\sqrt{\text{wBCpostKTx}}+0.29\,\text{antiHLAclass}_1$

◆ Ensembles in ParetoFront

■ The 26th Cross Validation with Leave-One-Out Method out of 51 turns

The Estimated value: 0.6148, The Observed value: 1

The Prediction: Right

Accuracy so far: 76.92% (50.98% completed)

◆ **Accuracies until the 26th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 2 min 16 sec

◆ **Error(= Predicted value - Observed value) in the 26th Cross Validation**

◇ **Average Error is 0.3668±0.3421 until the 26th turn in the LOO method.**

■ The 27th cross-validation out of 51 turns

□ The 27th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日⧈23時 39分 11秒

□ The 27th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日⧈23時 45分 51秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
500
400
300
200
100
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
40
30
20
10
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
20
40
60
80
100
120
140
160
Model Complexity

,

◆ **1025 models were created**

◇ **Quatiliy Box values are {46., 0.1585} in the 27th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1025 Selected models: 1 (0.09756%)

◆ Inning 0. Complexity: 46. Error: 0.1585 Number of Selected models: 1 (0.09756%)

◆ Inning 1. Complexity: 47. Error: 0.1685 Number of Selected models: 1 (0.09756%)

◆ Inning 2. Complexity: 48. Error: 0.1785 Number of Selected models: 1 (0.09756%)

◆ Inning 3. Complexity: 49. Error: 0.1885 Number of Selected models: 3 (0.2927%)

◆ Inning 4. Complexity: 50. Error: 0.1985 Number of Selected models: 6 (0.5854%)

◆ Inning 5. Complexity: 51. Error: 0.2085 Number of Selected models: 10 (0.9756%)

◆ Inning 6. Complexity: 52. Error: 0.2185 Number of Selected models: 22 (2.146%)

◆ Inning 7. Complexity: 53. Error: 0.2285 Number of Selected models: 31 (3.024%)

◆ Inning 8. Complexity: 54. Error: 0.2385 Number of Selected models: 48 (4.683%)

◆ Inning 9. Complexity: 55. Error: 0.2485 Number of Selected models: 56 (5.463%)

◆ Inning 10. Complexity: 56. Error: 0.2585 Number of Selected models: 60 (5.854%)

◆ Inning 11. Complexity: 57. Error: 0.2685 Number of Selected models: 81 (7.902%)

◆ Inning 12. Complexity: 58. Error: 0.2785 Number of Selected models: 97 (9.463%)

◆ **97 interesting models were selected**

◇ **Quatiliy Box values are {58., 0.27848}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, pyrexia, igG, cNIpostRej}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.268	$5.64\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+1.04\,b_{45}$
2	38	0.273	$-(2.87\times10^{-2})+(9.00\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+0.99\,b_{45}+0.36\,dR_{52}+(1.85\times10^{-2})\,\text{wBCpeakover}_5$
3	41	0.263	$2.21\times10^{-2}+0.60\,\text{cellInvasion igG}+0.94\,\text{respiratoryInfection antiHLAclass}_2+0.64\,b_{45}+(1.96\times10^{-2})\,\text{wBCpeakover}_5$
4	41	0.272	$6.96\times10^{-3}+0.11\,\text{cNIpostRej}+0.60\,\text{respiratoryInfection}+1.09\,b_{45}+0.10\,\text{hDperiod type2DM}\,dR_{18}$
5	41	0.275	$1.73\times10^{-2}+0.36\,(2.18-\text{pyrexia})\,\sqrt{\text{igG}+\text{respiratoryInfection}+b_{45}}$
6	42	0.245	$2.15\times10^{-2}+0.82\,\text{respiratoryInfection}-0.56\,\text{pyrexia respiratoryInfection}+0.98\,b_{45}+(4.98\times10^{-4})\,\text{wBCpeakover}_5{}^2$
7	42	0.266	$3.63\times10^{-2}+0.11\,\text{cNIpostRej}+0.36\,\text{respiratoryInfection}+1.06\,b_{45}+0.60\,\text{respiratoryInfection}\,\sqrt{dQ_7}$
8	43	0.211	$7.60\times10^{-2}+0.11\,\text{cNIpostRej}-\frac{1.82\times10^{-3}}{\text{hDperiod}}-0.43\,\text{pyrexia}+0.81\,\text{respiratoryInfection}+1.01\,b_{45}$
9	43	0.236	$6.88\times10^{-3}+0.47\,\text{igG}-0.39\,\text{pyrexia}+0.68\,\text{respiratoryInfection}+0.72\,b_{45}+(1.90\times10^{-2})\,\text{wBCpeakover}_5$
10	44	0.225	$-(1.75\times10^{-3})+0.95\,\text{cellInvasion igG}+(5.51\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+0.62\,\text{respiratoryInfection antiHLAclass}_2+(1.88\times10^{-2})\,\text{wBCpeakover}_5$
11	46	0.158	$5.29\times10^{-2}+0.11\,\text{cNIpostRej}-\frac{1.92\times10^{-3}}{\text{hDperiod}}+0.90\,\text{respiratoryInfection}-0.61\,\text{pyrexia respiratoryInfection}+1.04\,b_{45}$
12	46	0.175	$2.48\times10^{-2}+0.11\,\text{cNIpostRej}+0.41\,\text{igG}+0.79\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.86\,b_{45}$
13	46	0.219	$6.03\times10^{-2}-\frac{2.06\times10^{-3}}{\text{hDperiod}}+0.42\,\text{igG}+0.82\,\text{respiratoryInfection}-0.59\,\text{pyrexia respiratoryInfection}+0.73\,b_{45}$
14	46	0.220	$5.07\times10^{-2}+0.11\,\text{cNIpostRej}-0.27\,\text{pyrexia}+0.90\,\text{respiratoryInfection}-0.25\,\text{feverOnly respiratoryInfection}+1.04\,b_{45}$
15	49	0.197	$3.58\times10^{-2}+0.11\,\text{cNIpostRej}+0.64\,\text{respiratoryInfection}-0.42\,\text{pyrexia respiratoryInfection}+1.06\,b_{45}+0.32\,\text{respiratoryInfection}\,dQ_7$

◆ Ensembles in ParetoFront

■ **The 27th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.0391, The Observed value: 0

The Prediction: Right

Accuracy so far: 77.78% (52.94% completed)

◆ **Accuracies until the 27th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 2 min 9 sec

◆ **Error(= Predicted value - Observed value) in the 27th Cross Validation**

◇ **Average Error is 0.3547±0.3413 until the 27th turn in the LOO method.**

■ The 28th cross-validation out of 51 turns

□ The 28th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日 23時 45分 55秒

□ The 28th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日 23時 52分 13秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
100
200
300
400
Model Complexity

,

◆ **957 models were created**

◇ **Quatiliy Box values are {42., 0.2109} in the 28th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 957 Selected models: 1 (0.1045%)

◆ Inning 0. Complexity: 42. Error: 0.2109 Number of Selected models: 1 (0.1045%)

◆ Inning 1. Complexity: 43. Error: 0.2209 Number of Selected models: 2 (0.209%)

◆ Inning 2. Complexity: 44. Error: 0.2309 Number of Selected models: 3 (0.3135%)

◆ Inning 3. Complexity: 45. Error: 0.2409 Number of Selected models: 4 (0.418%)

◆ Inning 4. Complexity: 46. Error: 0.2509 Number of Selected models: 9 (0.9404%)

◆ Inning 5. Complexity: 47. Error: 0.2609 Number of Selected models: 11 (1.149%)

◆ Inning 6. Complexity: 48. Error: 0.2709 Number of Selected models: 19 (1.985%)

◆ Inning 7. Complexity: 49. Error: 0.2809 Number of Selected models: 25 (2.612%)

◆ Inning 8. Complexity: 50. Error: 0.2909 Number of Selected models: 31 (3.239%)

◆ Inning 9. Complexity: 51. Error: 0.3009 Number of Selected models: 53 (5.538%)

◆ Inning 10. Complexity: 52. Error: 0.3109 Number of Selected models: 60 (6.27%)

◆ Inning 11. Complexity: 53. Error: 0.3209 Number of Selected models: 75 (7.837%)

◆ Inning 12. Complexity: 54. Error: 0.3309 Number of Selected models: 103 (10.76%)

◆ **103 interesting models were selected**

  ◇ **Quatiliy Box values are {54., 0.330893}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, igG, pyrexia}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	33	0.312	$5.15\times10^{-2}+(5.57\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.95\,b_{45}+0.59\,\text{respiratoryInfection}\,dQ_8$
2	34	0.298	$3.30\times10^{-2}+(1.55\times10^{-2})\,\text{cNIpostRej}^2+0.84\,\text{igG}+(8.67\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}$
3	34	0.303	$5.06\times10^{-2}+0.12\,\text{cNIpostRej}+(9.58\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}^2+1.05\,b_{45}$
4	34	0.327	$4.51\times10^{-2}+0.62\,\text{igG}+(8.73\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.64\,b_{45}{}^2$
5	38	0.211	$3.01\times10^{-2}+0.11\,\text{cNIpostRej}+0.57\,\text{igG}+(9.37\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.78\,b_{45}$
6	38	0.228	$3.36\times10^{-2}+0.11\,\text{cNIpostRej}+1.10\,\text{respiratoryInfection}-0.47\,\text{banfi}\,\text{respiratoryInfection}+1.06\,b_{45}$
7	38	0.298	$3.30\times10^{-2}+(1.55\times10^{-2})\,\text{cNIpostRej}^2+0.84\,\text{igG}+(8.67\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}^2$
8	42	0.272	$4.16\times10^{-2}+0.46\,\text{igG}+0.77\,\text{respiratoryInfection}-0.69\,\sqrt{\text{pyrexia}}\,\text{respiratoryInfection}+0.73\,b_{45}$
9	42	0.277	$1.25\times10^{-2}+0.69\,\text{igG}+0.73\,\text{respiratoryInfection}-0.70\,\sqrt{\text{pyrexia}}\,\text{respiratoryInfection}+(1.95\times10^{-2})\,\text{wBCpeakover}_5$
10	43	0.218	$4.22\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.83\,b_{45}$
11	43	0.232	$1.14\times10^{-2}+0.12\,\text{cNIpostRej}-0.33\,\text{pyrexia}+0.70\,\text{respiratoryInfection}+1.09\,b_{45}+0.20\,dR_{53}$
12	43	0.246	$3.71\times10^{-2}+0.10\,\text{cNIpostRej}+0.58\,\text{igG}-0.34\,\text{pyrexia}+0.68\,\text{respiratoryInfection}+0.22\,\text{dSAandHSAclass}_1$
13	46	0.188	$3.28\times10^{-2}+0.10\,\text{cNIpostRej}+(1.12\times10^{-2})\,\text{igG}\,\text{pRAclass2pre}-0.38\,\text{pyrexia}+0.77\,\text{respiratoryInfection}+1.05\,b_{45}$
14	46	0.260	$-(2.54\times10^{-2})+0.12\,\text{cNIpostRej}+(9.01\times10^{-3})\,\text{igG}\,\text{pRAclass2pre}+0.62\,\text{respiratoryInfection}+1.12\,b_{45}+0.21\,dR_{53}$
15	47	0.237	$1.78\times10^{-2}+0.78\,b_{45}+0.95\,\text{respiratoryInfection}\,dQ_7+(8.11\times10^{-2})\,\text{maxWBC}\,\text{timeoftransplantation}\,c_3\,dQ_7+(1.95\times10^{-2})\,\text{wBCpeakover}_5$

◆ Ensembles in ParetoFront

■ **The 28th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.008674, The Observed value: 0

The Prediction: Right

Accuracy so far: 78.57% (54.9% completed)

◆ **Accuracies until the 28th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 2 min 3 sec

◆ **Error(= Predicted value - Observed value) in the 28th Cross Validation**

◇ **Average Error is 0.3423±0.3412 until the 28th turn in the LOO method.**

■ The 29th cross-validation out of 51 turns

□ The 29th Genetic Programming has started.

◆ Present Time: 2020年 7月 13日 23時 52分 17秒

□ The 29th Genetic Programming has ended.

◆ Present Time: 2020年 7月 13日 23時 58分 29秒

◆ Monitors Plot

0.01
0
200
400
600
800
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 – R2
0
100
200
300
400
Model Complexity

,

◆ **993 models were created**

◇ **Quatiliy Box values are {46., 0.1679} in the 29th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 993 Selected models: 1 (0.1007%)

◆ Inning 0. Complexity: 46. Error: 0.1679 Number of Selected models: 1 (0.1007%)

◆ Inning 1. Complexity: 47. Error: 0.1779 Number of Selected models: 1 (0.1007%)

◆ Inning 2. Complexity: 48. Error: 0.1879 Number of Selected models: 2 (0.2014%)

◆ Inning 3. Complexity: 49. Error: 0.1979 Number of Selected models: 4 (0.4028%)

◆ Inning 4. Complexity: 50. Error: 0.2079 Number of Selected models: 4 (0.4028%)

◆ Inning 5. Complexity: 51. Error: 0.2179 Number of Selected models: 13 (1.309%)

◆ Inning 6. Complexity: 52. Error: 0.2279 Number of Selected models: 15 (1.511%)

◆ Inning 7. Complexity: 53. Error: 0.2379 Number of Selected models: 16 (1.611%)

◆ Inning 8. Complexity: 54. Error: 0.2479 Number of Selected models: 24 (2.417%)

◆ Inning 9. Complexity: 55. Error: 0.2579 Number of Selected models: 30 (3.021%)

◆ Inning 10. Complexity: 56. Error: 0.2679 Number of Selected models: 35 (3.525%)

◆ Inning 11. Complexity: 57. Error: 0.2779 Number of Selected models: 45 (4.532%)

◆ Inning 12. Complexity: 58. Error: 0.2879 Number of Selected models: 50 (5.035%)

◆ Inning 13. Complexity: 59. Error: 0.2979 Number of Selected models: 58 (5.841%)

◆ Inning 14. Complexity: 60. Error: 0.3079 Number of Selected models: 68 (6.848%)

- Inning 15. Complexity: 61. Error: 0.3179 Number of Selected models: 77 (7.754%)
- Inning 16. Complexity: 62. Error: 0.3279 Number of Selected models: 86 (8.661%)

- **86 interesting models were selected**
  - **Quatiliy Box values are {62., 0.327888}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, cNIpostRej, b45, pyrexia, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.259	$6.08\times10^{-2}+0.12\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+1.04\,b_{45}$
2	38	0.290	$4.14\times10^{-2}+0.47\,\text{igG}+0.74\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.72\,b_{45}$
3	38	0.303	$2.14\times10^{-2}+0.13\,\text{aerobicGPC cNIpostRej}+0.55\,\text{igG}+0.58\,\text{respiratoryInfection}+0.70\,b_{45}$
4	38	0.304	$6.07\times10^{-2}+(9.64\times10^{-2})\,\text{cNIpostRej}+0.69\,\text{igG}+$ $0.72\,\text{respiratoryInfection}-0.50\,\text{pyrexia respiratoryInfection}$
5	42	0.310	$7.12\times10^{-2}+0.12\,\text{cNIpostRej}-0.19\,\text{pyrexia}+\frac{1.50\,\text{respiratoryInfection}}{\text{mMFpostRej}}+1.03\,b_{45}$
6	43	0.292	$-(5.36\times10^{-2})+0.16\,\text{cNIpostRej}-0.19\,\text{enterococcusfaecalis}+$ $0.66\,\text{respiratoryInfection}+0.21\,\text{antiHLAclass}_2+0.97\,b_{45}$
7	46	0.168	$2.92\times10^{-2}+0.12\,\text{cNIpostRej}+0.41\,\text{igG}+$ $0.79\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.87\,b_{45}$
8	46	0.181	$3.93\times10^{-2}+0.11\,\text{cNIpostRej}-0.38\,\text{pyrexia}+0.77\,\text{respiratoryInfection}+0.83\,\bullet\text{igA antiHLAclass}_2+1.05\,b_{45}$
9	46	0.213	$4.95\times10^{-2}+0.11\,\text{cNIpostRej}+0.71\,\text{igG}-0.35\,\text{pyrexia}+0.68\,\text{respiratoryInfection}+1.05\,b_{45}\,b_{62}$
10	49	0.166	$2.39\times10^{-2}+0.13\,\text{aerobicGPC cNIpostRej}+0.48\,\text{igG}+$ $0.77\,\text{respiratoryInfection}-0.51\,\text{pyrexia respiratoryInfection}+0.74\,b_{45}$
11	49	0.190	$4.01\times10^{-2}+0.12\,\text{cNIpostRej}+0.64\,\text{respiratoryInfection}-$ $0.42\,\text{pyrexia respiratoryInfection}+0.32\,\text{respiratoryInfection antiHLAclass}_2+1.06\,b_{45}$
12	51	0.210	$7.79\times10^{-2}+0.15\,\text{cNIpostRej}-0.34\,\text{pyrexia}+$ $0.79\,\text{respiratoryInfection}-(3.04\times10^{-2})\,\text{uTI}+1.06\,b_{45}+0.17\,dQ_6$
13	54	0.165	$3.15\times10^{-2}-0.12\,\text{calcification}+0.12\,\text{cNIpostRej}+0.45\,\text{igG}+$ $0.80\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.84\,b_{45}$
14	57	0.112	$3.55\times10^{-2}+0.14\,\text{cNIpostRej}-0.24\,\text{enterococcusfaecalis}+0.87\,\text{respiratoryInfection}-$ $0.57\,\text{pyrexia respiratoryInfection}+0.81\,\bullet\text{igA antiHLAclass}_2+1.08\,b_{45}$
15	57	0.122	$6.47\times10^{-2}+0.13\,\text{cNIpostRej}+0.91\,\text{respiratoryInfection}-$ $0.55\,\text{pyrexia respiratoryInfection}-(2.42\times10^{-2})\,\text{uTI}+0.81\,\bullet\text{igA antiHLAclass}_2+1.06\,b_{45}$

◆ Ensembles in ParetoFront

■ **The 29th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.2499, The Observed value: 0

The Prediction: Right

Accuracy so far: 79.31% (56.86% completed)

◆ **Accuracies until the 29th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 1 min 57 sec

◆ **Error(= Predicted value - Observed value) in the 29th Cross Validation**

◇ **Average Error is 0.3391±0.3355 until the 29th turn in the LOO method.**

■ The 30th cross-validation out of 51 turns

□ **The 30th Genetic Programming has started.**

◆ **Present Time: 2020年 7月 13日23時 58分 33秒**

LinkObject: Unable to communicate with closed link LinkObject['/Applications/Wolfram Desktop.app/Contents/MacOS/WolframKernel' −subkernel −noinit −nopaclet −wstp, 8510, 15].

KernelObject: Subkernel connected through KernelObject[Name: local KernelID: 2] appears dead.

□ **The 30th Genetic Programming has ended.**

◆ **Present Time: 2020年 7月 14日0時 5分 9秒**

◆ Monitors Plot

Error = 1 −
0.10
0.05
0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
120
100
80
60
40
20
0
−20

Pareto Fronts
Error = 1 − R²
1
0.50
0.10
0.05

◆ **760 models were created**

◇ **Quatiliy Box values are {60., 0.1501} in the 30th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 760 Selected models: 1 (0.1316%)

◆ Inning 0. Complexity: 60. Error: 0.1501 Number of Selected models: 1 (0.1316%)

◆ Inning 1. Complexity: 61. Error: 0.1601 Number of Selected models: 1 (0.1316%)

◆ Inning 2. Complexity: 62. Error: 0.1701 Number of Selected models: 1 (0.1316%)

◆ Inning 3. Complexity: 63. Error: 0.1801 Number of Selected models: 1 (0.1316%)

◆ Inning 4. Complexity: 64. Error: 0.1901 Number of Selected models: 2 (0.2632%)

◆ Inning 5. Complexity: 65. Error: 0.2001 Number of Selected models: 4 (0.5263%)

◆ Inning 6. Complexity: 66. Error: 0.2101 Number of Selected models: 4 (0.5263%)

◆ Inning 7. Complexity: 67. Error: 0.2201 Number of Selected models: 4 (0.5263%)

◆ Inning 8. Complexity: 68. Error: 0.2301 Number of Selected models: 8 (1.053%)

◆ Inning 9. Complexity: 69. Error: 0.2401 Number of Selected models: 12 (1.579%)

◆ Inning 10. Complexity: 70. Error: 0.2501 Number of Selected models: 16 (2.105%)

◆ Inning 11. Complexity: 71. Error: 0.2601 Number of Selected models: 26 (3.421%)

◆ Inning 12. Complexity: 72. Error: 0.2701 Number of Selected models: 32 (4.211%)

◆ Inning 13. Complexity: 73. Error: 0.2801 Number of Selected models: 35 (4.605%)

- Inning 14. Complexity: 74. Error: 0.2901 Number of Selected models: 45 (5.921%)
- Inning 15. Complexity: 75. Error: 0.3001 Number of Selected models: 52 (6.842%)
- Inning 16. Complexity: 76. Error: 0.3101 Number of Selected models: 65 (8.553%)

- **65 interesting models were selected**
  - **Quatiliy Box values are {76., 0.310128}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, igG, candida, dR7, pyrexia}**

◆ Defining Ensembles

graftLoss

	Complexity	$1-R^2$	Function
1	38	0.307	$4.87\times10^{-2}+0.75\,\text{igG}-0.33\,\text{pyrexia}+0.59\,\text{respiratoryInfection}+0.18\,\text{denovoDSA}\,\text{dR}_7$
2	43	0.306	$0.12+0.73\,\text{candida}+0.75\,\text{igG}-0.33\,\text{pyrexia}+0.64\,\text{respiratoryInfection}-(3.13\times10^{-2})\,\text{uTI}$
3	46	0.197	$2.26\times10^{-2}+0.72\,\text{candida}+0.80\,\text{igG}-0.28\,\text{pyrexia}+0.52\,\text{respiratoryInfection}+0.19\,\text{denovoDSA}\,\text{dR}_7$
4	46	0.277	$3.19\times10^{-2}+0.54\,\text{igG}-0.34\,\text{pyrexia}+0.64\,\sqrt{\text{candida}+\text{respiratoryInfection}+\text{b}_{44}}$
5	51	0.222	$7.34\times10^{-3}+0.71\,\text{candida}+0.63\,\text{igG}-0.29\,\text{pyrexia}+$ $0.56\,\text{respiratoryInfection}+0.19\,\text{dR}_7+0.17\,\text{dSAandHSAclass}_1$
6	51	0.244	$1.17\times10^{-2}+0.55\,\text{candida}+(4.07\times10^{-2})\,\text{cRPpostRej}+$ $0.63\,\text{igG}-0.31\,\text{pyrexia}+0.59\,\text{respiratoryInfection}+0.18\,\text{dSAandHSAclass}_1$
7	53	0.285	$4.11+0.56\,\text{respiratoryInfection}+0.62\,\text{b}_{45}-\frac{133.72}{32.40+\text{banfptc}\,\text{cNIpostRej}+\text{denovoDSA}+\text{dR}_{51}}$
8	54	0.194	$3.03\times10^{-2}+0.70\,\text{candida}+0.82\,\text{igG}-0.29\,\text{pyrexia}+$ $0.53\,\text{respiratoryInfection}-(7.61\times10^{-2})\,\text{dP}_{17}+0.20\,\text{denovoDSA}\,\text{dR}_7$
9	54	0.224	$9.95\times10^{-3}+0.82\,\text{candida}+0.83\,\text{igG}+$ $0.35\,\text{respiratoryInfection}+0.14\,\text{b}_{13}+0.71\,(\text{respiratoryInfection}+\text{a}_{34})\,\text{dR}_7$
10	60	0.150	$2.26-\frac{3.79}{1.71+\text{candida}+\text{igG}+\text{coaglationnecrosis}\,\text{respiratoryInfection}+\text{respiratoryInfection}\,\text{antiHLAclass}_2+\text{b}_{45}^2}$
11	62	0.207	$-(1.28\times10^{-2})+0.66\,\text{candida}+0.37\,\text{coaglationnecrosis}+0.49\,\text{igG}+$ $0.28\,\text{respiratoryInfection}+0.42\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.67\,\text{b}_{45}+0.19\,\text{dR}_7$
12	62	0.233	$-(4.19\times10^{-3})+0.65\,\text{candida}+0.51\,\text{igG}+0.34\,\text{respiratoryInfection}+$ $0.11\,\text{a}_{34}+0.36\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.60\,\text{b}_{45}+0.18\,\text{dR}_7$
13	65	0.231	$1.84-\frac{4.79}{2.60+3\,\text{candida}+2\,\text{igG}+\text{respiratoryInfection}+\text{respiratoryInfection}\,\text{antiHLAclass}_2+\text{b}_{45}}$
14	68	0.185	$2.11\times10^{-2}+0.73\,\text{candida}+0.69\,\text{igG}-0.27\,\text{pyrexia}+$ $0.50\,\text{respiratoryInfection}+0.18\,(\text{denovoDSA}+2\,\text{igG}+\text{respiratoryInfection})\,\text{dR}_7$

◆ Ensembles in ParetoFront

■ The 30th Cross Validation with Leave-One-Out Method out of 51 turns

The Estimated value: 0.8225, The Observed value: 0

The Prediction: Wrong

Accuracy so far: 76.67% (58.82% completed)

◆ **Accuracies until the 30th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 1 min 50 sec

◆ **Error(= Predicted value - Observed value) in the 30th Cross Validation**

◇ **Average Error is 0.3553±0.3413 until the 30th turn in the LOO method.**

■ The 31st cross-validation out of 51 turns

□ **The 31st Genetic Programming has started.**

◆ **Present Time: 2020年 7月 14日⣿0時 5分 13秒**

(kernel 5) Global`x::shdw : Symbol x appears in multiple contexts {Global`, DataModeler`SymbolicRegression`}; definitions in context Global` may shadow or be shadowed by other definitions.

(kernel 5) Global`n::shdw : Symbol n appears in multiple contexts {Global`, DataModeler`SymbolicRegression`}; definitions in context Global` may shadow or be shadowed by other definitions.

(kernel 5) Global`g::shdw : Symbol g appears in multiple contexts {Global`, DataModeler`SymbolicRegression`}; definitions in context Global` may shadow or be shadowed by other definitions.

□ **The 31th Genetic Programming has ended.**

◆ **Present Time: 2020年 7月 14日⣿0時 11分 25秒**

◆ Monitors Plot

Error = 1 − R²
0.10
0.05
0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
60
40
20
0

Pareto Fronts
Error = 1 − R²
1
0.50
0.10
0.05

◆ **1052 models were created**

◇ **Quatiliy Box values are {54., 0.181} in the 31st turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1052 Selected models: 1 (0.09506%)

◆ Inning 0. Complexity: 54. Error: 0.181 Number of Selected models: 1 (0.09506%)

◆ Inning 1. Complexity: 55. Error: 0.191 Number of Selected models: 1 (0.09506%)

◆ Inning 2. Complexity: 56. Error: 0.201 Number of Selected models: 2 (0.1901%)

◆ Inning 3. Complexity: 57. Error: 0.211 Number of Selected models: 6 (0.5703%)

◆ Inning 4. Complexity: 58. Error: 0.221 Number of Selected models: 6 (0.5703%)

◆ Inning 5. Complexity: 59. Error: 0.231 Number of Selected models: 9 (0.8555%)

- Inning 6. Complexity: 60. Error: 0.241 Number of Selected models: 13 (1.236%)
- Inning 7. Complexity: 61. Error: 0.251 Number of Selected models: 17 (1.616%)
- Inning 8. Complexity: 62. Error: 0.261 Number of Selected models: 34 (3.232%)
- Inning 9. Complexity: 63. Error: 0.271 Number of Selected models: 43 (4.087%)
- Inning 10. Complexity: 64. Error: 0.281 Number of Selected models: 54 (5.133%)
- Inning 11. Complexity: 65. Error: 0.291 Number of Selected models: 69 (6.559%)
- Inning 12. Complexity: 66. Error: 0.301 Number of Selected models: 73 (6.939%)
- Inning 13. Complexity: 67. Error: 0.311 Number of Selected models: 94 (8.935%)

- **94 interesting models were selected**
  - **Quatiliy Box values are {67., 0.311039}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, cNIpostRej, b45, igG, feverOnly}**

- **Defining Ensembles**

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.306	$-(2.36\times10^{-2})+0.13\,\text{cNIpostRej}+0.59\,\text{respiratoryInfection}+1.13\,b_{45}+0.28\,dR_{53}$
2	38	0.227	$3.23\times10^{-2}+0.11\,\text{cNIpostRej}+1.11\,\text{respiratoryInfection}-0.47\,\text{banfi}\,\text{respiratoryInfection}+1.06\,b_{45}$
3	38	0.302	$1.83\times10^{-2}+0.13\,\text{aerobicGPC}\,\text{cNIpostRej}+0.56\,\text{igG}+0.59\,\text{respiratoryInfection}+0.70\,b_{45}$
4	39	0.310	$1.31\times10^{-2}+0.12\,\sqrt{\text{cNIpostRej}^2}+0.88\,b_{45}+0.94\,\text{respiratoryInfection}\,dQ_7$
5	43	0.288	$-(3.48\times10^{-2})+0.13\,\text{cNIpostRej}+$ $(9.17\times10^{-2})\,\text{denovoDSA}+0.55\,\text{respiratoryInfection}+0.82\,b_{45}+0.29\,dR_{15}$
6	43	0.291	$-(1.82\times10^{-2})+0.12\,\text{cNIpostRej}+$ $(7.63\times10^{-3})\,\text{hSAclass2number}+0.41\,\text{igG}+0.60\,\text{respiratoryInfection}+0.88\,b_{45}$
7	46	0.222	$2.25\times10^{-2}+0.11\,\text{cNIpostRej}+0.40\,\text{igG}+$ $0.84\,\text{respiratoryInfection}-0.32\,\text{feverOnly}\,\text{respiratoryInfection}+0.87\,b_{45}$
8	49	0.235	$3.23\times10^{-2}+0.11\,\text{cNIpostRej}+0.71\,\text{respiratoryInfection}-$ $0.27\,\text{feverOnly}\,\text{respiratoryInfection}+1.06\,b_{45}+0.35\,\text{respiratoryInfection}\,dQ_6$
9	51	0.203	$4.47\times10^{-2}+0.10\,\text{cNIpostRej}+0.50\,\text{igG}-0.34\,\text{pyrexia}+$ $0.87\,\text{respiratoryInfection}-0.22\,\text{upperRespiratoryInfection}+0.90\,b_{45}$
10	51	0.210	$6.49\times10^{-2}+0.12\,\text{cNIpostRej}-(5.61\times10^{-2})\,\text{feverOnly}+$ $0.41\,\text{igG}-0.33\,\text{pyrexia}+0.73\,\text{respiratoryInfection}+0.86\,b_{45}$
11	51	0.232	$-(2.40\times10^{-2})+(1.55\times10^{-2})\,\text{hDperiod}+0.56\,\text{igG}-0.34\,\text{pyrexia}+$ $0.94\,\text{respiratoryInfection}-0.33\,\text{upperRespiratoryInfection}+0.88\,b_{45}$
12	53	0.206	$1.91\times10^{-2}+0.10\,\text{cNIpostRej}+0.90\,\text{igG}+0.81\,\text{respiratoryInfection}-$ $0.61\,\text{aerobicGPC}\,\text{respiratoryInfection}+0.23\,\text{cRPpostRej}^2\,b_{61}$
13	54	0.181	$3.73\times10^{-2}+0.11\,\text{cNIpostRej}+0.38\,\text{igG}-0.26\,\text{pyrexia}+$ $0.85\,\text{respiratoryInfection}-0.22\,\text{feverOnly}\,\text{respiratoryInfection}+0.86\,b_{45}$
14	54	0.196	$-(3.00\times10^{-2})+0.13\,\text{cNIpostRej}+0.38\,\text{coaglationnecrosis}+$ $0.81\,\text{respiratoryInfection}-0.31\,\text{feverOnly}\,\text{respiratoryInfection}+1.14\,b_{45}+0.23\,dQ_6$
15	54	0.259	$-(1.87\times10^{-2})+0.13\,\text{cNIpostRej}+0.11\,\text{denovoDSA}+0.77\,\text{respiratoryInfection}-$ $0.49\,\text{aerobicGPC}\,\text{upperRespiratoryInfection}+0.73\,b_{45}+(4.94\times10^{-2})\,dQ_8$

◆ Ensembles in ParetoFront

■ **The 31st Cross Validation with Leave-One-Out Method out of 51 turns**

```
The Estimated value: -0.06965, The Observed value: 0
The Prediction: Right
Accuracy so far: 77.42%   (60.78% completed)
```

◆ **Accuracies until the 31st turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 1 min 44 sec

◆ **Error(= Predicted value - Observed value) in the 31st Cross Validation**

◇ **Average Error is 0.346±0.3395 until the 31st turn in the LOO method.**

■ The 32nd cross-validation out of 51 turns

□ The 32nd Genetic Programming has started.

◆ Present Time: 2020年 7月 14日0時 11分 29秒

□ The 32th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日0時 17分 45秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
50
100
150
200
250
Model Complexity

,

◆ **974 models were created**

◇ **Quatiliy Box values are {41., 0.1744} in the 32nd turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 974 Selected models: 1 (0.1027%)

◆ Inning 0. Complexity: 41. Error: 0.1744 Number of Selected models: 1 (0.1027%)

◆ Inning 1. Complexity: 42. Error: 0.1844 Number of Selected models: 1 (0.1027%)

◆ Inning 2. Complexity: 43. Error: 0.1944 Number of Selected models: 1 (0.1027%)

◆ Inning 3. Complexity: 44. Error: 0.2044 Number of Selected models: 2 (0.2053%)

◆ Inning 4. Complexity: 45. Error: 0.2144 Number of Selected models: 2 (0.2053%)

◆ Inning 5. Complexity: 46. Error: 0.2244 Number of Selected models: 6 (0.616%)

◆ Inning 6. Complexity: 47. Error: 0.2344 Number of Selected models: 8 (0.8214%)

◆ Inning 7. Complexity: 48. Error: 0.2444 Number of Selected models: 8 (0.8214%)

◆ Inning 8. Complexity: 49. Error: 0.2544 Number of Selected models: 15 (1.54%)

◆ Inning 9. Complexity: 50. Error: 0.2644 Number of Selected models: 20 (2.053%)

◆ Inning 10. Complexity: 51. Error: 0.2744 Number of Selected models: 31 (3.183%)

◆ Inning 11. Complexity: 52. Error: 0.2844 Number of Selected models: 38 (3.901%)

◆ Inning 12. Complexity: 53. Error: 0.2944 Number of Selected models: 41 (4.209%)

◆ Inning 13. Complexity: 54. Error: 0.3044 Number of Selected models: 56 (5.749%)

◆ Inning 14. Complexity: 55. Error: 0.3144 Number of Selected models: 68 (6.982%)

- Inning 15. Complexity: 56. Error: 0.3244 Number of Selected models: 71 (7.29%)
- Inning 16. Complexity: 57. Error: 0.3344 Number of Selected models: 87 (8.932%)

- **87 interesting models were selected**
  - **Quatiliy Box values are {57., 0.334382}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, inflammationdatefirst, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.325	$7.14\times10^{-2}+0.93\,(\text{respiratoryInfection}+\text{igA})\,\text{antiHLAclass}_2+0.93\,b_{45}$
2	30	0.327	$4.51\times10^{-2}+0.62\,\text{igG}+(8.73\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.64\,b_{45}$
3	33	0.309	$7.66\times10^{-2}+0.12\,\text{cNIpostRej}\,\text{surgery}+0.92\,b_{45}+0.92\,\text{respiratoryInfection}\,dQ_7$
4	33	0.312	$5.15\times10^{-2}+(5.57\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+$ $0.95\,b_{45}+0.59\,\text{respiratoryInfection}\,dQ_8$
5	35	0.308	$-(2.01\times10^{-2})+0.13\,\text{cNIpostRej}+0.59\,\text{respiratoryInfection}+1.13\,b_{45}+0.28\,dR_{53}$
6	35	0.332	$1.56\times10^{-2}+0.11\,\text{cNIpostRej}+0.63\,\text{igG}+0.57\,\text{respiratoryInfection}+0.23\,\text{dSAandHSAclass}_1$
7	38	0.211	$3.12\times10^{-2}+0.11\,\text{cNIpostRej}+0.57\,\text{igG}+(9.35\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.78\,b_{45}$
8	38	0.285	$3.29\times10^{-2}+0.12\,\text{cNIpostRej}+0.22\,\text{respiratoryInfection}+$ $(7.14\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.07\,b_{45}$
9	38	0.290	$4.14\times10^{-2}+0.47\,\text{igG}+0.74\,\text{respiratoryInfection}-0.52\,\text{pyrexia}\,\text{respiratoryInfection}+0.72\,b_{45}$
10	38	0.295	$3.63\times10^{-2}+0.12\,\text{cNIpostRej}+0.11\,\text{gERD}+$ $(9.69\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.01\,b_{45}$
11	41	0.174	$2.14\times10^{-2}+0.86\,\text{respiratoryInfection}-$ $0.58\,\text{pyrexia}\,\text{respiratoryInfection}+0.15\,\text{cNIpostRej}\,\text{surgery}+0.98\,b_{45}$
12	41	0.197	$3.71\times10^{-2}+0.11\,\text{cNIpostRej}+$ $(6.43\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.06\,b_{45}+0.55\,\text{respiratoryInfection}\,dQ_8$
13	41	0.204	$3.50\times10^{-2}+0.80\,\text{respiratoryInfection}+0.15\,\text{cNIpostRej}\,\text{surgery}-0.49\,\text{pyrexia}\,\text{virusInfection}+0.96\,b_{45}$
14	41	0.300	$5.25\times10^{-2}+(9.71\times10^{-2})\,\text{cNIpostRej}+0.83\,\text{igG}+$ $0.45\,\text{bTF}\,\text{respiratoryInfection}+(8.26\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}$
15	46	0.164	$-(1.33\times10^{-2})+0.12\,\text{cNIpostRej}+0.42\,\text{igG}+$ $(9.11\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.90\,b_{45}+0.23\,dR_{53}$

◆ Ensembles in ParetoFront

■ **The 32nd Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.02476, The Observed value: 0

The Prediction: Right

Accuracy so far: 78.13% (62.75% completed)

◆ **Accuracies until the 32nd turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 1 min 37 sec

◆ **Error(= Predicted value - Observed value) in the 32nd Cross Validation**

◇ **Average Error is 0.336±0.3387 until the 32nd turn in the LOO method.**

■ The 33rd cross-validation out of 51 turns

□ The 33rd Genetic Programming has started.

◆ Present Time: 2020年 7月 14日0時 17分 48秒

□ The 33th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日0時 24分 4秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
−200
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
100
200
300
400
500
600
700
Model Complexity

,

◆ **1016 models were created**

◇ **Quatiliy Box values are {42., 0.2075} in the 33rd turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1016 Selected models: 1 (0.09843%)

◆ Inning 0. Complexity: 42. Error: 0.2075 Number of Selected models: 1 (0.09843%)

◆ Inning 1. Complexity: 43. Error: 0.2175 Number of Selected models: 1 (0.09843%)

◆ Inning 2. Complexity: 44. Error: 0.2275 Number of Selected models: 2 (0.1969%)

◆ Inning 3. Complexity: 45. Error: 0.2375 Number of Selected models: 4 (0.3937%)

◆ Inning 4. Complexity: 46. Error: 0.2475 Number of Selected models: 12 (1.181%)

◆ Inning 5. Complexity: 47. Error: 0.2575 Number of Selected models: 12 (1.181%)

◆ Inning 6. Complexity: 48. Error: 0.2675 Number of Selected models: 15 (1.476%)

◆ Inning 7. Complexity: 49. Error: 0.2775 Number of Selected models: 24 (2.362%)

◆ Inning 8. Complexity: 50. Error: 0.2875 Number of Selected models: 30 (2.953%)

◆ Inning 9. Complexity: 51. Error: 0.2975 Number of Selected models: 48 (4.724%)

◆ Inning 10. Complexity: 52. Error: 0.3075 Number of Selected models: 54 (5.315%)

◆ Inning 11. Complexity: 53. Error: 0.3175 Number of Selected models: 63 (6.201%)

◆ Inning 12. Complexity: 54. Error: 0.3275 Number of Selected models: 88 (8.661%)

◆ **88 interesting models were selected**

  ◇ **Quatiliy Box values are {54., 0.327522}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, pyrexia, igG, cNIpostRej}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.268	$5.30\times10^{-2}+0.12\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+1.04\,b_{45}$
2	35	0.308	$-(2.88\times10^{-2})+0.13\,\text{cNIpostRej}+0.60\,\text{respiratoryInfection}+1.14\,b_{45}+0.27\,dQ_6$
3	38	0.223	$4.50\times10^{-2}-0.42\,\text{pyrexia}+0.77\,\text{respiratoryInfection}+0.15\,\text{cNIpostRej surgery}+0.96\,b_{45}$
4	38	0.227	$3.26\times10^{-2}+0.11\,\text{cNIpostRej}+1.11\,\text{respiratoryInfection}-0.47\,\text{banfi respiratoryInfection}+1.06\,b_{45}$
5	38	0.288	$-(3.89\times10^{-2})+0.15\,\text{cRPpostRej}+0.66\,\text{igG}+0.70\,\text{respiratoryInfection}-0.47\,\text{pyrexia respiratoryInfection}$
6	38	0.308	$4.42\times10^{-2}+0.37\,\text{igG}+1.00\,\text{respiratoryInfection}-0.44\,\text{banfi respiratoryInfection}+0.77\,b_{45}$
7	38	0.310	$2.01\times10^{-2}+0.11\,\text{cNIpostRej}+0.78\,\text{igG}+0.58\,\text{respiratoryInfection}+0.54\,\text{banfi}\,b_{45}$
8	41	0.292	$9.57\times10^{-2}-0.42\,\text{pyrexia}+0.15\,\text{hDperiod respiratoryInfection}+0.12\,\text{cNIpostRej surgery}+0.90\,b_{45}$
9	41	0.297	$-(2.79\times10^{-2})+0.14\,\text{cRPpostRej}+1.08\,\text{respiratoryInfection}-$ $0.49\,\text{banfi respiratoryInfection}+0.19\,\text{denovoDSA}\,b_{45}$
10	42	0.208	$-(5.98\times10^{-3})+1.00\,\text{respiratoryInfection}-$ $0.27\,\text{banfi}^2\,\text{respiratoryInfection}+0.96\,b_{45}+(2.08\times10^{-2})\,\text{wBCpeakover}_5$
11	43	0.218	$4.11\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.84\,b_{45}$
12	46	0.193	$3.21\times10^{-2}+0.11\,\text{cNIpostRej}+1.02\,\text{respiratoryInfection}-0.25\,\text{banfi}^2\,\text{respiratoryInfection}^2+1.06\,b_{45}$
13	46	0.221	$4.47\times10^{-2}-(3.71\times10^{-2})\,\text{cNIpostRej}-0.43\,\text{pyrexia}+$ $0.77\,\text{respiratoryInfection}+0.18\,\text{cNIpostRej surgery}+0.92\,b_{45}$
14	46	0.234	$-(4.31\times10^{-2})+0.14\,\text{cRPpostRej}+0.37\,\text{igG}+$ $1.00\,\text{respiratoryInfection}-0.43\,\text{banfi respiratoryInfection}+0.62\,b_{45}$
15	49	0.186	$4.80\times10^{-2}-0.45\,\text{pyrexia}+0.53\,\text{respiratoryInfection}+$ $(6.44\times10^{-2})\,\text{hDperiod respiratoryInfection}+0.14\,\text{cNIpostRej surgery}+0.95\,b_{45}$

◆ Ensembles in ParetoFront

■ **The 33rd Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: -0.001676, The Observed value: 0

The Prediction: Right

Accuracy so far: 78.79% (64.71% completed)

◆ **Accuracies until the 33rd turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 1 min 31 sec

◆ **Error(= Predicted value - Observed value) in the 33rd Cross Validation**

◇ **Average Error is 0.3259±0.3385 until the 33rd turn in the LOO method.**

■ The 34th cross-validation out of 51 turns

□ The 34th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日⣿0時 24分 8秒

□ The 34th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日⣿0時 30分 22秒

◆ Monitors Plot

0.01
0
200
400
600
800
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
100
200
300
400
500
600
700
Model Complexity

,

◆ **1007 models were created**

◇ **Quatiliy Box values are {54., 0.1515} in the 34th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1007 Selected models: 1 (0.0993%)

◆ Inning 0. Complexity: 54. Error: 0.1515 Number of Selected models: 1 (0.0993%)

◆ Inning 1. Complexity: 55. Error: 0.1615 Number of Selected models: 1 (0.0993%)

◆ Inning 2. Complexity: 56. Error: 0.1715 Number of Selected models: 2 (0.1986%)

◆ Inning 3. Complexity: 57. Error: 0.1815 Number of Selected models: 2 (0.1986%)

◆ Inning 4. Complexity: 58. Error: 0.1915 Number of Selected models: 7 (0.6951%)

◆ Inning 5. Complexity: 59. Error: 0.2015 Number of Selected models: 10 (0.993%)

◆ Inning 6. Complexity: 60. Error: 0.2115 Number of Selected models: 10 (0.993%)

◆ Inning 7. Complexity: 61. Error: 0.2215 Number of Selected models: 13 (1.291%)

◆ Inning 8. Complexity: 62. Error: 0.2315 Number of Selected models: 17 (1.688%)

◆ Inning 9. Complexity: 63. Error: 0.2415 Number of Selected models: 21 (2.085%)

◆ Inning 10. Complexity: 64. Error: 0.2515 Number of Selected models: 23 (2.284%)

◆ Inning 11. Complexity: 65. Error: 0.2615 Number of Selected models: 36 (3.575%)

◆ Inning 12. Complexity: 66. Error: 0.2715 Number of Selected models: 39 (3.873%)

◆ Inning 13. Complexity: 67. Error: 0.2815 Number of Selected models: 52 (5.164%)

◆ Inning 14. Complexity: 68. Error: 0.2915 Number of Selected models: 53 (5.263%)

- Inning 15. Complexity: 69. Error: 0.3015 Number of Selected models: 57 (5.66%)
- Inning 16. Complexity: 70. Error: 0.3115 Number of Selected models: 70 (6.951%)
- Inning 17. Complexity: 71. Error: 0.3215 Number of Selected models: 79 (7.845%)
- Inning 18. Complexity: 72. Error: 0.3315 Number of Selected models: 92 (9.136%)

- **92 interesting models were selected**
  - **Quatiliy Box values are {72., 0.331543}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, banfi, b45, cNIpostRej, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	34	0.314	$5.41\times10^{-2}+0.98\,\text{respiratoryInfection}-0.26\,\text{banfi}^2\,\text{respiratoryInfection}+0.95\,b_{45}$
2	35	0.269	$5.46\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+1.04\,b_{45}$
3	38	0.297	$5.21\times10^{-2}+0.64\,\text{igG}-0.33\,\text{pyrexia}+0.59\,\text{respiratoryInfection}+0.17\,\text{denovoDSA antiHLAclass}_1$
4	38	0.299	$1.02\times10^{-2}+0.21\,\text{cRPpostRej heartDisease}+0.52\,\text{igG}+0.49\,\text{respiratoryInfection}+0.73\,b_{45}$
5	42	0.194	$3.37\times10^{-2}+0.11\,\text{cNIpostRej}+1.01\,\text{respiratoryInfection}-0.25\,\text{banfi}^2\,\text{respiratoryInfection}+1.06\,b_{45}$
6	43	0.280	$-(5.60\times10^{-2})+0.17\,\text{cRPpostRej}+0.63\,\text{igG}-0.30\,\text{pyrexia}+0.62\,\text{respiratoryInfection}+0.18\,dR_7$
7	43	0.285	$8.35\times10^{-2}-(9.07\times10^{-2})\,\text{banfi}+0.15\,\text{cRPpostRej}-0.33\,\text{pyrexia}+0.68\,\text{respiratoryInfection}+0.75\,b_{45}$
8	50	0.162	$2.52\times10^{-2}+0.11\,\text{cNIpostRej}+0.35\,\text{igG}+$ $0.96\,\text{respiratoryInfection}-0.23\,\text{banfi}^2\,\text{respiratoryInfection}+0.89\,b_{45}$
9	50	0.259	$4.93\times10^{-2}+0.11\,\text{cNIpostRej}-(3.25\times10^{-2})\,\text{hypertention}^2+$ $0.81\,\text{igG}+0.48\,\text{respiratoryInfection}+0.53\,\text{banfi antiHLAclass}_1$
10	54	0.196	$-(4.11\times10^{-2})+0.14\,\text{cRPpostRej}+0.40\,\text{igG}+$ $0.90\,\text{respiratoryInfection}-0.22\,\text{banfi}^2\,\text{respiratoryInfection}+0.59\,\sqrt{b_{45}}$
11	58	0.147	$7.75\times10^{-2}+0.13\,\text{cNIpostRej}+0.36\,\text{igG}+1.04\,\text{respiratoryInfection}-$ $0.22\,\text{banfi}^2\,\text{respiratoryInfection}-(3.07\times10^{-2})\,\text{uTI}+0.87\,b_{45}$
12	58	0.158	$6.29\times10^{-4}+(8.89\times10^{-2})\,\text{cNIpostRej}+(4.75\times10^{-2})\,\text{cRPpostRej}+$ $0.36\,\text{igG}+0.95\,\text{respiratoryInfection}-0.22\,\text{banfi}^2\,\text{respiratoryInfection}+0.81\,b_{45}$
13	62	0.147	$2.69\times10^{-2}+0.11\,\text{cNIpostRej}+0.44\,\text{igG}+0.87\,\text{respiratoryInfection}-$ $(5.36\times10^{-2})\,\text{banfi}^4\,\text{respiratoryInfection}+0.84\,b_{45}-0.16\,dP_{13}$
14	62	0.175	$6.45\times10^{-2}+(9.56\times10^{-2})\,\text{cNIpostRej}+1.09\,\text{respiratoryInfection}-$ $0.25\,\text{banfi}^2\,\text{respiratoryInfection}-(2.78\times10^{-2})\,\text{uTI}+1.01\,\sqrt{b_{45}}+(8.12\times10^{-3})\,\text{wBCpeakover}_5$
15	65	0.127	$9.87\times10^{-2}+0.12\,\text{cNIpostRej}+0.73\,\text{igG}+0.81\,\text{respiratoryInfection}-$ $(4.35\times10^{-2})\,\text{banfi}^4\,\text{respiratoryInfection}-(4.16\times10^{-2})\,\text{uTI}+0.46\,\text{banfi antiHLAclass}_1$

◆ Ensembles in ParetoFront

■ **The 34th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.06975, The Observed value: 0

The Prediction: Right

Accuracy so far: 79.41% (66.67% completed)

◆ **Accuracies until the 34th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 1 min 25 sec

◆ **Error(= Predicted value - Observed value) in the 34th Cross Validation**

◇ **Average Error is 0.3183±0.3362 until the 34th turn in the LOO method.**

■ The 35th cross-validation out of 51 turns

□ The 35th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日0時 30分 26秒

□ The 35th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日0時 36分 41秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
100
80
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
100
200
300
400
500
Model Complexity

,

◆ **1076 models were created**

◇ **Quatiliy Box values are {49., 0.1067} in the 35th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1076 Selected models: 1 (0.09294%)

◆ Inning 0. Complexity: 49. Error: 0.1067 Number of Selected models: 1 (0.09294%)

◆ Inning 1. Complexity: 50. Error: 0.1167 Number of Selected models: 1 (0.09294%)

◆ Inning 2. Complexity: 51. Error: 0.1267 Number of Selected models: 2 (0.1859%)

◆ Inning 3. Complexity: 52. Error: 0.1367 Number of Selected models: 2 (0.1859%)

◆ Inning 4. Complexity: 53. Error: 0.1467 Number of Selected models: 3 (0.2788%)

◆ Inning 5. Complexity: 54. Error: 0.1567 Number of Selected models: 9 (0.8364%)

◆ Inning 6. Complexity: 55. Error: 0.1667 Number of Selected models: 13 (1.208%)

◆ Inning 7. Complexity: 56. Error: 0.1767 Number of Selected models: 21 (1.952%)

◆ Inning 8. Complexity: 57. Error: 0.1867 Number of Selected models: 44 (4.089%)

◆ Inning 9. Complexity: 58. Error: 0.1967 Number of Selected models: 62 (5.762%)

◆ Inning 10. Complexity: 59. Error: 0.2067 Number of Selected models: 75 (6.97%)

◆ Inning 11. Complexity: 60. Error: 0.2167 Number of Selected models: 86 (7.993%)

◆ Inning 12. Complexity: 61. Error: 0.2267 Number of Selected models: 101 (9.387%)

◆ **101 interesting models were selected**

  ◇ **Quatiliy Box values are {61., 0.22667}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, igG, b45, pyrexia, inflammationdatefirst}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	36	0.209	$1.48\times10^{-2}+(8.96\times10^{-2})$ inflammationdatefirst respiratoryInfection $+0.80\sqrt{\text{igG}+b_{45}}$
2	38	0.192	$2.20\times10^{-2}+0.98$ banf t igG -0.40 pyrexia $+0.76$ respiratoryInfection $+0.98\,b_{45}$
3	38	0.213	$2.80\times10^{-2}+0.18$ hLAABmm igG -0.38 pyrexia $+0.71$ respiratoryInfection $+0.70\,b_{45}$
4	38	0.218	$9.90\times10^{-3}+0.61$ igG $+0.73$ respiratoryInfection $-$ 0.50 pyrexia respiratoryInfection $+0.20$ dSAandHSAclass$_1$
5	38	0.222	$5.15\times10^{-2}-0.45$ pyrexia $+0.83$ respiratoryInfection $-$ 0.88 enterococcusfaecalis respiratoryInfection $+0.95\,b_{45}$
6	41	0.167	$-(3.14\times10^{-17})+1.00$ banf t igG $+0.33$ respiratoryInfection $+1.00\,b_{45}+0.67$ respiratoryInfection dQ_8
7	44	0.206	$2.23\times10^{-2}-(6.69\times10^{-2})$ nS $+(9.05\times10^{-2})$ inflammationdatefirst respiratoryInfection $+0.79\sqrt{\text{igG}+b_{45}}$
8	46	0.161	$4.02\times10^{-2}-0.11$ banfct $+0.53$ igG $+0.83$ respiratoryInfection -0.54 pyrexia respiratoryInfection $+0.81\,b_{45}$
9	46	0.161	$3.74\times10^{-2}+0.46$ igG -0.42 pyrexia $+0.79$ respiratoryInfection $-$ 0.82 enterococcusfaecalis respiratoryInfection $+0.73\,b_{45}$
10	46	0.168	$1.46\times10^{-2}+0.32$ calcification -0.42 pyrexia $+0.75$ respiratoryInfection $+0.99\,b_{45}+0.99$ igG dR_7
11	48	0.151	$4.31\times10^{-4}+0.80\sqrt{\text{igG}+b_{45}}+$ (8.50×10^{-2}) respiratoryInfection (inflammationdatefirst $+$ wBCpreRej $+dQ_7$)
12	48	0.166	$7.66\times10^{-3}+0.77\sqrt{\text{igG}+b_{45}}+(8.49\times10^{-2})$ respiratoryInfection (inflammationdatefirst $+dQ_4+dQ_7$)
13	49	0.107	$2.47\times10^{-2}-0.45$ pyrexia $+0.85$ respiratoryInfection $-$ 0.88 enterococcusfaecalis respiratoryInfection $+0.98\,b_{45}+0.98$ igG dR_7
14	49	0.124	$1.42\times10^{-2}+0.99$ banf t igG -0.26 pyrexia $+$ 0.49 respiratoryInfection $+0.99\,b_{45}+0.50$ respiratoryInfection dQ_8
15	49	0.125	$1.93\times10^{-2}-(7.71\times10^{-2})$ banfct $+0.98$ banf t igG $+$ 0.88 respiratoryInfection -0.58 pyrexia respiratoryInfection $+1.06\,b_{45}$

◆ Ensembles in ParetoFront

■ **The 35th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.01653, The Observed value: 1

The Prediction: Wrong

Accuracy so far: 77.14% (68.63% completed)

◆ **Accuracies until the 35th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 1 min 19 sec

◆ **Error(= Predicted value - Observed value) in the 35th Cross Validation**

◇ **Average Error is 0.3373±0.3498 until the 35th turn in the LOO method.**

■ The 36th cross-validation out of 51 turns

□ The 36th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日0時 36分 46秒

□ The 36th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日0時 43分 8秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1– R2
0
100
200
300
Model Complexity

,

◆ **1006 models were created**

◇ **Quatiliy Box values are {41., 0.1859} in the 36th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1006 Selected models: 1 (0.0994%)

◆ Inning 0. Complexity: 41. Error: 0.1859 Number of Selected models: 1 (0.0994%)

◆ Inning 1. Complexity: 42. Error: 0.1959 Number of Selected models: 1 (0.0994%)

◆ Inning 2. Complexity: 43. Error: 0.2059 Number of Selected models: 1 (0.0994%)

◆ Inning 3. Complexity: 44. Error: 0.2159 Number of Selected models: 1 (0.0994%)

◆ Inning 4. Complexity: 45. Error: 0.2259 Number of Selected models: 3 (0.2982%)

◆ Inning 5. Complexity: 46. Error: 0.2359 Number of Selected models: 9 (0.8946%)

◆ Inning 6. Complexity: 47. Error: 0.2459 Number of Selected models: 10 (0.994%)

◆ Inning 7. Complexity: 48. Error: 0.2559 Number of Selected models: 15 (1.491%)

◆ Inning 8. Complexity: 49. Error: 0.2659 Number of Selected models: 19 (1.889%)

◆ Inning 9. Complexity: 50. Error: 0.2759 Number of Selected models: 37 (3.678%)

◆ Inning 10. Complexity: 51. Error: 0.2859 Number of Selected models: 49 (4.871%)

◆ Inning 11. Complexity: 52. Error: 0.2959 Number of Selected models: 60 (5.964%)

◆ Inning 12. Complexity: 53. Error: 0.3059 Number of Selected models: 70 (6.958%)

◆ Inning 13. Complexity: 54. Error: 0.3159 Number of Selected models: 89 (8.847%)

◆ **89 interesting models were selected**

  ◇ **Quatiliy Box values are {54., 0.315935}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, pyrexia, b45, cNIpostRej, igG}**

◆ Defining Ensembles

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	Complexity	$1-R^2$	graftLoss Function
1	33	0.286	$3.33\times10^{-2}+0.75\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.25\,\text{dSAandHLAclass1pre wBCpeakover}_5$
2	34	0.314	$5.41\times10^{-2}+0.98\,\text{respiratoryInfection}-0.26\,\text{banfi}^2\,\text{respiratoryInfection}+0.95\,b_{45}$
3	35	0.269	$5.33\times10^{-2}+0.12\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+1.04\,b_{45}$
4	35	0.304	$-(1.75\times10^{-2})+0.12\,\text{cNIpostRej}+0.58\,\text{respiratoryInfection}+1.12\,b_{45}+0.30\,dR_{53}$
5	38	0.221	$3.16\times10^{-2}+0.12\,\text{cNIpostRej}+0.84\,\text{respiratoryInfection}-0.55\,\text{pyrexia respiratoryInfection}+1.07\,b_{45}$
6	41	0.186	$-(2.47\times10^{-2})+0.77\,\text{respiratoryInfection}-0.54\,\text{pyrexia respiratoryInfection}+(2.01\times10^{-2})\,\text{wBCpeakover}_5+0.25\,\text{dSAandHLAclass1pre wBCpeakover}_5$
7	41	0.244	$2.78\times10^{-2}+0.97\,\text{dSAandHLAclass1pre lymphinvasion}+0.81\,\text{respiratoryInfection}-0.56\,\text{pyrexia respiratoryInfection}+0.97\,b_{45}$
8	42	0.194	$3.23\times10^{-2}+0.11\,\text{cNIpostRej}+1.02\,\text{respiratoryInfection}-0.25\,\text{banfi}^2\,\text{respiratoryInfection}+1.06\,b_{45}$
9	42	0.268	$-(4.69\times10^{-3})+(9.45\times10^{-2})\,\text{cNIpostRej}+(2.93\times10^{-3})\,\text{infectionCount}^2+1.06\,b_{45}+0.77\,\text{respiratoryInfection}\,dQ_8$
10	42	0.272	$-(3.97\times10^{-2})+0.16\,\text{cRPpostRej}+0.60\,\text{igG}+0.86\,\text{respiratoryInfection}-0.21\,\text{banfi}^2\,\text{respiratoryInfection}$
11	42	0.300	$-(6.09\times10^{-3})+1.00\,\text{dSAandHLAclass1pre lymphinvasion}+0.64\,\text{respiratoryInfection}+1.00\,b_{45}+(5.08\times10^{-4})\,\text{wBCpeakover}_5{}^2$
12	43	0.218	$4.14\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.83\,b_{45}$
13	43	0.227	$-(9.11\times10^{-4})+0.77\,\text{candida}+0.34\,\text{respiratoryInfection}+1.00\,b_{45}-0.66\,dR_{12}+0.63\,dR_{53}$
14	43	0.262	$2.45\times10^{-2}+0.10\,\text{cNIpostRej}+0.38\,\text{gERD}+0.73\,\text{igG}-0.44\,\text{pyrexia}+0.70\,\text{respiratoryInfection}$
15	45	0.175	$-(6.41\times10^{-4})+0.78\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.25\,\text{dSAandHLAclass1pre wBCpeakover}_5+(5.08\times10^{-4})\,\text{wBCpeakover}_5{}^2$

◆ Ensembles in ParetoFront

■ **The 36th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.06832, The Observed value: 0

The Prediction: Right

Accuracy so far: 77.78% (70.59% completed)

◆ **Accuracies until the 36th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 1 min 12 sec

◆ **Error(= Predicted value - Observed value) in the 36th Cross Validation**

◇ **Average Error is 0.3299±0.3476 until the 36th turn in the LOO method.**

■ The 37th cross-validation out of 51 turns

□ The 37th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日0時 43分 12秒

□ The 37th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日0時 49分 26秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
ModelAge
80
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
50
100
150
200
Model Complexity

,

◆ **919 models were created**

◇ **Quatiliy Box values are {45., 0.1971} in the 37th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 919 Selected models: 1 (0.1088%)

◆ Inning 0. Complexity: 45. Error: 0.1971 Number of Selected models: 1 (0.1088%)

◆ Inning 1. Complexity: 46. Error: 0.2071 Number of Selected models: 1 (0.1088%)

◆ Inning 2. Complexity: 47. Error: 0.2171 Number of Selected models: 2 (0.2176%)

◆ Inning 3. Complexity: 48. Error: 0.2271 Number of Selected models: 4 (0.4353%)

◆ Inning 4. Complexity: 49. Error: 0.2371 Number of Selected models: 9 (0.9793%)

◆ Inning 5. Complexity: 50. Error: 0.2471 Number of Selected models: 10 (1.088%)

◆ Inning 6. Complexity: 51. Error: 0.2571 Number of Selected models: 11 (1.197%)

◆ Inning 7. Complexity: 52. Error: 0.2671 Number of Selected models: 17 (1.85%)

◆ Inning 8. Complexity: 53. Error: 0.2771 Number of Selected models: 20 (2.176%)

◆ Inning 9. Complexity: 54. Error: 0.2871 Number of Selected models: 26 (2.829%)

◆ Inning 10. Complexity: 55. Error: 0.2971 Number of Selected models: 31 (3.373%)

◆ Inning 11. Complexity: 56. Error: 0.3071 Number of Selected models: 39 (4.244%)

◆ Inning 12. Complexity: 57. Error: 0.3171 Number of Selected models: 48 (5.223%)

◆ Inning 13. Complexity: 58. Error: 0.3271 Number of Selected models: 63 (6.855%)

◆ Inning 14. Complexity: 59. Error: 0.3371 Number of Selected models: 71 (7.726%)

- Inning 15. Complexity: 60. Error: 0.3471 Number of Selected models: 80 (8.705%)

- **80 interesting models were selected**
  - **Quatiliy Box values are {60., 0.347103}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, igG, inflammationdatefirst}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.303	$5.19\times10^{-2}+0.12\,\text{cNIpostRej}+(9.57\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.05\,b_{45}$
2	34	0.304	$1.80\times10^{-2}+(3.69\times10^{-2})\,\text{cRPpostRej}^2+0.83\,\text{igG}+(8.47\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}$
3	34	0.327	$6.58\times10^{-2}+0.93\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.93\,b_{45}+(4.73\times10^{-4})\,\text{wBCpeakover}_5{}^2$
4	35	0.268	$5.55\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+1.04\,b_{45}$
5	35	0.344	$0.13-(9.02\times10^{-2})\,\text{banfi}+0.12\,\text{cNIpostRej}+0.63\,\text{respiratoryInfection}+1.06\,b_{45}$
6	38	0.211	$3.14\times10^{-2}+0.11\,\text{cNIpostRej}+0.57\,\text{igG}+(9.35\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.78\,b_{45}$
7	38	0.308	$5.76\times10^{-2}-0.37\,\text{pyrexia}+0.66\,\text{respiratoryInfection}+0.94\,b_{45}+0.61\,\text{igG}\,dR_{52}$
8	42	0.248	$-(4.69\times10^{-2})+0.14\,\text{cNIpostRej}+(9.59\times10^{-2})\,\text{inflammationdatefirst}\,\sqrt{\text{respiratoryInfection}}+0.20\,\text{antiHLAclass}_2+0.96\,b_{45}$
9	43	0.235	$2.77\times10^{-2}+0.12\,\text{cNIpostRej}-0.35\,\text{pyrexia}+0.73\,\text{respiratoryInfection}+1.07\,b_{45}+0.24\,dR_{52}$
10	43	0.246	$3.84\times10^{-2}+0.10\,\text{cNIpostRej}+0.58\,\text{igG}-0.34\,\text{pyrexia}+0.68\,\text{respiratoryInfection}+0.22\,\text{dSAandHSAclass}_1$
11	43	0.250	$1.86\times10^{-2}+0.12\,\text{cNIpostRej}+(6.70\times10^{-3})\,\text{hSAclass2number}-0.35\,\text{pyrexia}+0.73\,\text{respiratoryInfection}+1.05\,b_{45}$
12	43	0.251	$2.83\times10^{-2}+0.12\,\text{cNIpostRej}+(5.99\times10^{-2})\,\text{denovoDSA}-0.35\,\text{pyrexia}+0.70\,\text{respiratoryInfection}+0.86\,b_{45}$
13	46	0.203	$1.97\times10^{-2}+0.11\,\text{cNIpostRej}+0.55\,\text{igG}+0.15\,\text{respiratoryInfection}+(7.74\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.80\,b_{45}$
14	46	0.265	$-(4.05\times10^{-2})+0.13\,\text{cRPpostRej}+0.43\,\text{igG}+0.32\,\text{respiratoryInfection}+0.60\,b_{45}+0.54\,\text{respiratoryInfection}\,dQ_7$
15	49	0.193	$2.17\times10^{-2}+(8.39\times10^{-2})\,\text{cNIpostRej}+(6.20\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.57\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+1.04\,b_{45}+(6.62\times10^{-3})\,\text{wBCpeakover}_5$

◆ Ensembles in ParetoFront

■ **The 37th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.02124, The Observed value: 0

The Prediction: Right

Accuracy so far: 78.38% (72.55% completed)

◆ **Accuracies until the 37th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 1 min 6 sec

◆ **Error(= Predicted value - Observed value) in the 37th Cross Validation**

◇ **Average Error is 0.3215±0.3465 until the 37th turn in the LOO method.**

■ The 38th cross-validation out of 51 turns

□ The 38th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日⣿0時 49分 29秒

□ The 38th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日⣿0時 56分 10秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
120
100
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
100
200
300
400
500
600
Model Complexity

,

◆ **1022 models were created**

◇ **Quatiliy Box values are {46., 0.1754} in the 38th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1022 Selected models: 1 (0.09785%)

◆ Inning 0. Complexity: 46. Error: 0.1754 Number of Selected models: 1 (0.09785%)

◆ Inning 1. Complexity: 47. Error: 0.1854 Number of Selected models: 1 (0.09785%)

◆ Inning 2. Complexity: 48. Error: 0.1954 Number of Selected models: 1 (0.09785%)

◆ Inning 3. Complexity: 49. Error: 0.2054 Number of Selected models: 1 (0.09785%)

◆ Inning 4. Complexity: 50. Error: 0.2154 Number of Selected models: 1 (0.09785%)

◆ Inning 5. Complexity: 51. Error: 0.2254 Number of Selected models: 3 (0.2935%)

◆ Inning 6. Complexity: 52. Error: 0.2354 Number of Selected models: 5 (0.4892%)

◆ Inning 7. Complexity: 53. Error: 0.2454 Number of Selected models: 8 (0.7828%)

◆ Inning 8. Complexity: 54. Error: 0.2554 Number of Selected models: 12 (1.174%)

◆ Inning 9. Complexity: 55. Error: 0.2654 Number of Selected models: 18 (1.761%)

◆ Inning 10. Complexity: 56. Error: 0.2754 Number of Selected models: 19 (1.859%)

◆ Inning 11. Complexity: 57. Error: 0.2854 Number of Selected models: 20 (1.957%)

◆ Inning 12. Complexity: 58. Error: 0.2954 Number of Selected models: 26 (2.544%)

◆ Inning 13. Complexity: 59. Error: 0.3054 Number of Selected models: 30 (2.935%)

◆ Inning 14. Complexity: 60. Error: 0.3154 Number of Selected models: 45 (4.403%)

- Inning 15. Complexity: 61. Error: 0.3254 Number of Selected models: 55 (5.382%)
- Inning 16. Complexity: 62. Error: 0.3354 Number of Selected models: 65 (6.36%)
- Inning 17. Complexity: 63. Error: 0.3454 Number of Selected models: 74 (7.241%)
- Inning 18. Complexity: 64. Error: 0.3554 Number of Selected models: 86 (8.415%)

- **86 interesting models were selected**
  - **Quatiliy Box values are {64., 0.355434}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, pyrexia, cNIpostRej, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.303	$5.18\times10^{-2}+0.12\,\text{cNIpostRej}+(9.57\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.05\,b_{45}$
2	30	0.341	$8.64\times10^{-2}+(9.29\times10^{-2})\,\text{cNIpostRej}+0.99\,b_{45}+0.91\,\text{respiratoryInfection}\,dQ_7$
3	35	0.268	$5.54\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+1.04\,b_{45}$
4	37	0.299	$3.90\times10^{-2}+0.77\,\text{igG}+(8.70\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}^3+0.43\,\text{hDperiod}\,b_{45}$
5	37	0.349	$6.30\times10^{-2}+(7.27\times10^{-2})\,\text{banfi}\,\text{cNIpostRej}+$ $0.82\,\text{igG}+(8.69\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}^3$
6	38	0.222	$3.38\times10^{-2}+0.12\,\text{cNIpostRej}+0.84\,\text{respiratoryInfection}-0.55\,\text{pyrexia}\,\text{respiratoryInfection}+1.07\,b_{45}$
7	38	0.246	$-(5.40\times10^{-3})+0.81\,\text{respiratoryInfection}-$ $0.59\,\text{pyrexia}\,\text{respiratoryInfection}+0.96\,b_{45}+(2.06\times10^{-2})\,\text{wBCpeakover}_5$
8	42	0.262	$2.10\times10^{-2}+0.12\,\text{cNIpostRej}-0.26\,(-3.69+\text{banfi})\,\text{respiratoryInfection}^3+1.08\,b_{45}$
9	42	0.328	$7.45\times10^{-3}+0.76\,\text{igG}+(5.78\times10^{-4})\,\text{cRPpostRej}^2\,\text{mMFpostRej}^4+0.49\,\text{respiratoryInfection}$
10	42	0.330	$4.28\times10^{-2}+0.42\,\text{igG}+0.29\,\text{respiratoryInfection}+0.75\,b_{45}+0.58\,\text{respiratoryInfection}^2\,dQ_7$
11	43	0.218	$4.35\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.83\,b_{45}$
12	43	0.249	$-(2.65\times10^{-2})-0.35\,\text{pyrexia}+0.65\,\text{respiratoryInfection}+$ $0.98\,b_{45}+0.24\,dR_{53}+(2.10\times10^{-2})\,\text{wBCpeakover}_5$
13	43	0.270	$3.65\times10^{-2}+0.42\,\text{candida}+0.51\,\text{igG}-0.35\,\text{pyrexia}+0.64\,\text{respiratoryInfection}+0.71\,b_{45}$
14	43	0.292	$-(8.76\times10^{-3})+(8.32\times10^{-2})\,\text{denovoDSA}+0.57\,\text{igG}-$ $0.34\,\text{pyrexia}+0.57\,\text{respiratoryInfection}+(1.94\times10^{-2})\,\text{wBCpeakover}_5$
15	47	0.250	$-(2.21\times10^{-3})+0.48\,\text{igG}-0.22\,\text{pyrexia}^2+$ $0.67\,\text{respiratoryInfection}+0.72\,b_{45}+(1.92\times10^{-2})\,\text{wBCpeakover}_5$

◆ Ensembles in ParetoFront

■ **The 38th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.03615, The Observed value: 0

The Prediction: Right

Accuracy so far: 78.95% (74.51% completed)

◆ **Accuracies until the 38th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 0 min 59 sec

◆ **Error(= Predicted value - Observed value) in the 38th Cross Validation**

◇ **Average Error is 0.314±0.3449 until the 38th turn in the LOO method.**

■ The 39th cross-validation out of 51 turns

□ The 39th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日0時 56分 15秒

□ The 39th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日1時 3分 22秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
100
80
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
200
400
600
800
Model Complexity

,

◆ **1023 models were created**

◇ **Quatiliy Box values are {46., 0.1903} in the 39th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1023 Selected models: 1 (0.09775%)

◆ Inning 0. Complexity: 46. Error: 0.1903 Number of Selected models: 1 (0.09775%)

◆ Inning 1. Complexity: 47. Error: 0.2003 Number of Selected models: 1 (0.09775%)

◆ Inning 2. Complexity: 48. Error: 0.2103 Number of Selected models: 1 (0.09775%)

◆ Inning 3. Complexity: 49. Error: 0.2203 Number of Selected models: 4 (0.391%)

◆ Inning 4. Complexity: 50. Error: 0.2303 Number of Selected models: 9 (0.8798%)

◆ Inning 5. Complexity: 51. Error: 0.2403 Number of Selected models: 18 (1.76%)

◆ Inning 6. Complexity: 52. Error: 0.2503 Number of Selected models: 19 (1.857%)

◆ Inning 7. Complexity: 53. Error: 0.2603 Number of Selected models: 22 (2.151%)

◆ Inning 8. Complexity: 54. Error: 0.2703 Number of Selected models: 37 (3.617%)

◆ Inning 9. Complexity: 55. Error: 0.2803 Number of Selected models: 48 (4.692%)

◆ Inning 10. Complexity: 56. Error: 0.2903 Number of Selected models: 56 (5.474%)

◆ Inning 11. Complexity: 57. Error: 0.3003 Number of Selected models: 73 (7.136%)

◆ Inning 12. Complexity: 58. Error: 0.3103 Number of Selected models: 88 (8.602%)

◆ **88 interesting models were selected**

  ◇ **Quatiliy Box values are {58., 0.310304}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, pyrexia, cNIpostRej, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.269	$5.31\times10^{-2}+0.12\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+1.04\,b_{45}$
2	35	0.304	$-(1.75\times10^{-2})+0.12\,\text{cNIpostRej}+0.58\,\text{respiratoryInfection}+1.12\,b_{45}+0.29\,dR_{53}$
3	38	0.221	$3.14\times10^{-2}+0.12\,\text{cNIpostRej}+0.84\,\text{respiratoryInfection}-0.55\,\text{pyrexia respiratoryInfection}+1.07\,b_{45}$
4	38	0.288	$-(3.90\times10^{-2})+0.15\,\text{cRPpostRej}+0.66\,\text{igG}+$ $0.70\,\text{respiratoryInfection}-0.47\,\text{pyrexia upperRespiratoryInfection}$
5	38	0.308	$7.69\times10^{-2}+(8.82\times10^{-2})\,\text{cNIpostRej}+0.36\,\text{igG}+0.82\,b_{45}+0.85\,\text{respiratoryInfection}\,dQ_7$
6	38	0.309	$-(7.02\times10^{-2})+0.14\,\text{cRPpostRej}+0.76\,\text{igG}+0.51\,\text{respiratoryInfection}+0.17\,\text{denovoDSA}\,dR_7$
7	41	0.299	$-(4.88\times10^{-3})+0.14\,\text{cRPpostRej}+0.61\,\text{igG}+$ $0.77\,\text{respiratoryInfection type2DM}+0.85\,\text{respiratoryInfection antiHLAclass}_1$
8	42	0.266	$2.10\times10^{-2}+(1.57\times10^{-2})\,\text{cNIpostRej}^2+0.31\,\text{respiratoryInfection}+0.97\,b_{45}+0.67\,\text{respiratoryInfection}\,dQ_7$
9	42	0.282	$4.94\times10^{-2}+(1.65\times10^{-3})\,\text{hDperiod}^3\,\text{igG}-0.39\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.95\,b_{45}$
10	43	0.218	$4.12\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.84\,b_{45}$
11	46	0.190	$-(1.69\times10^{-2})+0.45\,\text{igG}+0.76\,\text{respiratoryInfection}-$ $0.55\,\text{pyrexia upperRespiratoryInfection}+0.75\,b_{45}+(2.01\times10^{-2})\,\text{wBCpeakover}_5$
12	46	0.209	$3.91\times10^{-2}+0.11\,\text{cNIpostRej}+0.47\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}-1.00\,\text{cNIpostRej}\,b_{45}$
13	46	0.221	$2.28\times10^{-2}+0.11\,\text{cNIpostRej}+(1.53\times10^{-2})\,\text{cRPpostRej}+$ $0.84\,\text{respiratoryInfection}-0.55\,\text{pyrexia respiratoryInfection}+1.05\,b_{45}$
14	46	0.230	$2.39\times10^{-2}+0.11\,\text{cNIpostRej}+0.37\,\text{igG}+$ $0.37\,\text{respiratoryInfection}+0.88\,b_{45}+0.53\,\text{respiratoryInfection}\,dQ_7$
15	53	0.179	$-(7.64\times10^{-3})+(3.61\times10^{-2})\,\text{cRPpostRej}^2+0.64\,\text{igG}+0.69\,\text{respiratoryInfection}-$ $0.46\,\text{pyrexia respiratoryInfection}+(1.94\times10^{-2})\,\text{pRAclass1after type2DM}$

◆ Ensembles in ParetoFront

■ **The 39th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: -0.01744, The Observed value: 0

The Prediction: Right

Accuracy so far: 79.49% (76.47% completed)

◆ **Accuracies until the 39th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 0 min 52 sec

◆ **Error(= Predicted value - Observed value) in the 39th Cross Validation**

◇ **Average Error is 0.3064±0.3436 until the 39th turn in the LOO method.**

■ The 40th cross-validation out of 51 turns

□ The 40th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日1時 3分 27秒

□ The 40th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日1時 9分 39秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
100
80
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
50
100
150
200
Model Complexity

,

◆ **978 models were created**

◇ **Quatiliy Box values are {46., 0.1903} in the 40th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 978 Selected models: 1 (0.1022%)

◆ Inning 0. Complexity: 46. Error: 0.1903 Number of Selected models: 1 (0.1022%)

◆ Inning 1. Complexity: 47. Error: 0.2003 Number of Selected models: 1 (0.1022%)

◆ Inning 2. Complexity: 48. Error: 0.2103 Number of Selected models: 1 (0.1022%)

◆ Inning 3. Complexity: 49. Error: 0.2203 Number of Selected models: 2 (0.2045%)

◆ Inning 4. Complexity: 50. Error: 0.2303 Number of Selected models: 4 (0.409%)

◆ Inning 5. Complexity: 51. Error: 0.2403 Number of Selected models: 7 (0.7157%)

◆ Inning 6. Complexity: 52. Error: 0.2503 Number of Selected models: 8 (0.818%)

◆ Inning 7. Complexity: 53. Error: 0.2603 Number of Selected models: 10 (1.022%)

◆ Inning 8. Complexity: 54. Error: 0.2703 Number of Selected models: 20 (2.045%)

◆ Inning 9. Complexity: 55. Error: 0.2803 Number of Selected models: 25 (2.556%)

◆ Inning 10. Complexity: 56. Error: 0.2903 Number of Selected models: 30 (3.067%)

◆ Inning 11. Complexity: 57. Error: 0.3003 Number of Selected models: 43 (4.397%)

◆ Inning 12. Complexity: 58. Error: 0.3103 Number of Selected models: 53 (5.419%)

◆ Inning 13. Complexity: 59. Error: 0.3203 Number of Selected models: 62 (6.339%)

◆ Inning 14. Complexity: 60. Error: 0.3303 Number of Selected models: 80 (8.18%)

- 80 interesting models were selected
  - Quatiliy Box values are {60., 0.330304}.

- Variable Presence (Popularity of each variable) FOCUSED on important variables
- TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, pyrexia, igG, b45, wBCpeakover5}

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	38	0.246	$-(6.02\times10^{-3})+0.81\,\text{respiratoryInfection}-0.59\,\text{pyrexia respiratoryInfection}+0.96\,b_{45}+(2.06\times10^{-2})\,\text{wBCpeakover}_5$
2	38	0.274	$-(4.35\times10^{-2})+0.12\,\text{cNIpostRej}+0.15\,\text{denovoDSA}+0.43\,\text{aBOI dSAclass1number}+0.53\,\text{respiratoryInfection}$
3	38	0.295	$-(2.82\times10^{-2})+0.15\,\text{cRPpostRej}+0.88\,\text{aBOI igG}-0.37\,\text{pyrexia}+0.72\,\text{respiratoryInfection}$
4	38	0.296	$1.14\times10^{-2}+0.69\,\text{igG}+0.71\,\text{respiratoryInfection}-0.53\,\text{pyrexia respiratoryInfection}+(1.94\times10^{-2})\,\text{wBCpeakover}_5$
5	38	0.327	$4.75\times10^{-2}+0.62\,\text{igG}+(8.70\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+0.69\,b_{45}-(4.75\times10^{-2})\,b_{75}$
6	39	0.318	$-(1.46\times10^{-2})-0.44\,\text{pyrexia}+0.69\,\text{respiratoryInfection}+0.89\,b_{45}+(9.00\times10^{-2})\,\sqrt{\text{wBCpeakover}_5}$
7	42	0.305	$-(8.44\times10^{-2})+0.14\,\text{cRPpostRej}+0.71\,\text{igG}+(8.23\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+0.12\,\text{antiHLAclass}_2{}^2$
8	43	0.236	$6.88\times10^{-3}+0.47\,\text{igG}-0.39\,\text{pyrexia}+0.68\,\text{respiratoryInfection}+0.72\,b_{45}+(1.90\times10^{-2})\,\text{wBCpeakover}_5$
9	43	0.298	$8.69\times10^{-2}-0.11\,\text{banfct}+0.53\,\text{igG}-0.38\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.76\,b_{45}$
10	43	0.318	$-(2.86\times10^{-2})+0.53\,\text{candida}+0.45\,\text{igG}+0.50\,\text{respiratoryInfection}+0.80\,b_{45}+0.22\,dR_{53}$
11	46	0.190	$-(1.69\times10^{-2})+0.45\,\text{igG}+0.76\,\text{respiratoryInfection}-0.55\,\text{pyrexia respiratoryInfection}+0.75\,b_{45}+(2.01\times10^{-2})\,\text{wBCpeakover}_5$
12	46	0.204	$-(1.39\times10^{-2})+0.11\,\text{cNIpostRej}+0.13\,\text{denovoDSA}+0.43\,\text{aBOI dSAclass1number}-0.31\,\text{pyrexia}+0.64\,\text{respiratoryInfection}$
13	46	0.228	$-(3.90\times10^{-2})+0.12\,\text{cRPpostRej}+0.48\,\text{igG}+0.74\,\text{respiratoryInfection}-0.49\,\text{pyrexia respiratoryInfection}+0.58\,b_{45}$
14	46	0.228	$-(9.26\times10^{-2})+0.33\,\text{asthma}+0.15\,\text{cRPpostRej}+0.75\,\text{igG}+(8.59\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+0.27\,dR_7$
15	46	0.246	$1.33\times10^{-3}-(1.12\times10^{-2})\,\text{lymphinvasion}+0.81\,\text{respiratoryInfection}-0.58\,\text{pyrexia respiratoryInfection}+0.96\,b_{45}+(2.04\times10^{-2})\,\text{wBCpeakover}_5$

◆ Ensembles in ParetoFront

■ **The 40th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: -0.01353, The Observed value: 0

The Prediction: Right

Accuracy so far: 80.% (78.43% completed)

◆ **Accuracies until the 40th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 0 min 46 sec

◆ **Error(= Predicted value - Observed value) in the 40th Cross Validation**

◇ **Average Error is 0.2991±0.3423 until the 40th turn in the LOO method.**

■ The 41st cross-validation out of 51 turns

□ The 41st Genetic Programming has started.

◆ Present Time: 2020年 7月 14日1時 9分 43秒

□ The 41th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日1時 16分 20秒

◆ Monitors Plot

0.01
0
200
400
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 – R2
0
50
100
150
200
250
300
Model Complexity

,

◆ **963 models were created**

◇ **Quatiliy Box values are {42., 0.1986} in the 41st turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 963 Selected models: 1 (0.1038%)

◆ Inning 0. Complexity: 42. Error: 0.1986 Number of Selected models: 1 (0.1038%)

◆ Inning 1. Complexity: 43. Error: 0.2086 Number of Selected models: 1 (0.1038%)

◆ Inning 2. Complexity: 44. Error: 0.2186 Number of Selected models: 1 (0.1038%)

◆ Inning 3. Complexity: 45. Error: 0.2286 Number of Selected models: 1 (0.1038%)

◆ Inning 4. Complexity: 46. Error: 0.2386 Number of Selected models: 5 (0.5192%)

◆ Inning 5. Complexity: 47. Error: 0.2486 Number of Selected models: 10 (1.038%)

◆ Inning 6. Complexity: 48. Error: 0.2586 Number of Selected models: 11 (1.142%)

◆ Inning 7. Complexity: 49. Error: 0.2686 Number of Selected models: 15 (1.558%)

◆ Inning 8. Complexity: 50. Error: 0.2786 Number of Selected models: 21 (2.181%)

◆ Inning 9. Complexity: 51. Error: 0.2886 Number of Selected models: 33 (3.427%)

◆ Inning 10. Complexity: 52. Error: 0.2986 Number of Selected models: 39 (4.05%)

◆ Inning 11. Complexity: 53. Error: 0.3086 Number of Selected models: 46 (4.777%)

◆ Inning 12. Complexity: 54. Error: 0.3186 Number of Selected models: 60 (6.231%)

◆ Inning 13. Complexity: 55. Error: 0.3286 Number of Selected models: 73 (7.58%)

◆ Inning 14. Complexity: 56. Error: 0.3386 Number of Selected models: 81 (8.411%)

- **81 interesting models were selected**
  - **Quatiliy Box values are {56., 0.338612}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, cNIpostRej, b45, pyrexia, igG}**

◆ Defining Ensembles

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	Complexity	$1-R^2$	Function
			graftLoss
1	30	0.295	$-(1.05\times10^{-2})+0.13\,\text{cNIpostRej}+0.15\,\text{denovoDSA}+(8.21\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}$
2	34	0.248	$1.51\times10^{-2}+0.94\,\text{antiHLAclass}_2\,(\text{respiratoryInfection}+\bullet\text{igA}+b_{45})+(1.94\times10^{-2})\,\text{wBCpeakover}_5$
3	34	0.284	$6.62\times10^{-2}+(7.97\times10^{-2})\,\text{cNIpostRej}+0.93\,\text{antiHLAclass}_2\,(\text{respiratoryInfection}+\bullet\text{igA}+b_{45})$
4	38	0.238	$3.29\times10^{-2}+0.12\,\text{cNIpostRej}+0.84\,\text{respiratoryInfection}-0.55\,\text{pyrexia}\,\text{respiratoryInfection}+1.08\,b_{45}$
5	38	0.251	$-(1.18\times10^{-2})+0.12\,\text{cNIpostRej}+0.13\,\text{denovoDSA}+(8.45\times10^{-2})\,\text{inflammationdatefirst}\,(\text{igG}+\text{respiratoryInfection})$
6	38	0.269	$-(3.93\times10^{-3})+0.12\,\text{cNIpostRej}+0.12\,\text{denovoDSA}+0.70\,\text{respiratoryInfection}-0.47\,\text{pyrexia}\,\text{respiratoryInfection}$
7	38	0.327	$2.99\times10^{-2}+0.11\,\text{cNIpostRej}+(9.61\times10^{-2})\,\text{inflammationdatefirst}\,(\text{igG}+\text{respiratoryInfection})+0.27\,dR_{13}$
8	39	0.302	$4.53\times10^{-2}+0.11\,\text{cNIpostRej}+(2.90\times10^{-2})\,\text{denovoDSA}^2-0.33\,\text{pyrexia}+0.63\,\text{respiratoryInfection}$
9	41	0.264	$-(5.84\times10^{-3})+0.81\,\text{respiratoryInfection}-0.59\,\text{pyrexia}\,\text{respiratoryInfection}+0.96\,\text{antiHLAclass}_2\,b_{45}+(2.06\times10^{-2})\,\text{wBCpeakover}_5$
10	41	0.305	$7.26\times10^{-3}+0.73\,\text{respiratoryInfection}-0.54\,\text{pyrexia}\,\text{respiratoryInfection}+0.56\,\text{igG}\,\text{antiHLAclass}_2+(1.96\times10^{-2})\,\text{wBCpeakover}_5$
11	42	0.199	$-(1.95\times10^{-2})+0.24\,\text{respiratoryInfection}+0.80\,\text{antiHLAclass}_2\,(\text{respiratoryInfection}+\bullet\text{igA}+b_{45})+(1.96\times10^{-2})\,\text{wBCpeakover}_5$
12	42	0.248	$1.56\times10^{-2}+0.95\,\text{antiHLAclass}_2\,(\text{respiratoryInfection}+\bullet\text{igA}+b_{45})-(1.73\times10^{-2})\,cw_9+(1.94\times10^{-2})\,\text{wBCpeakover}_5$
13	42	0.291	$1.82\times10^{-2}+0.25\,\text{respiratoryInfection}+0.12\,\bullet\text{igA}+0.79\,\text{antiHLAclass}_2\,(\text{respiratoryInfection}+\bullet\text{igA}+b_{45})$
14	43	0.253	$3.49\times10^{-2}+0.11\,\text{cNIpostRej}+0.45\,\text{igG}-0.35\,\text{pyrexia}+0.70\,\text{respiratoryInfection}+0.22\,\text{dSAandHSAclass}_1$
15	43	0.274	$1.81\times10^{-2}+0.12\,\text{cNIpostRej}-0.34\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.18\,dR_{18}+0.24\,\text{dSAandHSAclass}_1$

◆ Ensembles in ParetoFront

■ **The 41st Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.7268, The Observed value: 1

The Prediction: Right

Accuracy so far: 80.49% (80.39% completed)

◆ **Accuracies until the 41st turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 0 min 39 sec

◆ **Error(= Predicted value - Observed value) in the 41st Cross Validation**

◇ **Average Error is 0.2985±0.3381 until the 41st turn in the LOO method.**

■ The 42nd cross-validation out of 51 turns

□ The 42nd Genetic Programming has started.

◆ Present Time: 2020年 7月 14日曜日 1時 16分 24秒

□ The 42th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日曜日 1時 22分 40秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

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Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
100
200
300
400
500
Model Complexity

,

◆ **912 models were created**

◇ **Quatiliy Box values are {41., 0.1784} in the 42nd turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 912 Selected models: 1 (0.1096%)

◆ Inning 0. Complexity: 41. Error: 0.1784 Number of Selected models: 1 (0.1096%)

◆ Inning 1. Complexity: 42. Error: 0.1884 Number of Selected models: 1 (0.1096%)

◆ Inning 2. Complexity: 43. Error: 0.1984 Number of Selected models: 1 (0.1096%)

◆ Inning 3. Complexity: 44. Error: 0.2084 Number of Selected models: 1 (0.1096%)

◆ Inning 4. Complexity: 45. Error: 0.2184 Number of Selected models: 1 (0.1096%)

◆ Inning 5. Complexity: 46. Error: 0.2284 Number of Selected models: 6 (0.6579%)

◆ Inning 6. Complexity: 47. Error: 0.2384 Number of Selected models: 11 (1.206%)

◆ Inning 7. Complexity: 48. Error: 0.2484 Number of Selected models: 12 (1.316%)

◆ Inning 8. Complexity: 49. Error: 0.2584 Number of Selected models: 23 (2.522%)

◆ Inning 9. Complexity: 50. Error: 0.2684 Number of Selected models: 31 (3.399%)

◆ Inning 10. Complexity: 51. Error: 0.2784 Number of Selected models: 52 (5.702%)

◆ Inning 11. Complexity: 52. Error: 0.2884 Number of Selected models: 59 (6.469%)

◆ Inning 12. Complexity: 53. Error: 0.2984 Number of Selected models: 68 (7.456%)

◆ Inning 13. Complexity: 54. Error: 0.3084 Number of Selected models: 78 (8.553%)

◆ **78 interesting models were selected**

  ◇ **Quatiliy Box values are {54., 0.30838}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, pyrexia, hLAmm}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	33	0.289	$5.41\times10^{-2}+0.95\,\text{respiratoryInfection}-0.22\,\text{feverOnly hLAmm respiratoryInfection}+0.95\,b_{45}$
2	35	0.268	$5.27\times10^{-2}+0.12\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+1.04\,b_{45}$
3	35	0.306	$-(2.36\times10^{-2})+0.13\,\text{cNIpostRej}+0.59\,\text{respiratoryInfection}+1.13\,b_{45}+0.28\,dR_{53}$
4	38	0.221	$3.11\times10^{-2}+0.12\,\text{cNIpostRej}+0.84\,\text{respiratoryInfection}-0.55\,\text{pyrexia respiratoryInfection}+1.07\,b_{45}$
5	41	0.178	$3.28\times10^{-2}+0.11\,\text{cNIpostRej}+0.99\,\text{respiratoryInfection}-$ $0.20\,\text{feverOnly hLAmm respiratoryInfection}+1.06\,b_{45}$
6	41	0.285	$1.87\times10^{-2}+0.77\,\text{respiratoryInfection}-$ $0.52\,\text{pyrexia respiratoryInfection}+0.98\,b_{45}+(9.34\times10^{-2})\,\text{hLAmm}\,dR_{51}$
7	43	0.266	$-(1.78\times10^{-2})+0.12\,\text{cRPpostRej}+0.49\,\text{igG}-0.35\,\text{pyrexia}+0.67\,\text{respiratoryInfection}+0.56\,b_{45}$
8	46	0.175	$2.11\times10^{-2}+0.11\,\text{cNIpostRej}+0.41\,\text{igG}+$ $0.80\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.87\,b_{45}$
9	46	0.186	$-(1.30\times10^{-2})+0.45\,\text{igG}+0.76\,\text{respiratoryInfection}-$ $0.55\,\text{pyrexia respiratoryInfection}+0.75\,b_{45}+(2.08\times10^{-2})\,\text{wBCpeakover}_5$
10	46	0.189	$5.29\times10^{-3}+0.12\,\text{cNIpostRej}+0.81\,\text{respiratoryInfection}-$ $0.51\,\text{pyrexia respiratoryInfection}+1.10\,b_{45}+0.23\,dR_{51}$
11	46	0.200	$4.55\times10^{-3}+0.12\,\text{cNIpostRej}+0.83\,\text{respiratoryInfection}-$ $0.52\,\text{pyrexia respiratoryInfection}+1.02\,b_{45}+0.16\,dR_7$
12	46	0.205	$-(2.59\times10^{-2})+0.12\,\text{cNIpostRej}+1.00\,b_{45}+0.25\,(\text{coaglationnecrosis}+\text{respiratoryInfection}+dQ_7)^2$
13	46	0.206	$1.67\times10^{-2}+0.11\,\text{cNIpostRej}-0.35\,\text{pyrexia}+$ $0.74\,\text{respiratoryInfection}+1.08\,b_{45}+(9.09\times10^{-2})\,\text{hLAmm}\,dR_{51}$
14	46	0.234	$4.70\times10^{-2}+0.11\,\text{cNIpostRej}-0.27\,\text{pyrexia}+$ $1.18\,\text{respiratoryInfection}-(2.98\times10^{-2})\,\text{maxWBC respiratoryInfection}+1.05\,b_{45}$
15	49	0.205	$-(4.67\times10^{-3})+0.11\,\text{cNIpostRej}+1.29\,\text{respiratoryInfection}-$ $(4.31\times10^{-2})\,\text{maxWBC respiratoryInfection}+1.10\,b_{45}+(9.74\times10^{-2})\,\text{hLAmm}\,dR_{51}$

◆ Ensembles in ParetoFront

■ **The 42nd Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: -0.02046, The Observed value: 0

The Prediction: Right

Accuracy so far: 80.95% (82.35% completed)

◆ **Accuracies until the 42nd turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 0 min 33 sec

◆ **Error(= Predicted value - Observed value) in the 42nd Cross Validation**

◇ **Average Error is 0.2918±0.3367 until the 42nd turn in the LOO method.**

■ The 43rd cross-validation out of 51 turns

□ The 43rd Genetic Programming has started.

◆ Present Time: 2020年 7月 14日1時 22分 45秒

□ The 43th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日1時 29分 23秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
100
80
60
40
20
0
−20

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
50
100
150
200
250
Model Complexity

,

◆ **993 models were created**

◇ **Quatiliy Box values are {42., 0.2032} in the 43rd turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 993 Selected models: 1 (0.1007%)

◆ Inning 0. Complexity: 42. Error: 0.2032 Number of Selected models: 1 (0.1007%)

◆ Inning 1. Complexity: 43. Error: 0.2132 Number of Selected models: 2 (0.2014%)

◆ Inning 2. Complexity: 44. Error: 0.2232 Number of Selected models: 2 (0.2014%)

◆ Inning 3. Complexity: 45. Error: 0.2332 Number of Selected models: 2 (0.2014%)

◆ Inning 4. Complexity: 46. Error: 0.2432 Number of Selected models: 5 (0.5035%)

◆ Inning 5. Complexity: 47. Error: 0.2532 Number of Selected models: 7 (0.7049%)

◆ Inning 6. Complexity: 48. Error: 0.2632 Number of Selected models: 7 (0.7049%)

◆ Inning 7. Complexity: 49. Error: 0.2732 Number of Selected models: 10 (1.007%)

◆ Inning 8. Complexity: 50. Error: 0.2832 Number of Selected models: 16 (1.611%)

◆ Inning 9. Complexity: 51. Error: 0.2932 Number of Selected models: 29 (2.92%)

◆ Inning 10. Complexity: 52. Error: 0.3032 Number of Selected models: 37 (3.726%)

◆ Inning 11. Complexity: 53. Error: 0.3132 Number of Selected models: 42 (4.23%)

◆ Inning 12. Complexity: 54. Error: 0.3232 Number of Selected models: 50 (5.035%)

◆ Inning 13. Complexity: 55. Error: 0.3332 Number of Selected models: 59 (5.942%)

◆ Inning 14. Complexity: 56. Error: 0.3432 Number of Selected models: 65 (6.546%)

- Inning 15. Complexity: 57. Error: 0.3532 Number of Selected models: 74 (7.452%)
- Inning 16. Complexity: 58. Error: 0.3632 Number of Selected models: 87 (8.761%)

- **87 interesting models were selected**
  - **Quatiliy Box values are {58., 0.363159}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, igG, cNIpostRej, wBCpeakover5}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.323	$1.06\times10^{-2}+0.76\,\text{igG}+(8.67\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.33\,\text{dR}_7$
2	34	0.314	$5.41\times10^{-2}+0.98\,\text{respiratoryInfection}-0.26\,\text{banfi}^2\,\text{respiratoryInfection}+0.95\,\text{b}_{45}$
3	34	0.344	$-(7.01\times10^{-2})+0.17\,\text{cRPpostRej}+0.58\,\text{respiratoryInfection}+(7.63\times10^{-2})\,\text{dSAandHLAclass1pre}\,\text{wBCpeakover}_5{}^2$
4	35	0.269	$5.44\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+1.04\,\text{b}_{45}$
5	35	0.358	$-(2.80\times10^{-2})+0.53\,\text{candida}+0.50\,\text{respiratoryInfection}+1.03\,\text{b}_{45}+0.33\,\text{dR}_{53}$
6	35	0.363	$1.09\times10^{-2}+0.12\,\text{cNIpostRej}+(4.58\times10^{-3})\,\text{pRAclass1pre}+0.65\,\text{respiratoryInfection}+0.92\,\text{b}_{45}$
7	38	0.238	$-(4.18\times10^{-3})+1.11\,\text{respiratoryInfection}-0.52\,\text{banfi}\,\text{respiratoryInfection}+0.96\,\text{b}_{45}+(2.05\times10^{-2})\,\text{wBCpeakover}_5$
8	41	0.324	$3.64\times10^{-2}+0.92\,\text{b}_{45}+0.93\,\sqrt{\text{respiratoryInfection}\,\text{dQ}_7}+(2.00\times10^{-2})\,\text{wBCpeakover}_5$
9	42	0.203	$-(2.56\times10^{-2})+(1.63\times10^{-2})\,\text{cNIpostRej}^2+0.78\,\text{igG}+(9.02\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.35\,\text{dR}_7$
10	42	0.207	$-(4.91\times10^{-3})+1.00\,\text{respiratoryInfection}-0.27\,\text{banfi}^2\,\text{respiratoryInfection}+0.96\,\text{b}_{45}+(2.08\times10^{-2})\,\text{wBCpeakover}_5$
11	42	0.236	$2.16\times10^{-2}+1.11\,\text{respiratoryInfection}-0.50\,\text{banfi}\,\text{respiratoryInfection}+0.98\,\text{b}_{45}+(4.98\times10^{-4})\,\text{wBCpeakover}_5{}^2$
12	42	0.270	$-(3.71\times10^{-2})+0.16\,\text{cRPpostRej}+0.60\,\text{igG}+0.86\,\text{respiratoryInfection}-0.21\,\text{banfi}^2\,\text{respiratoryInfection}$
13	42	0.345	$7.60\times10^{-2}+0.82\,\sqrt{\text{igG}+\text{b}_{45}+\text{respiratoryInfection}\,\text{dQ}_7}$
14	43	0.264	$2.73\times10^{-2}+0.12\,\text{cNIpostRej}+\frac{5.56\times10^{-3}}{\text{cRPpostRej}}-0.40\,\text{pyrexia}+0.77\,\text{respiratoryInfection}+1.07\,\text{b}_{45}$
15	43	0.273	$2.24\times10^{-2}+0.10\,\text{cNIpostRej}+0.33\,\text{gERD}+0.73\,\text{igG}-0.42\,\text{pyrexia}+0.70\,\text{respiratoryInfection}$

◆ Ensembles in ParetoFront

■ **The 43rd Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.09581, The Observed value: 0

The Prediction: Right

Accuracy so far: 81.4% (84.31% completed)

◆ **Accuracies until the 43rd turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 0 min 26 sec

◆ **Error(= Predicted value - Observed value) in the 43rd Cross Validation**

◇ **Average Error is 0.2873±0.334 until the 43rd turn in the LOO method.**

■ The 44th cross-validation out of 51 turns

□ The 44th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日1時 29分 27秒

□ The 44th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日1時 36分 5秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
−200
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
200
400
600
800
Model Complexity

,

◆ **969 models were created**

◇ **Quatiliy Box values are {46., 0.1475} in the 44th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 969 Selected models: 1 (0.1032%)

◆ Inning 0. Complexity: 46. Error: 0.1475 Number of Selected models: 1 (0.1032%)

◆ Inning 1. Complexity: 47. Error: 0.1575 Number of Selected models: 1 (0.1032%)

◆ Inning 2. Complexity: 48. Error: 0.1675 Number of Selected models: 1 (0.1032%)

◆ Inning 3. Complexity: 49. Error: 0.1775 Number of Selected models: 1 (0.1032%)

◆ Inning 4. Complexity: 50. Error: 0.1875 Number of Selected models: 1 (0.1032%)

◆ Inning 5. Complexity: 51. Error: 0.1975 Number of Selected models: 4 (0.4128%)

◆ Inning 6. Complexity: 52. Error: 0.2075 Number of Selected models: 5 (0.516%)

◆ Inning 7. Complexity: 53. Error: 0.2175 Number of Selected models: 8 (0.8256%)

◆ Inning 8. Complexity: 54. Error: 0.2275 Number of Selected models: 14 (1.445%)

◆ Inning 9. Complexity: 55. Error: 0.2375 Number of Selected models: 16 (1.651%)

◆ Inning 10. Complexity: 56. Error: 0.2475 Number of Selected models: 24 (2.477%)

◆ Inning 11. Complexity: 57. Error: 0.2575 Number of Selected models: 26 (2.683%)

◆ Inning 12. Complexity: 58. Error: 0.2675 Number of Selected models: 34 (3.509%)

◆ Inning 13. Complexity: 59. Error: 0.2775 Number of Selected models: 40 (4.128%)

◆ Inning 14. Complexity: 60. Error: 0.2875 Number of Selected models: 52 (5.366%)

- Inning 15. Complexity: 61. Error: 0.2975 Number of Selected models: 61 (6.295%)
- Inning 16. Complexity: 62. Error: 0.3075 Number of Selected models: 64 (6.605%)
- Inning 17. Complexity: 63. Error: 0.3175 Number of Selected models: 78 (8.05%)

- **78 interesting models were selected**
  - **Quatiliy Box values are {63., 0.317471}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, igG, pyrexia, wBCpeakover5}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.303	$5.05\times10^{-2}+0.12\,\text{cNIpostRej}+(9.58\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.05\,b_{45}$
2	33	0.309	$8.57\times10^{-3}+0.72\,\text{igG}+(3.20\times10^{-2})\,\text{denovoDSA}\,\text{mMFpostRej}+(7.79\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}$
3	35	0.269	$5.40\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.76\,\text{respiratoryInfection}+1.04\,b_{45}$
4	35	0.313	$9.71\times10^{-2}-\frac{2.11\times10^{-3}}{\text{hDperiod}}-0.46\,\text{pyrexia}+0.78\,\text{respiratoryInfection}+0.91\,b_{45}$
5	38	0.211	$3.00\times10^{-2}+0.11\,\text{cNIpostRej}+0.57\,\text{igG}+(9.37\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.78\,b_{45}$
6	38	0.307	$2.85\times10^{-2}+(9.65\times10^{-2})\,\text{cNIpostRej}+0.76\,\text{igG}+(5.59\times10^{-2})\,\text{preDSA}+(9.14\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}$
7	41	0.285	$-(4.79\times10^{-2})+0.13\,\text{cRPpostRej}+0.70\,\text{igG}+(4.35\times10^{-3})\,\text{denovoDSA}\,\text{maxWBC}+(7.77\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}$
8	42	0.245	$-(5.61\times10^{-2})+0.13\,\text{cNIpostRej}+0.15\,\text{denovoDSA}+(9.67\times10^{-3})\,\text{pRAclass1pre}+(8.55\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}^2$
9	42	0.253	$2.49\times10^{-3}+0.13\,\text{cNIpostRej}+(9.89\times10^{-2})\,\text{denovoDSA}+(8.79\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}^2+0.76\,b_{45}$
10	42	0.287	$3.53\times10^{-2}+0.72\,\text{igG}+0.72\,\text{respiratoryInfection}-0.50\,\text{pyrexia}\,\text{respiratoryInfection}+(4.87\times10^{-4})\,\text{wBCpeakover}_5{}^2$
11	42	0.290	$4.14\times10^{-2}+0.47\,\text{igG}+0.74\,\text{respiratoryInfection}-0.52\,\text{pyrexia}\,\text{respiratoryInfection}+0.72\,b_{45}{}^2$
12	43	0.236	$6.88\times10^{-3}+0.47\,\text{igG}-0.39\,\text{pyrexia}+0.68\,\text{respiratoryInfection}+0.72\,b_{45}+(1.90\times10^{-2})\,\text{wBCpeakover}_5$
13	43	0.260	$2.10\times10^{-2}-0.42\,\text{polyp}-0.38\,\text{pyrexia}+0.74\,\text{respiratoryInfection}+0.93\,b_{45}+(2.23\times10^{-2})\,\text{wBCpeakover}_5$
14	43	0.275	$2.09\times10^{-2}+0.11\,\text{cNIpostRej}-0.62\,\text{hypoplastickidney}+0.47\,\text{igG}+0.66\,\text{respiratoryInfection}+0.84\,b_{45}$
15	46	0.147	$-(2.00\times10^{-2})+0.12\,\text{cNIpostRej}+0.55\,\text{igG}+(9.69\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.70\,b_{45}+0.28\,dR_7$

◆ Ensembles in ParetoFront

■ **The 44th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.003397, The Observed value: 0

The Prediction: Right

Accuracy so far: 81.82% (86.27% completed)

◆ **Accuracies until the 44th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 0 min 19 sec

◆ **Error(= Predicted value - Observed value) in the 44th Cross Validation**

◇ **Average Error is 0.2808±0.3328 until the 44th turn in the LOO method.**

■ The 45th cross-validation out of 51 turns

□ The 45th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日1時 36分 10秒

□ The 45th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日1時 42分 39秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
40
30
20
10
0

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
50
100
150
200
250
300
350
Model Complexity

◆ **1054 models were created**

◇ **Quatiliy Box values are {41., 0.1923} in the 45th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1054 Selected models: 1 (0.09488%)

◆ Inning 0. Complexity: 41. Error: 0.1923 Number of Selected models: 1 (0.09488%)

◆ Inning 1. Complexity: 42. Error: 0.2023 Number of Selected models: 1 (0.09488%)

◆ Inning 2. Complexity: 43. Error: 0.2123 Number of Selected models: 2 (0.1898%)

◆ Inning 3. Complexity: 44. Error: 0.2223 Number of Selected models: 2 (0.1898%)

◆ Inning 4. Complexity: 45. Error: 0.2323 Number of Selected models: 2 (0.1898%)

◆ Inning 5. Complexity: 46. Error: 0.2423 Number of Selected models: 5 (0.4744%)

◆ Inning 6. Complexity: 47. Error: 0.2523 Number of Selected models: 7 (0.6641%)

◆ Inning 7. Complexity: 48. Error: 0.2623 Number of Selected models: 9 (0.8539%)

◆ Inning 8. Complexity: 49. Error: 0.2723 Number of Selected models: 13 (1.233%)

◆ Inning 9. Complexity: 50. Error: 0.2823 Number of Selected models: 16 (1.518%)

◆ Inning 10. Complexity: 51. Error: 0.2923 Number of Selected models: 20 (1.898%)

◆ Inning 11. Complexity: 52. Error: 0.3023 Number of Selected models: 28 (2.657%)

◆ Inning 12. Complexity: 53. Error: 0.3123 Number of Selected models: 36 (3.416%)

◆ Inning 13. Complexity: 54. Error: 0.3223 Number of Selected models: 45 (4.269%)

◆ Inning 14. Complexity: 55. Error: 0.3323 Number of Selected models: 57 (5.408%)

- Inning 15. Complexity: 56. Error: 0.3423 Number of Selected models: 59 (5.598%)
- Inning 16. Complexity: 57. Error: 0.3523 Number of Selected models: 69 (6.546%)
- Inning 17. Complexity: 58. Error: 0.3623 Number of Selected models: 71 (6.736%)
- Inning 18. Complexity: 59. Error: 0.3723 Number of Selected models: 84 (7.97%)
- Inning 19. Complexity: 60. Error: 0.3823 Number of Selected models: 100 (9.488%)

- **100 interesting models were selected**
  - **Quatiliy Box values are {60., 0.382297}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, igG, inflammationdatefirst}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	27	0.381	$3.07\times10^{-2}+0.12\,\text{cNIpostRej}+0.64\,\text{respiratoryInfection}+1.07\,b_{45}$
2	30	0.303	$4.95\times10^{-2}+0.12\,\text{cNIpostRej}+(9.60\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.05\,b_{45}$
3	30	0.319	$1.83\times10^{-2}+(8.99\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.98\,b_{45}+0.47\,dR_{15}$
4	30	0.322	$5.34\times10^{-2}+(9.39\times10^{-2})\,\text{cNIpostRej}+0.82\,\text{igG}+(8.84\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}$
5	30	0.342	$8.48\times10^{-2}+(9.28\times10^{-2})\,\text{cNIpostRej}+0.99\,b_{45}+0.91\,\text{respiratoryInfection}\,dQ_8$
6	30	0.376	$5.41\times10^{-2}+0.28\,\text{respiratoryInfection}+0.95\,b_{45}+0.67\,\text{respiratoryInfection}\,dQ_8$
7	33	0.301	$3.96\times10^{-2}+0.85\,\text{igG}+(8.63\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.96\,a_{26}\,b_{45}$
8	35	0.344	$-(1.03\times10^{-2})+0.13\,\text{cNIpostRej}+0.60\,\text{respiratoryInfection}+1.03\,b_{45}+0.18\,dQ_8$
9	35	0.353	$-(6.72\times10^{-3})+0.11\,\text{cNIpostRej}+0.12\,\text{denovoDSA}+0.55\,\text{igG}+0.48\,\text{respiratoryInfection}$
10	35	0.370	$-(7.17\times10^{-2})+0.17\,\text{cRPpostRej}+0.65\,\text{igG}+0.51\,\text{respiratoryInfection}+0.26\,dR_{15}$
11	38	0.210	$1.73\times10^{-2}+0.11\,\text{cNIpostRej}+0.69\,\text{igG}+(9.26\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.24\,\text{dSAandHSAclass}_1$
12	38	0.280	$-(2.04\times10^{-2})+0.12\,\text{cNIpostRej}+(8.67\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.26\,dQ_7+0.28\,\text{dSAandHSAclass}_1$
13	38	0.285	$3.04\times10^{-2}+0.12\,\text{cNIpostRej}+0.23\,\text{respiratoryInfection}+(7.14\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.07\,b_{45}$
14	38	0.287	$5.02\times10^{-2}+0.47\,\text{banf g igG}-0.40\,\text{pyrexia}+0.73\,\text{respiratoryInfection}+0.95\,b_{45}$
15	38	0.291	$-(5.50\times10^{-2})+(9.15\times10^{-2})\,\text{cNIpostRej}+(3.05\times10^{-2})\,\text{infectionCount}+1.04\,b_{45}+0.81\,\text{respiratoryInfection}\,dQ_8$

◆ Ensembles in ParetoFront

■ **The 45th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.01057, The Observed value: 0

The Prediction: Right

Accuracy so far: 82.22% (88.24% completed)

◆ **Accuracies until the 45th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 0 min 13 sec

◆ **Error(= Predicted value - Observed value) in the 45th Cross Validation**

◇ **Average Error is 0.2748±0.3315 until the 45th turn in the LOO method.**

■ The 46th cross-validation out of 51 turns

□ The 46th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日1時 42分 43秒

□ The 46th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日1時 48分 59秒

◆ Monitors Plot

0.01
0
200
400
600
Generation Sequence

Model Quality Distribution
ModelComplexity
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
100
200
300
400
Model Complexity

,

◆ **940 models were created**

◇ **Quatiliy Box values are {50., 0.2106} in the 46th turn.**

- Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.
- Generated models: 940 Selected models: 1 (0.1064%)
- Inning 0. Complexity: 50. Error: 0.2106 Number of Selected models: 1 (0.1064%)
- Inning 1. Complexity: 51. Error: 0.2206 Number of Selected models: 3 (0.3191%)
- Inning 2. Complexity: 52. Error: 0.2306 Number of Selected models: 4 (0.4255%)
- Inning 3. Complexity: 53. Error: 0.2406 Number of Selected models: 8 (0.8511%)
- Inning 4. Complexity: 54. Error: 0.2506 Number of Selected models: 12 (1.277%)
- Inning 5. Complexity: 55. Error: 0.2606 Number of Selected models: 21 (2.234%)
- Inning 6. Complexity: 56. Error: 0.2706 Number of Selected models: 24 (2.553%)
- Inning 7. Complexity: 57. Error: 0.2806 Number of Selected models: 30 (3.191%)
- Inning 8. Complexity: 58. Error: 0.2906 Number of Selected models: 43 (4.574%)
- Inning 9. Complexity: 59. Error: 0.3006 Number of Selected models: 58 (6.17%)
- Inning 10. Complexity: 60. Error: 0.3106 Number of Selected models: 62 (6.596%)
- Inning 11. Complexity: 61. Error: 0.3206 Number of Selected models: 78 (8.298%)

- **78 interesting models were selected**
  - **Quatiliy Box values are {61., 0.320568}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, igG, cRPpostRej, pyrexia}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.268	$5.54\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+1.04\,b_{45}$
2	41	0.260	$-(5.11\times10^{-2})+0.16\,\text{cRPpostRej}+0.39\,\text{hLADRmm igG}+0.99\,\text{respiratoryInfection}-0.42\,\text{banfi respiratoryInfection}$
3	41	0.295	$5.41\times10^{-2}+1.27\,\text{respiratoryInfection}-0.59\,\text{banfi respiratoryInfection}-0.26\,\text{birthhistory respiratoryInfection}+0.95\,b_{45}$
4	42	0.251	$9.45\times10^{-3}+(3.53\times10^{-2})\,\text{cRPpostRej}^2+1.10\,\text{respiratoryInfection}-0.50\,\text{banfi respiratoryInfection}+0.88\,b_{45}$
5	42	0.290	$-(8.95\times10^{-2})+0.56\,\text{respiratoryInfection}+(1.19\times10^{-2})\,\text{hLAmm}^2\,(\text{cRPpostRej}+\text{igG}+b_{50}+dR_{53})$
6	43	0.218	$4.34\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.83\,b_{45}$
7	43	0.257	$3.70\times10^{-2}+0.12\,\text{cGN}+0.12\,\text{cNIpostRej}-0.41\,\text{pyrexia}+0.74\,\text{respiratoryInfection}+1.06\,b_{45}$
8	43	0.281	$-(5.19\times10^{-2})+0.14\,\text{cNIpostRej}+0.37\,\text{coaglationnecrosis}+0.57\,\text{respiratoryInfection}+1.03\,b_{45}+0.27\,dQ_7$
9	46	0.234	$-(4.29\times10^{-2})+0.13\,\text{cRPpostRej}+0.37\,\text{igG}+1.00\,\text{respiratoryInfection}-0.43\,\text{banfi respiratoryInfection}+0.62\,b_{45}$
10	46	0.271	$-(1.99\times10^{-2})+0.50\,\text{coaglationnecrosis}+0.13\,\text{cRPpostRej}+0.42\,\text{igG}+0.58\,b_{45}+0.84\,\text{respiratoryInfection}\,dQ_7$
11	50	0.211	$-(2.58\times10^{-3})+(3.64\times10^{-2})\,\text{cRPpostRej}^2+0.39\,\text{igG}+1.01\,\text{respiratoryInfection}-0.43\,\text{banfi respiratoryInfection}+0.69\,b_{45}$
12	50	0.235	$-(6.40\times10^{-2})+0.13\,\text{cRPpostRej}+0.91\,\text{respiratoryInfection}-0.22\,\text{banfi}^2\,\text{respiratoryInfection}+0.77\,b_{45}+0.12\,dQ_7$
13	50	0.240	$-(2.38\times10^{-3})+(3.51\times10^{-2})\,\text{cRPpostRej}^2+0.45\,\text{igG}+0.33\,\text{respiratoryInfection}+0.67\,b_{45}+0.55\,\text{respiratoryInfection}\,dQ_7$
14	54	0.235	$-(6.40\times10^{-2})+0.13\,\text{cRPpostRej}+0.91\,\text{respiratoryInfection}-0.22\,\text{banfi}^2\,\text{respiratoryInfection}^3+0.77\,b_{45}+0.12\,dQ_7$
15	57	0.257	$-(3.83\times10^{-2})+0.13\,\text{cRPpostRej}+0.43\,\text{igG}+0.24\,\text{respiratoryInfection}+0.22\,\text{orthopedics respiratoryInfection}+0.61\,b_{45}+0.62\,\text{respiratoryInfection}\,dQ_7$

◆ Ensembles in ParetoFront

■ **The 46th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.003716, The Observed value: 0

The Prediction: Right

Accuracy so far: 82.61% (90.2% completed)

◆ **Accuracies until the 46th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr 0 min 6 sec

◆ **Error(= Predicted value - Observed value) in the 46th Cross Validation**

◇ **Average Error is 0.2689±0.3302 until the 46th turn in the LOO method.**

■ The 47th cross-validation out of 51 turns

□ The 47th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日1時 49分 3秒

□ The 47th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日1時 55分 19秒

◆ Monitors Plot

0.01
0
200
400
600
800
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

,

Pareto Fronts
Error = 1 – R2
1
0.50
0.10
0.05
0.01
0
50
100
150
200
250
300
350
Model Complexity

,

◆ **902 models were created**

◇ **Quatiliy Box values are {49., 0.1455} in the 47th turn.**

- Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.
- Generated models: 902 Selected models: 1 (0.1109%)
- Inning 0. Complexity: 49. Error: 0.1455 Number of Selected models: 1 (0.1109%)
- Inning 1. Complexity: 50. Error: 0.1555 Number of Selected models: 1 (0.1109%)
- Inning 2. Complexity: 51. Error: 0.1655 Number of Selected models: 1 (0.1109%)
- Inning 3. Complexity: 52. Error: 0.1755 Number of Selected models: 1 (0.1109%)
- Inning 4. Complexity: 53. Error: 0.1855 Number of Selected models: 3 (0.3326%)
- Inning 5. Complexity: 54. Error: 0.1955 Number of Selected models: 3 (0.3326%)
- Inning 6. Complexity: 55. Error: 0.2055 Number of Selected models: 5 (0.5543%)
- Inning 7. Complexity: 56. Error: 0.2155 Number of Selected models: 13 (1.441%)
- Inning 8. Complexity: 57. Error: 0.2255 Number of Selected models: 21 (2.328%)
- Inning 9. Complexity: 58. Error: 0.2355 Number of Selected models: 27 (2.993%)
- Inning 10. Complexity: 59. Error: 0.2455 Number of Selected models: 34 (3.769%)
- Inning 11. Complexity: 60. Error: 0.2555 Number of Selected models: 40 (4.435%)
- Inning 12. Complexity: 61. Error: 0.2655 Number of Selected models: 44 (4.878%)
- Inning 13. Complexity: 62. Error: 0.2755 Number of Selected models: 59 (6.541%)
- Inning 14. Complexity: 63. Error: 0.2855 Number of Selected models: 70 (7.761%)

- Inning 15. Complexity: 64. Error: 0.2955 Number of Selected models: 76 (8.426%)

- **76 interesting models were selected**
  - **Quatiliy Box values are {64., 0.295495}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, cNIpostRej, igG, inflammationdatefirst}**

◆ Defining Ensembles

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	Complexity	$1-R^2$	Function
			graftLoss
1	34	0.294	$2.88\times10^{-2}+0.12\,\text{cNIpostRej}+\frac{8.92\,\text{respiratoryInfection}}{\text{maxWBC}}+1.07\,b_{45}$
2	38	0.240	$-(5.36\times10^{-3})+0.11\,\text{cNIpostRej}+0.12\,\text{denovoDSA}+0.61\,\text{igG}+(8.11\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}$
3	38	0.285	$3.38\times10^{-2}+0.12\,\text{cNIpostRej}+0.22\,\text{respiratoryInfection}+(7.14\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+1.07\,b_{45}$
4	41	0.197	$3.79\times10^{-2}+0.11\,\text{cNIpostRej}+(6.43\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+1.06\,b_{45}+0.55\,\text{respiratoryInfection}\,dQ_7$
5	42	0.266	$3.61\times10^{-2}+0.11\,\text{cNIpostRej}+0.36\,\text{respiratoryInfection}+0.60\,\text{respiratoryInfection}^2\,\text{antiHLAclass}_2+1.06\,b_{45}$
6	42	0.268	$2.74\times10^{-4}+0.12\,\text{cNIpostRej}+(3.76\times10^{-2})\,\text{denovoDSA}^2+(8.12\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+0.38\,dR_{15}$
7	43	0.265	$-(9.69\times10^{-3})+0.73\,\text{candida}+0.39\,\text{respiratoryInfection}+1.01\,b_{45}-0.56\,dR_{12}+0.53\,dR_{53}$
8	43	0.270	$3.65\times10^{-2}+0.42\,\text{candida}+0.51\,\text{igG}-0.35\,\text{pyrexia}+0.64\,\text{respiratoryInfection}+0.71\,b_{45}$
9	43	0.280	$-(2.39\times10^{-2})+0.12\,\text{cNIpostRej}+0.35\,\text{igG}+0.58\,\text{respiratoryInfection}+0.86\,b_{45}+0.18\,dQ_7$
10	46	0.203	$2.04\times10^{-2}+0.11\,\text{cNIpostRej}+0.55\,\text{igG}+0.15\,\text{respiratoryInfection}+(7.74\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+0.80\,b_{45}$
11	46	0.207	$1.50\times10^{-2}+(3.19\times10^{-2})\,\text{banfah}+0.11\,\text{cNIpostRej}+0.59\,\text{igG}+(9.36\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+0.77\,b_{45}$
12	46	0.209	$4.24\times10^{-2}+0.10\,\text{cNIpostRej}+0.65\,\text{igG}-0.35\,\text{pyrexia}+0.69\,\text{respiratoryInfection}+(4.87\times10^{-2})\,\text{maxWBC}\,b_{45}$
13	46	0.272	$4.40\times10^{-2}+0.43\,\text{igG}-0.15\,\text{inflammation}+0.70\,b_{45}+0.87\,\text{respiratoryInfection}\,dQ_7+(1.96\times10^{-2})\,\text{wBCpeakover}_5$
14	49	0.145	$2.47\times10^{-2}+0.11\,\text{cNIpostRej}+0.44\,\text{igG}+(6.85\times10^{-2})\,\text{inflammationdatefirst respiratoryInfection}+0.84\,b_{45}+0.44\,\text{respiratoryInfection}\,dQ_7$
15	50	0.170	$3.70\times10^{-2}+0.10\,\text{cNIpostRej}+0.49\,\text{igG}-0.25\,\text{pyrexia}+\frac{9.13\,\text{respiratoryInfection}}{\text{maxWBC}}+0.81\,b_{45}$

◆ Ensembles in ParetoFront

■ **The 47th Cross Validation**
with Leave-One-Out Method out of 51 turns

The Estimated value: 0.04193, The Observed value: 0

The Prediction: Right

Accuracy so far: 82.98% (92.16% completed)

◆ **Accuracies until the 47th turn in the**
Leave-One-Out Cross Validation out of 51 turns

◇ Estimated Remaining time: `` hour `` min `` sec hr 0 min 0 sec

◆ **Error(= Predicted value - Observed value) in the 47th Cross Validation**

◇ **Average Error is 0.2641±0.3283 until the 47th turn in the LOO method.**

■ The 48th cross-validation out of 51 turns

□ The 48th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日1時 55分 23秒

□ The 48th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日2時 2分 1秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
700
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
−200
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
100
80
60
40
20
0
−20

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
200
400
600
800
Model Complexity

,

◆ **1002 models were created**

◇ **Quatiliy Box values are {46., 0.1752} in the 48th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1002 Selected models: 1 (0.0998%)

◆ Inning 0. Complexity: 46. Error: 0.1752 Number of Selected models: 1 (0.0998%)

◆ Inning 1. Complexity: 47. Error: 0.1852 Number of Selected models: 1 (0.0998%)

◆ Inning 2. Complexity: 48. Error: 0.1952 Number of Selected models: 1 (0.0998%)

◆ Inning 3. Complexity: 49. Error: 0.2052 Number of Selected models: 3 (0.2994%)

◆ Inning 4. Complexity: 50. Error: 0.2152 Number of Selected models: 3 (0.2994%)

◆ Inning 5. Complexity: 51. Error: 0.2252 Number of Selected models: 9 (0.8982%)

◆ Inning 6. Complexity: 52. Error: 0.2352 Number of Selected models: 14 (1.397%)

◆ Inning 7. Complexity: 53. Error: 0.2452 Number of Selected models: 18 (1.796%)

◆ Inning 8. Complexity: 54. Error: 0.2552 Number of Selected models: 23 (2.295%)

◆ Inning 9. Complexity: 55. Error: 0.2652 Number of Selected models: 29 (2.894%)

◆ Inning 10. Complexity: 56. Error: 0.2752 Number of Selected models: 40 (3.992%)

◆ Inning 11. Complexity: 57. Error: 0.2852 Number of Selected models: 44 (4.391%)

◆ Inning 12. Complexity: 58. Error: 0.2952 Number of Selected models: 59 (5.888%)

◆ Inning 13. Complexity: 59. Error: 0.3052 Number of Selected models: 74 (7.385%)

◆ Inning 14. Complexity: 60. Error: 0.3152 Number of Selected models: 92 (9.182%)

- 92 interesting models were selected
  - Quatiliy Box values are {60., 0.315189}.

- Variable Presence (Popularity of each variable) FOCUSED on important variables
- TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, pyrexia, igG, cNIpostRej}

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.268	$5.62\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+1.04\,b_{45}$
2	38	0.221	$3.46\times10^{-2}+0.12\,\text{cNIpostRej}+0.83\,\text{respiratoryInfection}-0.55\,\text{pyrexia respiratoryInfection}+1.06\,b_{45}$
3	38	0.227	$3.57\times10^{-2}+0.11\,\text{cNIpostRej}+1.10\,\text{respiratoryInfection}-0.47\,\text{banfi respiratoryInfection}+1.06\,b_{45}$
4	38	0.311	$5.68\times10^{-2}+(9.06\times10^{-2})\,\text{cNIpostRej}+0.69\,\text{igG}+$ $0.72\,\text{respiratoryInfection}-0.50\,\text{pyrexia respiratoryInfection}$
5	42	0.307	$7.89\times10^{-2}+(8.86\times10^{-2})\,\text{cNIpostRej}+0.36\,\text{igG}+0.82\,b_{45}+0.85\,\text{respiratoryInfection}\,dQ_7{}^2$
6	43	0.218	$4.42\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.83\,b_{45}$
7	43	0.301	$3.81\times10^{-4}+0.12\,\text{cNIpostRej}+0.15\,\text{gERD}+0.53\,\text{igG}+0.61\,\text{respiratoryInfection}+0.76\,b_{45}$
8	46	0.175	$2.45\times10^{-2}+0.11\,\text{cNIpostRej}+0.41\,\text{igG}+$ $0.79\,\text{respiratoryInfection}-0.52\,\text{pyrexia respiratoryInfection}+0.86\,b_{45}$
9	46	0.207	$-(8.76\times10^{-3})+0.46\,\text{igG}+0.73\,\text{respiratoryInfection}+$ $0.74\,b_{45}+(1.99\times10^{-2})\,\text{wBCpeakover}_5-0.13\,\text{pyrexia wBCpeakover}_5$
10	46	0.231	$7.57\times10^{-3}-0.36\,\text{pyrexia}+0.64\,\text{respiratoryInfection}+$ $0.74\,b_{45}+0.43\,\text{aBOI}\,dQ_7+(1.89\times10^{-2})\,\text{wBCpeakover}_5$
11	46	0.260	$-(2.01\times10^{-2})+0.12\,\text{cRPpostRej}+0.52\,\text{igG}-$ $0.34\,\text{pyrexia}+0.67\,\text{respiratoryInfection}+0.33\,\text{cRPpostRej}\,b_{45}$
12	46	0.277	$-(3.30\times10^{-3})+0.28\,\text{respiratoryInfection}+0.97\,b_{45}-$ $(1.11\times10^{-2})\,b_{50}+0.69\,\text{respiratoryInfection}\,dQ_7+(1.99\times10^{-2})\,\text{wBCpeakover}_5$
13	49	0.195	$2.55\times10^{-2}+0.11\,\text{cNIpostRej}+0.48\,\text{igG}+$ $0.99\,\text{respiratoryInfection}-0.39\,\text{banfi respiratoryInfection}+0.22\,\text{denovoDSA}\,b_{57}$
14	50	0.239	$2.95\times10^{-2}+(1.54\times10^{-2})\,\text{cNIpostRej}^2-(9.89\times10^{-2})\,\text{hypothyroidism}+$ $0.81\,\text{respiratoryInfection}-0.54\,\text{pyrexia respiratoryInfection}+0.96\,b_{45}$
15	53	0.154	$2.44\times10^{-2}+0.11\,\text{cNIpostRej}+0.50\,\text{igG}+$ $0.93\,\text{respiratoryInfection}-0.22\,\text{banfi}^2\,\text{respiratoryInfection}+0.22\,\text{denovoDSA}\,b_{57}$

◆ Ensembles in ParetoFront

■ **The 48th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.03725, The Observed value: 0

The Prediction: Right

Accuracy so far: 83.33% (94.12% completed)

◆ **Accuracies until the 48th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr -1 min 53 sec

◆ **Error(= Predicted value - Observed value) in the 48th Cross Validation**

◇ **Average Error is 0.2594±0.3264 until the 48th turn in the LOO method.**

■ The 49th cross-validation out of 51 turns

□ The 49th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日⣿2時 2分 5秒

□ The 49th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日⣿2時 8分 20秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
80
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R²
0
100
200
300
400
500
Model Complexity

,

◆ **998 models were created**

◇ **Quatiliy Box values are {38., 0.2462} in the 49th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 998 Selected models: 1 (0.1002%)

◆ Inning 0. Complexity: 38. Error: 0.2462 Number of Selected models: 1 (0.1002%)

◆ Inning 1. Complexity: 39. Error: 0.2562 Number of Selected models: 1 (0.1002%)

◆ Inning 2. Complexity: 40. Error: 0.2662 Number of Selected models: 1 (0.1002%)

◆ Inning 3. Complexity: 41. Error: 0.2762 Number of Selected models: 2 (0.2004%)

◆ Inning 4. Complexity: 42. Error: 0.2862 Number of Selected models: 4 (0.4008%)

◆ Inning 5. Complexity: 43. Error: 0.2962 Number of Selected models: 15 (1.503%)

◆ Inning 6. Complexity: 44. Error: 0.3062 Number of Selected models: 19 (1.904%)

◆ Inning 7. Complexity: 45. Error: 0.3162 Number of Selected models: 31 (3.106%)

◆ Inning 8. Complexity: 46. Error: 0.3262 Number of Selected models: 47 (4.709%)

◆ Inning 9. Complexity: 47. Error: 0.3362 Number of Selected models: 66 (6.613%)

◆ Inning 10. Complexity: 48. Error: 0.3462 Number of Selected models: 75 (7.515%)

◆ Inning 11. Complexity: 49. Error: 0.3562 Number of Selected models: 79 (7.916%)

◆ Inning 12. Complexity: 50. Error: 0.3662 Number of Selected models: 91 (9.118%)

◆ **91 interesting models were selected**

◇ **Quatiliy Box values are {50., 0.366166}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, wBCpeakover5, pyrexia, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	30	0.325	$3.52\times10^{-2}+0.93\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.93\,b_{45}+(1.99\times10^{-2})\,\text{wBCpeakover}_5$
2	30	0.351	$5.41\times10^{-2}+0.79\,\text{respiratoryInfection}-0.56\,\text{pyrexia}\,\text{respiratoryInfection}+0.95\,b_{45}$
3	35	0.267	$5.71\times10^{-2}+0.12\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+1.04\,b_{45}$
4	35	0.313	$3.20\times10^{-2}+(9.87\times10^{-2})\,\text{cNIpostRej}+0.79\,\text{igG}+0.49\,\text{respiratoryInfection}+0.76\,b_{61}$
5	35	0.344	$-(6.45\times10^{-2})+0.54\,\text{respiratoryInfection}+1.02\,b_{45}+0.30\,dR_{53}+(2.14\times10^{-2})\,\text{wBCpeakover}_5$
6	38	0.246	$-(6.02\times10^{-3})+0.81\,\text{respiratoryInfection}-$ $0.59\,\text{pyrexia}\,\text{respiratoryInfection}+0.96\,b_{45}+(2.06\times10^{-2})\,\text{wBCpeakover}_5$
7	38	0.314	$-(2.66\times10^{-2})+0.12\,\text{cRPpostRej}+0.31\,\text{respiratoryInfection}+0.81\,b_{45}+0.63\,\text{respiratoryInfection}\,dQ_8$
8	38	0.329	$-(4.01\times10^{-2})+0.16\,\text{cRPpostRej}+0.62\,\text{igG}+$ $0.31\,\text{respiratoryInfection}+0.50\,\text{respiratoryInfection}\,\text{antiHLAclass}_2$
9	39	0.316	$5.37\times10^{-2}+(1.50\times10^{-2})\,\text{cNIpostRej}^2+0.72\,\text{igG}-0.36\,\text{pyrexia}+0.65\,\text{respiratoryInfection}$
10	42	0.266	$3.70\times10^{-2}+0.11\,\text{cNIpostRej}+0.36\,\text{respiratoryInfection}+1.06\,b_{45}+0.60\,\text{respiratoryInfection}\,dQ_8{}^2$
11	42	0.271	$2.16\times10^{-2}+0.31\,\text{respiratoryInfection}+$ $0.67\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+0.98\,b_{45}+(4.96\times10^{-4})\,\text{wBCpeakover}_5{}^2$
12	42	0.284	$5.63\times10^{-2}+0.67\,\text{igG}+0.94\,a_{26}+0.81\,\text{respiratoryInfection}\,\text{antiHLAclass}_2+(4.76\times10^{-4})\,\text{wBCpeakover}_5{}^2$
13	42	0.331	$4.30\times10^{-2}+0.68\,\text{igG}+0.29\,\text{respiratoryInfection}+0.96\,a_{34}+0.53\,\text{respiratoryInfection}\,\text{antiHLAclass}_2{}^2$
14	43	0.217	$4.51\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.71\,\text{respiratoryInfection}+0.83\,b_{45}$
15	43	0.220	$4.60\times10^{-2}+0.10\,\text{cNIpostRej}+0.72\,\text{igG}-0.35\,\text{pyrexia}+0.68\,\text{respiratoryInfection}+1.05\,a_{34}$

◆ Ensembles in ParetoFront

■ The 49th Cross Validation with Leave-One-Out Method out of 51 turns

The Estimated value: 0.1469, The Observed value: 0

The Prediction: Right

Accuracy so far: 83.67% (96.08% completed)

◆ **Accuracies until the 49th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr -1 min 47 sec

◆ **Error(= Predicted value - Observed value) in the 49th Cross Validation**

◇ **Average Error is 0.2571±0.3234 until the 49th turn in the LOO method.**

■ The 50th cross-validation out of 51 turns

□ The 50th Genetic Programming has started.

◆ Present Time: 2020年 7月 14日2時 8分 24秒

□ The 50th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日2時 14分 35秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
1000
800
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
60
50
40
30
20
10
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1– R2
0
200
400
600
800
1000
Model Complexity

,

◆ **923 models were created**

◇ **Quatiliy Box values are {46., 0.1747} in the 50th turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 923 Selected models: 1 (0.1083%)

◆ Inning 0. Complexity: 46. Error: 0.1747 Number of Selected models: 1 (0.1083%)

◆ Inning 1. Complexity: 47. Error: 0.1847 Number of Selected models: 1 (0.1083%)

◆ Inning 2. Complexity: 48. Error: 0.1947 Number of Selected models: 1 (0.1083%)

◆ Inning 3. Complexity: 49. Error: 0.2047 Number of Selected models: 3 (0.325%)

◆ Inning 4. Complexity: 50. Error: 0.2147 Number of Selected models: 4 (0.4334%)

◆ Inning 5. Complexity: 51. Error: 0.2247 Number of Selected models: 11 (1.192%)

◆ Inning 6. Complexity: 52. Error: 0.2347 Number of Selected models: 15 (1.625%)

◆ Inning 7. Complexity: 53. Error: 0.2447 Number of Selected models: 17 (1.842%)

◆ Inning 8. Complexity: 54. Error: 0.2547 Number of Selected models: 25 (2.709%)

◆ Inning 9. Complexity: 55. Error: 0.2647 Number of Selected models: 29 (3.142%)

◆ Inning 10. Complexity: 56. Error: 0.2747 Number of Selected models: 36 (3.9%)

◆ Inning 11. Complexity: 57. Error: 0.2847 Number of Selected models: 43 (4.659%)

◆ Inning 12. Complexity: 58. Error: 0.2947 Number of Selected models: 63 (6.826%)

◆ Inning 13. Complexity: 59. Error: 0.3047 Number of Selected models: 78 (8.451%)

◆ **78 interesting models were selected**

◇ **Quatiliy Box values are {59., 0.304683}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, b45, pyrexia, cNIpostRej, igG}**

◆ Defining Ensembles

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graftLoss

	Complexity	$1-R^2$	Function
1	35	0.267	$5.70\times10^{-2}+0.12\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+1.04\,b_{45}$
2	38	0.293	$-(4.69\times10^{-3})+0.84\,\text{igG}+0.40\,\text{malignantHypertention}+(8.47\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+(1.82\times10^{-2})\,\text{wBCpeakover}_5$
3	38	0.295	$5.21\times10^{-2}-0.40\,\text{pyrexia}+0.73\,\sqrt{\text{igG}+\text{respiratoryInfection}+b_{45}}$
4	42	0.266	$3.69\times10^{-2}+0.11\,\text{cNIpostRej}+0.36\,\text{respiratoryInfection}+1.06\,b_{45}+0.60\,\text{respiratoryInfection}^2\,dQ_8$
5	43	0.217	$4.50\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.71\,\text{respiratoryInfection}+0.83\,b_{45}$
6	43	0.285	$2.28\times10^{-2}+0.11\,\text{cNIpostRej}+0.10\,\text{denovoDSA}+0.53\,\text{igG}-0.31\,\text{pyrexia}+0.59\,\text{respiratoryInfection}$
7	45	0.281	$6.17\times10^{-2}+0.41\,\text{igG}+0.94\,\text{coaglationnecrosis}\,\text{respiratoryInfection}^2+0.73\,b_{45}+0.86\,\text{respiratoryInfection}\,dQ_7$
8	46	0.175	$2.53\times10^{-2}+0.11\,\text{cNIpostRej}+0.41\,\text{igG}+0.79\,\text{respiratoryInfection}-0.52\,\text{pyrexia}\,\text{respiratoryInfection}+0.86\,b_{45}$
9	46	0.200	$9.73\times10^{-3}+0.12\,\text{cNIpostRej}+0.82\,\text{respiratoryInfection}-0.52\,\text{pyrexia}\,\text{respiratoryInfection}+1.01\,b_{45}+0.16\,dR_7$
10	46	0.203	$3.97\times10^{-2}+0.11\,\text{cNIpostRej}+0.60\,\text{cNIpostRej}\,\text{igG}-0.39\,\text{pyrexia}+0.77\,\text{respiratoryInfection}+1.27\,b_{45}$
11	46	0.218	$1.97\times10^{-2}+0.64\,\text{igG}+(9.02\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.66\,b_{45}+(2.61\times10^{-7})\,\text{wBCpeakover}_5{}^4$
12	47	0.217	$4.50\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.71\,\text{respiratoryInfection}+0.83\,b_{45}{}^2$
13	49	0.181	$1.50\times10^{-2}+(9.87\times10^{-2})\,\text{cNIpostRej}+0.29\,\text{birthhistory}\,\text{igG}+0.37\,\text{respiratoryInfection}+1.07\,b_{45}+0.61\,\text{respiratoryInfection}\,dQ_8$
14	49	0.260	$7.43\times10^{-2}+(8.14\times10^{-2})\,\text{cNIpostRej}+0.28\,\text{birthhistory}\,\text{igG}+0.99\,b_{45}+0.93\,\text{respiratoryInfection}\,dQ_8-(3.87\times10^{-2})\,dR_{14}$
15	51	0.204	$8.88\times10^{-3}+0.45\,\text{igG}-0.40\,\text{polyp}-0.35\,\text{pyrexia}+0.70\,\text{respiratoryInfection}+0.72\,b_{45}+(2.17\times10^{-2})\,\text{wBCpeakover}_5$

◆ Ensembles in ParetoFront

■ **The 50th Cross Validation with Leave-One-Out Method out of 51 turns**

The Estimated value: 0.0677, The Observed value: 0

The Prediction: Right

Accuracy so far: 84.% (98.04% completed)

◆ **Accuracies until the 50th turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr -1 min 41 sec

◆ **Error(= Predicted value - Observed value) in the 50th Cross Validation**

◇ **Average Error is 0.2533±0.3212 until the 50th turn in the LOO method.**

■ The 51st cross-validation out of 51 turns

□ The 51st Genetic Programming has started.

◆ Present Time: 2020年 7月 14日2時 14分 39秒

□ The 51th Genetic Programming has ended.

◆ Present Time: 2020年 7月 14日2時 20分 57秒

◆ Monitors Plot

0.01
0
100
200
300
400
500
600
Generation Sequence

Model Quality Distribution
ModelComplexity
600
400
200
0
ModelAccuracy
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ModelAge
60
40
20
0

,

Pareto Fronts
1
0.50
0.10
0.05
0.01
Error = 1 − R2
0
50
100
150
200
250
300
Model Complexity

,

◆ **1012 models were created**

◇ **Quatiliy Box values are {46., 0.1954} in the 51st turn.**

■ Process for adjusting levels of Quality Box is initiated mainly to limit the selected models between 8.`% and 20.`% of all generated models.

■ Generated models: 1012 Selected models: 1 (0.09881%)

◆ Inning 0. Complexity: 46. Error: 0.1954 Number of Selected models: 1 (0.09881%)

◆ Inning 1. Complexity: 47. Error: 0.2054 Number of Selected models: 2 (0.1976%)

◆ Inning 2. Complexity: 48. Error: 0.2154 Number of Selected models: 2 (0.1976%)

◆ Inning 3. Complexity: 49. Error: 0.2254 Number of Selected models: 5 (0.4941%)

◆ Inning 4. Complexity: 50. Error: 0.2354 Number of Selected models: 8 (0.7905%)

◆ Inning 5. Complexity: 51. Error: 0.2454 Number of Selected models: 25 (2.47%)

◆ Inning 6. Complexity: 52. Error: 0.2554 Number of Selected models: 25 (2.47%)

◆ Inning 7. Complexity: 53. Error: 0.2654 Number of Selected models: 33 (3.261%)

◆ Inning 8. Complexity: 54. Error: 0.2754 Number of Selected models: 43 (4.249%)

◆ Inning 9. Complexity: 55. Error: 0.2854 Number of Selected models: 48 (4.743%)

◆ Inning 10. Complexity: 56. Error: 0.2954 Number of Selected models: 54 (5.336%)

◆ Inning 11. Complexity: 57. Error: 0.3054 Number of Selected models: 66 (6.522%)

◆ Inning 12. Complexity: 58. Error: 0.3154 Number of Selected models: 85 (8.399%)

◆ **85 interesting models were selected**

  ◇ **Quatiliy Box values are {58., 0.31538}.**

- **Variable Presence (Popularity of each variable) FOCUSED on important variables**
- **TOP FIVE HIGHLY USED vairbles: {respiratoryInfection, igG, cNIpostRej, pyrexia, b44}**

◆ Defining Ensembles

Page 1 | Page 2

graftLoss

	Complexity	$1-R^2$	Function
1	30	0.301	$3.96\times10^{-2}+0.85\,\text{igG}+(8.63\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.96\,\text{cw}_9$
2	30	0.303	$5.22\times10^{-2}+0.12\,\text{cNIpostRej}+(9.56\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+1.05\,\text{b}_{44}$
3	34	0.298	$3.29\times10^{-2}+(1.55\times10^{-2})\,\text{cNIpostRej}^2+0.84\,\text{igG}+(8.67\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}$
4	35	0.268	$5.58\times10^{-2}+0.11\,\text{cNIpostRej}-0.39\,\text{pyrexia}+0.75\,\text{respiratoryInfection}+1.04\,\text{b}_{45}$
5	35	0.310	$-(8.15\times10^{-2})+0.14\,\text{cNIpostRej}+0.65\,\text{respiratoryInfection}+0.23\,\text{antiHLAclass}_2+0.97\,\text{b}_{13}$
6	35	0.313	$9.70\times10^{-2}-\frac{2.11\times10^{-3}}{\text{hDperiod}}-0.46\,\text{pyrexia}+0.78\,\text{respiratoryInfection}+0.91\,\text{b}_{44}$
7	38	0.307	$7.86\times10^{-2}+(8.84\times10^{-2})\,\text{cNIpostRej}+0.36\,\text{igG}+0.82\,\text{b}_{44}+0.85\,\text{respiratoryInfection}\,\text{dQ}_8$
8	38	0.312	$1.11\times10^{-2}+0.11\,\text{cNIpostRej}+0.69\,\sqrt{\text{igG}+\text{respiratoryInfection}+\text{b}_{44}}$
9	42	0.244	$-(7.59\times10^{-2})+(1.70\times10^{-2})\,\text{cNIpostRej}^2+0.25\,(\text{respiratoryInfection}+\text{type2DM}+\text{antiHLAclass}_1)^2$
10	43	0.218	$4.38\times10^{-2}+0.11\,\text{cNIpostRej}+0.43\,\text{igG}-0.36\,\text{pyrexia}+0.72\,\text{respiratoryInfection}+0.83\,\text{b}_{13}$
11	43	0.266	$6.74\times10^{-2}+0.11\,\text{cNIpostRej}-(1.02\times10^{-4})\,\text{infectiondatelast}-$ $0.40\,\text{pyrexia}+0.79\,\text{respiratoryInfection}+1.04\,\text{b}_{13}$
12	43	0.278	$5.60\times10^{-2}-\frac{1.80\times10^{-3}}{\text{hDperiod}}+0.66\,\text{igG}-0.42\,\text{pyrexia}+0.69\,\text{respiratoryInfection}+(1.73\times10^{-2})\,\text{wBCpeakover}_5$
13	46	0.195	$3.63\times10^{-2}+0.10\,\text{cNIpostRej}-0.38\,\text{pyrexia}+0.76\,\sqrt{\text{igG}+\text{respiratoryInfection}+\text{b}_{44}}$
14	46	0.200	$-(1.52\times10^{-3})+(9.74\times10^{-2})\,\text{hDperiod}\,\text{igG}-0.39\,\text{pyrexia}+$ $0.69\,\text{respiratoryInfection}+0.94\,\text{b}_{44}+(1.88\times10^{-2})\,\text{wBCpeakover}_5$
15	46	0.203	$2.00\times10^{-2}+0.11\,\text{cNIpostRej}+0.55\,\text{igG}+0.15\,\text{respiratoryInfection}+$ $(7.74\times10^{-2})\,\text{inflammationdatefirst}\,\text{respiratoryInfection}+0.80\,\text{b}_{44}$

◆ Ensembles in ParetoFront

■ The 51st Cross Validation with Leave-One-Out Method out of 51 turns

The Estimated value: 0.615, The Observed value: 0

The Prediction: Wrong

Accuracy so far: 82.35% (100.% completed)

◆ **Accuracies until the 51st turn in the Leave-One-Out Cross Validation out of 51 turns**

◇ Estimated Remaining time: `` hour `` min `` sec hr -1 min 34 sec

◆ **Error(= Predicted value - Observed value) in the 51st Cross Validation**

◇ **Average Error is 0.2604±0.322 until the 51st turn in the LOO method.**

■ The End of Leave-One-Out Cross Validation Loop

■ Summary of The 51-fold Cross Validation with Leave-One-Out Method

■ 0. Report of Hyper-parameter Settings in LOO-CV

◆ BuildModel version 2.6.4 made on July 12th, 2020

1. TimeConstraint: 3min, N of Evolutions: 8, Processor Count in the computer: 8
2. Evolution Strategy: BalancedGP, Selection Strategy: ParetoFrontSelect, RobustModels: True
3. Computation time for one evolution: {0, 24, 0}, Total computation tiem: {20, 24, 0}
4. Initial QuatlityBox values: Comlexity < 43., Error < 0.1761
5. Subset size for model evaluation: 100%
6. Gradient for setting the QualityBox: 0.75`

■ 1. Classification Performance with Leave-One-Out cross validation

■ Confusion Matrix

	Observed as 1	Observed as 0	Total
Predicted as 1	6	4	10
Predicted as 0	5	36	41
Total	11	40	51

1. Sample size: 51 Number of explanatory variables 211
2. Accuracy: 82.35%
3. Precision(精度=陽性的中率): 60.%
   Negative Predictie Value(陰性的中率): 87.8%
4. Recall(再現率=感度): 54.55% Specificity(特異度): 90.%
5. F1-score(F1値): 0.5714 C-statistic(C統計値): 0.7841
6. AUC of ROC curve: 0.784
7. Average Error in the Target Value: 0.2604 ± 0.322

◆ The data in the analysis was exported in the home directory with the following name: BuildModelLOOvaluesNo1Date202071422111.xlsx

◆ The Raw Result of Leave-One-Out Cross Validation is expressed as QUARTETBAG that is made of {predicted value, rounded value, observed value, LOOCV value}. And it is exported in an Excel file named BuildModelLOOvalues....xlsx

The head of data was not a list.

◆ The Total Result of Leave-One-Out Cross Validation is expressed as TOTALBAG that is made of raw data with {predicted value, rounded value, observed value}. And it is exported in an Excel file named BuildModelLOOCVresult...xlsx

■ 2. Receiver Operating Characteristics Analysis

◆ ROC curve

◆ **AUC of ROC curve: 0.783**

◆ **Effect of THRESHOLD between positive and negative**

■ 3. Results of Leave-One-Out Cross-Validation and its Prediction in Each Case

◆ Numbers of functions generated by Genetic Programming

	The 1st CV	The 2nd CV	The 3rd CV	The 4th CV	The 5th C
All Generated Models	893	1025	956	996	870
All Selected Models	72	84	85	94	81

◆ Estimated values and Observed values

	The 1st CV	The 2nd CV	The 3rd CV	The 4th CV	The 5th CV	The
Predicted	-0.77345	0.768011	-0.0120491	0.510085	0.095396	1.80
Observed	0	1	0	0	0	1
Right/Wrong	right	right	right	**WRONG**	right	righ

■ 4. FREQUENTLY USED Variables in the 51-fold Cross Validation with Leave-One-Out

- **N of all generated models:**
  49803, n of all selected models: 4373

- **Explanatory Variable Presence Percentage in**
  all 4373 Selected Models in all 51 Cross-Validations

Variable Presence Chart
%
0
20
40
60

◆ **Explanatory Variable Presence Percentage FOCUSED on TOP 15 in all 4373 Selected Models in all 51 Cross-Validations**

◆ **Explanatory Variable Presence Percentage FOCUSED on TOP 10 in all 4373 Selected Models in all 51 Cross-Validations**

◆ **Explanatory Variable Presence Percentage FOCUSED on TOP 5 in all 4373 Selected Models in all 51 Cross-Validations**

◆Most Frequently Used Variables in all 4373 Selected Models;
Top Five: {respiratoryInfection, b45, igG, cNIpostRej, pyrexia}

	Frequency (%)	Variable Name
1	99.8628	respiratoryInfection
2	78.9161	b45
3	61.9255	igG
4	58.7011	cNIpostRej
5	57.4434	pyrexia
6	15.8701	wBCpeakover5
7	14.9783	cRPpostRej
8	10.9307	inflammationdatefirst
9	9.90167	dQ7
10	7.43197	denovoDSA
11	7.22616	banfi
12	6.81454	antiHLAclass2
13	4.84793	dQ8
14	4.68786	candida
15	3.95609	dR7
16	3.47587	dR15
17	3.3158	dR53
18	3.3158	coaglationnecrosis
19	2.88132	maxWBC
20	2.60691	hDperiod
21	2.4697	dSAandHSAclass1
22	2.42397	antiHLAclass1
23	2.30963	b13
24	2.28676	hLAmm
25	1.85228	feverOnly
26	1.82941	upperRespiratoryInfection
27	1.82941	gERD
28	1.73794	dQ6

29	1.66933	type2DM
30	1.64647	surgery
31	1.64647	hLADRmm
32	1.53213	heartDisease
33	1.39492	banfah
34	1.34919	c3
35	1.23485	•igA
36	1.21198	aerobicGPC
37	1.16625	banfct
38	1.12051	uTI
39	1.12051	enterococcusfaecalis
40	1.12051	dR51
41	1.02904	banfptc
42	0.937571	b44
43	0.868969	aBOI
44	0.846101	banfci
45	0.823233	rage
46	0.777498	polyp
47	0.777498	maxCRP
48	0.731763	dR52
49	0.686028	dSAclass1number
50	0.66316	dSAandHLAclass1pre
51	0.640293	gynecology
52	0.617425	wBCinUrine
53	0.594558	dSAclass2
54	0.594558	b63
55	0.57169	enterobacteraerogenes
56	0.57169	bTF
57	0.57169	b75
58	0.57169	b62
59	0.525955	wBCpreRej
60	0.503087	c4d
61	0.503087	a34
62	0.48022	hLAABmm
63	0.48022	banf t
64	0.457352	mMFatRej
65	0.457352	infectionCount
66	0.457352	cRPpreRej
67	0.457352	banfcv
68	0.457352	a26
69	0.457352	a25
70	0.434484	dP18
71	0.434484	b61
72	0.411617	dR18
73	0.411617	birthhistory
74	0.388749	staphylococcusaureus
75	0.388749	mMFpostRej
76	0.388749	hSAclass2number
77	0.388749	cellInvasion
78	0.388749	allergy
79	0.365882	dSAandHSAclass2
80	0.365882	dQ4
81	0.365882	cw9
82	0.365882	artificialAbortion
83	0.343014	aerobicGNR
84	0.320146	rMale
85	0.320146	preDSA
86	0.320146	dSAandHLAclass2pre
87	0.320146	citobacterdiversus
88	0.320146	cGN
89	0.320146	anemia
90	0.297279	wBCpostKTx
91	0.297279	pRAclass2pre
92	0.297279	pastheart
93	0.297279	lymphinvasion
94	0.297279	cMV

95	0.274411	urology
96	0.274411	pRAclass1pre
97	0.274411	interstitialHemorrhage
98	0.274411	dP9
99	0.274411	calcification
100	0.251544	streptococcusaureus
101	0.251544	dR103
102	0.251544	dR10
103	0.251544	dP13
104	0.251544	b49
105	0.251544	a66
106	0.228676	wBCpeakover9postRej
107	0.228676	infectiondatelast
108	0.228676	dR1
109	0.205808	wBCpeakover10
110	0.205808	pRAclass1after
111	0.205808	orthopedics
112	0.205808	hBV
113	0.205808	dR13
114	0.205808	dP17
115	0.205808	diarrhea
116	0.205808	b78
117	0.205808	b57
118	0.182941	woundInfection
119	0.182941	nS
120	0.182941	malignantHypertention
121	0.182941	infarctionhemohorrage
122	0.182941	hypertention
123	0.182941	dR14
124	0.182941	dQ9
125	0.182941	banfptcbm
126	0.182941	b53
127	0.160073	skin
128	0.160073	pRAclass2after
129	0.160073	inflammation
130	0.160073	hypoplastickidney
131	0.160073	hCV
132	0.160073	dSAclass1
133	0.160073	dP4
134	0.160073	dP3
135	0.160073	c5b
136	0.160073	banfg
137	0.160073	b47
138	0.160073	b38
139	0.160073	asthma
140	0.160073	appendicitis
141	0.137206	twinpeak
142	0.137206	timeoftransplantation
143	0.137206	thrombusformation
144	0.137206	regraft
145	0.137206	igM
146	0.137206	dR12
147	0.137206	dQ11
148	0.137206	cw17
149	0.137206	banfv
150	0.137206	b51
151	0.137206	b37
152	0.114338	virusInfection
153	0.114338	stone
154	0.114338	pregnancyhistory
155	0.114338	pastanemia
156	0.114338	dR9
157	0.114338	dR17
158	0.114338	dR11
159	0.114338	dQ2
160	0.114338	dP20

161	0.114338	dP15
162	0.114338	dP14
163	0.114338	cw6
164	0.114338	b54
165	0.114338	b42
166	0.114338	a23
167	0.0914704	naturalAbortion
168	0.0914704	hSAclass1number
169	0.0914704	enterobactereclacue
170	0.0914704	dR16
171	0.0914704	dQ5
172	0.0914704	dP5
173	0.0914704	dP11
174	0.0914704	dP10
175	0.0914704	banfcg
176	0.0914704	b82
177	0.0914704	b8
178	0.0914704	b55
179	0.0914704	b18
180	0.0686028	upperDigestivetract
181	0.0686028	sABC1q
182	0.0686028	pseudomonas
183	0.0686028	hypothyroidism
184	0.0686028	herpesZoster
185	0.0686028	dR4
186	0.0686028	b77
187	0.0686028	b71
188	0.0686028	b7
189	0.0686028	b59
190	0.0686028	b58
191	0.0686028	b56
192	0.0686028	b50
193	0.0686028	b27
194	0.0686028	a32
195	0.0457352	ulcer
196	0.0457352	pastliverbilialy
197	0.0457352	ocular
198	0.0457352	mFImax
199	0.0457352	igA
200	0.0457352	dSAclass2number
201	0.0457352	dP6
202	0.0457352	digestiveorgan
203	0.0457352	banfaah
204	0.0457352	ascites
205	0.0228676	kidney
206	0.0228676	dR8
207	0.0228676	dP19
208	0.0228676	bulbarsclerosis
209	0.0228676	b73
210	0.0228676	b35

◇ Exporting cases that were MIS-CATEGORIED in the LEAVE-ONE-OUT cross-validation as wrongcases・・・.xlsx in the home directory.

◆ The data in the analysis was exported in the home directory in 2 files with the following names:
{BuildModelWrongCasesNo1Date202071422141.xlsx, BuildModelWrongCasesNo2Date202071422142.xlsx}

◇ **Exporting cases that were CORRECTLY-CATEGORIED in the LEAVE-ONE-OUT cross-validation as rightcases・・・.xlsx in the home directory.**

◆ The data in the analysis was exported in the home directory in 2 files with the following names:
{BuildModelRightCasesNo1Date202071422141.xlsx,
BuildModelRightCasesNo2Date202071422142.xlsx}

■ 5. Result of Discrimination of all Cases with the Optimized Model created from All 4373 Selected Models

◆ 1. Defining Ensembles

graftLoss

The number of rows exceeds the MaxRowsTotal limit

◆ 2. Ensembles in ParetoFront

◆ 3. Prediction Performance

◆ 4. Selected Phenotype of Optimized Model from 4373 Selected Models

```
MedianAverage(
 {0.846161 igG + 0.0864108 inflammationdatefirst respiratoryInfection + 0.0386245,
  0.952381 antiHLAclass2 (b13 + respiratoryInfection + •igA) + 0.047619,
  0.102799 banfptc cNIpostRej + 0.700582 igG + 0.595647 respiratoryInfection + 0.0294566,
  0.981668 b45 + 0.473839 dR15 +
   0.0898571 inflammationdatefirst respiratoryInfection + 0.0183323,
  0.928571 b45 + 0.928571 antiHLAclass2 (respiratoryInfection + •igA) + 0.0714286,
  0.377234 cRPpreRej heartDisease + 0.875869 igG +
   0.0860939 inflammationdatefirst respiratoryInfection + 0.00933915,
  0.945946 b45 - 0.215517 feverOnly hLAmm respiratoryInfection +
   0.954567 respiratoryInfection + 0.0540541,
  -0.408121 pyrexia + 0.740964 √(igG + respiratoryInfection) + 0.0501855,
  0.957643 b45 + 0.662983 (allergy + antiHLAclass2 + coaglationnecrosis)
     respiratoryInfection + 0.0423573,
  0.484615 (b45 + heartDisease + respiratoryInfection) (c4d + type2DM) + 0.0261538,
  0.845325 igG + 0.086299 inflammationdatefirst respiratoryInfection +
   0.96039 √cw9 + 0.03961, 0.928571 respiratoryInfection dQ8^2 + 0.928571 b45 +
   0.928571 coaglationnecrosis + 0.0714286, 0.0763346 dSAandHLAclass1pre wBCpeakover5^2 +
   0.169835 cRPpostRej + 0.584882 respiratoryInfection - 0.070139,
  0.230325 antiHLAclass2 + 0.968762 b13 + 0.140044 cNIpostRej +
   0.652431 respiratoryInfection - 0.0815212, 0.476686 c3 + 0.108982 cNIpostRej -
   0.382261 pyrexia + 0.773915 respiratoryInfection + 0.0319886, 0.991371 b45 +
   0.0151127 hDperiod - 0.406121 pyrexia + 0.738206 respiratoryInfection - 0.0121421,
```

```
0.734346 √(dQ7 + type2DM) (c3 + respiratoryInfection) + 0.0520871,
1.05955 b45 + 0.1115 cNIpostRej - 0.619749 pyrexia respiratoryInfection +
 0.938582 respiratoryInfection + 0.034055, 0.19802 dSAandHSAclass1 + 0.613861 igG -
 0.49505 pyrexia respiratoryInfection + 0.732673 respiratoryInfection + 0.00990099,
0.948454 b45 - 0.453608 pyrexia - 0.881443 enterococcusfaecalis respiratoryInfection +
 0.829897 respiratoryInfection + 0.0515464, 0.107137 cNIpostRej + 0.149575 denovoDSA -
 0.460302 pyrexia respiratoryInfection + 0.674084 respiratoryInfection - 0.0170889,
0.722878 b45 + 0.467027 igG - 1.87848 cRPpostRej pyrexia +
 0.745217 respiratoryInfection + 0.0436082, 0.154488 hLAmm cRPpostRej -
 0.420537 cRPpostRej - 0.339971 pyrexia + 0.671579 respiratoryInfection + 0.0207191,
0.967897 b45 + 0.270728 dR15 - 0.516684 pyrexia respiratoryInfection +
 0.742922 respiratoryInfection + 0.0321031, 0.978578 a34 + 0.781149 antiHLAclass2 igG +
 0.537258 respiratoryInfection + 0.0183426 wBCpeakover5 - 0.0152629,
1.00202 b45 + 0.331984 dR15 + 0.746964 candida heartDisease +
 0.510121 respiratoryInfection - 0.00202429, 0.937091 a34 + 0.724466 igG +
 0.637874 respiratoryInfection - 0.41974 √pyrexia + 0.0629092,
0.00268283 cRPpostRej hLAmm^3 - 0.0371912 banfi maxWBC respiratoryInfection +
 1.1325 respiratoryInfection - 0.0316737,
0.947263 b45 - 0.450061 pyrexia + 0.827228 respiratoryInfection +
 0.138538 cNIpostRej hLADRmm staphylococcusaureus + 0.0527375,
0.407512 cRPpreRej heartDisease + 0.881272 igG - 0.00964699 maxCRP +
 0.0889581 inflammationdatefirst respiratoryInfection + 0.0455227,
1. b45 + 1. banf t igG + 0.666667 dQ8 respiratoryInfection +
 0.333333 respiratoryInfection - 3.14018 × 10^-17, 1.22285 b45 + 0.695688 cNIpostRej igG -
 0.642825 pyrexia respiratoryInfection + 0.932553 respiratoryInfection + 0.0316843,
1.05972 b45 + 0.110183 cNIpostRej - 0.203539 feverOnly hLAmm respiratoryInfection +
 0.986025 respiratoryInfection + 0.0327787, 0.129718 aerobicGPC banfptc cNIpostRej +
 0.732689 igG - 0.35344 pyrexia + 0.699841 respiratoryInfection + 0.0428659,
-0.544973 pyrexia respiratoryInfection + 0.766924 respiratoryInfection +
 0.246959 dSAandHLAclass1pre wBCpeakover5 + 0.0200706 wBCpeakover5 - 0.0247295,
1.05644 b45 + 0.117101 cNIpostRej + 0.542785 dQ7 respiratoryInfection +
 0.0642324 inflammationdatefirst respiratoryInfection + 0.04187,
0.856936 igG + 0.0793806 inflammationdatefirst respiratoryInfection +
 0.0890798 respiratoryInfection + 0.99247 heartDisease •igA + 0.00752967,
1. b45 + 0.666667 dQ7 respiratoryInfection + 0.333333 respiratoryInfection +
 0.666667 surgery •igA - 2.19813 × 10^-16,
0.972222 b45 + 0.972222 dSAandHLAclass1pre lymphinvasion -
 0.56 pyrexia respiratoryInfection + 0.812222 respiratoryInfection + 0.0277778,
1.09953 b45 + 0.116497 cNIpostRej + 0.332016 diarrhea dR53 hLADRmm +
 0.506966 respiratoryInfection - 0.0017267,
1.10919 b45 + 0.111745 cNIpostRej + 0.224436 cNIpostRej dQ7 +
 0.0947478 inflammationdatefirst respiratoryInfection + 0.0667386,
0.230783 b45 denovoDSA - 0.520377 banfi respiratoryInfection +
 1.10543 respiratoryInfection + 0.0203774 wBCpeakover5 + 0.00314436,
0.904264 b45 - 0.415752 pyrexia + 0.14593 hDperiod respiratoryInfection +
 0.123495 cNIpostRej surgery + 0.0957356,
0.945946 b45 - 0.587629 banfi respiratoryInfection - 0.262887 birthhistory
  respiratoryInfection + 1.26553 respiratoryInfection + 0.0540541,
0.137865 cRPpostRej + 0.614756 igG + 0.85227 antiHLAclass1 respiratoryInfection +
 0.771984 respiratoryInfection type2DM - 0.00487959, 1.04936 b45 +
 0.0956724 cNIpostRej + 0.913069 (antiHLAclass2 + coaglationnecrosis + 0.0830896)
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respiratoryInfection + 0.0309519, 1.03661 b45 + 0.0929635 cNIpostRej +
0.96926 (b45 + coaglationnecrosis + dQ8) respiratoryInfection + 0.0414329,
0.244673 respiratoryInfection + 0.0196082 wBCpeakover5 +
0.802765 antiHLAclass2 (b45 + respiratoryInfection + •igA) − 0.0195495,
0.00788768 $cRPpostRej^3$ + 0.709937 b45 + 0.43284 igG + 0.869517 dQ7 respiratoryInfection +
0.0297991, 0.840791 igG^2 + 0.11118 cNIpostRej + 0.244221 dSAandHSAclass1 +
0.0952402 inflammationdatefirst respiratoryInfection + 0.0141712,
0.936351 respiratoryInfection $dQ8^2$ + 1.02837 b45 + 0.105059 cNIpostRej +
1.03177 coaglationnecrosis + 0.0598289, −0.249023 respiratoryInfection $banfi^2$ +
0.157304 cRPpostRej + 0.8932 igG + 0.994314 respiratoryInfection − 0.0531389,
0.00428319 $infectionCount^2$ + 0.622529 antiHLAclass1 banfi +
0.0779311 cNIpostRej + 0.850547 igG − 0.0499232, 0.0169932 $cNIpostRej^2$ +
0.252596 $(antiHLAclass1 + respiratoryInfection + type2DM)^2$ − 0.07591,
0.972973 b45 + 0.56 (antiHLAclass2 + bTF + interstitialHemorrhage)
respiratoryInfection + 0.252973 respiratoryInfection + 0.027027,
1.03919 b45 + 0.118704 cNIpostRej − 0.320413 pyrexia + $\frac{4.32239\ \text{respiratoryInfection}}{\text{wBCinUrine}}$ +
0.0604642, 0.00047561 $wBCpeakover5^2$ + 0.94176 a26 + 0.670104 igG +
0.806883 antiHLAclass2 respiratoryInfection + 0.0563376, 0.128421 cNIpostRej +
0.130538 denovoDSA + 0.0863025 inflammationdatefirst respiratoryInfection +
0.196768 $\sqrt{\text{dSAclass1number}}$ − 0.0346477, 1.04814 b45 + 0.114448 cNIpostRej +
$\frac{8.94186\ \text{respiratoryInfection}}{\text{maxWBC}}$ − 0.0923429 upperDigestivetract + 0.0479384,
0.931512 b45 + 0.621008 respiratoryInfection (b18 + dQ9 + type2DM) +
0.0195922 wBCpeakover5 + 0.0293039, 0.0380337 $cRPpostRej^2$ + 0.904588 b45 +
0.495661 respiratoryInfection + 0.51359 dR53 type2DM − 0.0217582,
−0.118482 igG + 0.465874 (heartDisease + igG + respiratoryInfection) (c4d + type2DM) +
0.0314417, 1.02626 b45 + 0.116042 cNIpostRej − 0.192344 pyrexia +
$\frac{1.50389\ \text{respiratoryInfection}}{\text{mMFpostRej}}$ + 0.0711524, 1.04556 b45 + 0.110835 cNIpostRej −
0.833755 gynecology − 0.512187 pyrexia + 0.881975 respiratoryInfection + 0.0474897,
0.116307 cNIpostRej + 0.157197 denovoDSA + 0.845017 igG −
0.32073 pyrexia + 0.663393 respiratoryInfection − 0.0261993,
0.10607 cNIpostRej + 0.240122 dSAandHSAclass1 + 0.835877 igG −
0.366787 pyrexia + 0.756135 respiratoryInfection + 0.022188,
0.234866 $(antiHLAclass1 + dR15 + igG + respiratoryInfection)^2$ +
0.163902 cRPpostRej − 0.0977902, 1.05066 a34 + 0.102094 cNIpostRej +
0.716647 igG − 0.34778 pyrexia + 0.680237 respiratoryInfection + 0.0460485,
1.00091 b45 + 0.773386 candida − 0.656071 dR12 + 0.62788 dR53 +
0.338647 respiratoryInfection − 0.00091083, 0.922827 b44 − 0.461858 pyrexia +
0.783759 respiratoryInfection + 0.0182303 wBCpeakover5 − $\frac{0.00195133}{\text{hDperiod}}$ + 0.0429716,
0.348418 cRPpostRej − 0.186116 feverOnly + 0.581689 igG +
0.729044 respiratoryInfection − 0.0615758 uTI + 0.0659294,
0.102653 cNIpostRej + 0.343362 gERD + 0.968209 igG − 0.449501 pyrexia +
0.765433 respiratoryInfection + 0.0106217, 0.699797 b44 + 0.440927 igG −
0.428367 pyrexia + 0.735711 respiratoryInfection − $\frac{0.00195602}{\text{hDperiod}}$ + 0.0820046,
0.0836221 banfptc cNIpostRej + 0.85404 igG − 0.302692 aerobicGPC banfptc
respiratoryInfection + 0.797772 respiratoryInfection + 0.0237396,
0.945387 cellInvasion igG + 0.615057 antiHLAclass2 respiratoryInfection + 0.0551365

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  inflammationdatefirst respiratoryInfection + 0.0187863 wBCpeakover5 - 0.00174626,
0.129543 hLADRmm (cNIpostRej + denovoDSA + dQ7 + igG + 2 respiratoryInfection) -
 0.0436571, 0.000508318 wBCpeakover5^2 + 0.253803 dSAandHLAclass1pre wBCpeakover5 -
 0.522106 pyrexia respiratoryInfection + 0.776557 respiratoryInfection - 0.000641318,
0.00413708 respiratoryInfection inflammationdatefirst^2 + 0.817571 b45 +
 0.100961 cRPpostRej + 0.690701 dQ7 respiratoryInfection + 0.00690778,
0.462058 Sqrt[b62 + igG + respiratoryInfection] (coaglationnecrosis + cRPpostRej + dQ7) +
 0.0441539, 0.00518719 wBCinUrine cRPpostRej^2 + 0.764388 b45 +
 0.12339 dQ7 hLAABmm + 0.541288 respiratoryInfection - 0.0659972,
0.913069 (antiHLAclass2 + coaglationnecrosis + 0.0830896) respiratoryInfection^2 +
 1.04936 b45 + 0.0956724 cNIpostRej + 0.0309519,
0.704012 b45 + 0.117231 cNIpostRej + 0.277214 dR7 + 0.551531 igG +
 0.0969292 inflammationdatefirst respiratoryInfection - 0.0199699,
1.0848 b45 + 0.110852 cNIpostRej + 0.530302 igG - 0.507277 pyrexia respiratoryInfection +
 0.783471 respiratoryInfection + 0.0202076,
0.140839 cRPpostRej + 0.167579 dSAandHSAclass1 + 0.84154 igG -
 0.528689 banfi respiratoryInfection + 1.17652 respiratoryInfection - 0.0685274,
0.949309 b45 - 0.632566 pyrexia respiratoryInfection + 0.862527 respiratoryInfection +
 0.0196156 wBCpeakover5 - 0.00201454/hDperiod + 0.0137918, 0.68146 b45 + 0.628054 igG +
 0.0836558 respiratoryInfection (c4d + igG + inflammationdatefirst + wBCpreRej) +
 0.00451313, -0.056097 respiratoryInfection banfi^4 + 1.06507 b45 +
 0.11705 cNIpostRej + 0.906253 respiratoryInfection + 0.0331933,
1.066 b45 + 0.117916 cNIpostRej - 0.859317 (pyrexia + 14) respiratoryInfection +
 12.901 respiratoryInfection + 0.032986,
0.147765 antiHLAclass2 + 0.99881 b45 + 0.129086 cNIpostRej -
 1.72197 cRPpostRej pyrexia + 0.822253 respiratoryInfection - 0.038208,
0.715165 candida + 0.193768 denovoDSA dR7 + 0.802574 igG -
 0.279183 pyrexia + 0.524456 respiratoryInfection + 0.0226072,
1.06491 b45 + 0.130763 cNIpostRej + 0.109566 dQ7 + 0.286732 dR51 +
 0.0926177 inflammationdatefirst respiratoryInfection - 0.00992005,
0.49955 antiHLAclass1 banfi + 0.095362 cNIpostRej + 0.775627 igG -
 0.267758 pyrexia + 0.527915 respiratoryInfection + 0.0385383,
0.937777 b44 + 0.0974427 hDperiod igG - 0.385033 pyrexia +
 0.692449 respiratoryInfection + 0.0188001 wBCpeakover5 - 0.00152164,
0.00788768 cRPpostRej^3 + 0.869517 dQ7 respiratoryInfection^2 + 0.709937 b45 +
 0.43284 igG + 0.0297991, 1.12341 b45 + 0.126036 cNIpostRej + 0.254934 dR15 +
 0.166999 dR53 + 0.0960752 inflammationdatefirst respiratoryInfection - 0.0176024,
1.14047 b45 - 0.0239694 banfah + 0.10656 cNIpostRej + 0.907627 respiratoryInfection -
 1.05087 upperRespiratoryInfection wBCpreRej + 0.0640059,
0.00523935 inflammationdatefirst^2 respiratoryInfection^2 +
 0.317483 respiratoryInfection + 0.107461 cNIpostRej + 0.836518 igG + 0.0185964,
0.876863 b45 + 0.150369 dSAclass2 - 0.58097 pyrexia respiratoryInfection +
 0.784794 respiratoryInfection + 0.0221186 wBCpeakover5 - 0.0714687,
0.296104 antiHLAclass1 + 0.191998 cRPpostRej + 0.701519 igG +
 0.680734 allergy respiratoryInfection + 0.318217 respiratoryInfection - 0.0912313,
0.228084 (antiHLAclass1 + respiratoryInfection + type2DM)^2 + 0.353115 igG +
 0.0214927 wBCpeakover5 - 0.101846, 0.830772 b45 + 0.11714 cNIpostRej + 0.518147 igG +
 0.0502691 (inflammationdatefirst + 7) respiratoryInfection + 0.00849362,
0.836865 b45 + 0.110026 cNIpostRej + 0.439505 igG + 0.703232 respiratoryInfection -
 0.0137384 pyrexia wBCpeakover9postRej + 0.0357499,
0.242528 (coaglationnecrosis + dQ7 + respiratoryInfection)^2 - 0.001412 b45
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$0.242528\,(\text{coaglationnecrosis} + \text{dQ7} + \text{respiratoryInfection})^2 + 0.901413\,\text{b45} +$
$0.0224965\,\text{wBCpeakover5} - 0.06767,\ 0.520996\,\text{b45} + 0.162413\,\text{cRPpostRej} + 0.478874\,\text{igG} -$
$0.285202\,\text{feverOnly pyrexia} + 0.70142\,\text{respiratoryInfection} - 0.0427875,$
$0.150203\,\text{cRPpostRej} + 0.616334\,\text{igG} - 0.532563\,\text{pyrexia respiratoryInfection} +$
$0.774841\,\text{respiratoryInfection} - \frac{0.0019662}{\text{hDperiod}} - 0.0178535,$
$0.636794\,\text{b45} - 0.00726273\,\text{pRAclass1pre} +$
$0.555807\,(\text{c3} + \text{respiratoryInfection})\,(\text{dQ7} + \text{type2DM}) + 0.0698006,$
$0.227334\,\text{antiHLAclass1} + 0.186089\,\text{cRPpostRej} + 0.653323\,\text{igG} -$
$0.0457655\,\text{maxWBC respiratoryInfection} + 1.21034\,\text{respiratoryInfection} - 0.0762541,$
$0.708301\,\text{b45} + 0.538704\,\text{igG} - 0.0489432\,\text{maxWBC respiratoryInfection} +$
$1.30825\,\text{respiratoryInfection} + 0.0186609\,\text{wBCpeakover5} - 0.0149752,$
$0.817236\,\text{b45} + 0.123334\,\text{cRPpostRej} + 0.482742\,\text{banfg igG} -$
$0.369618\,\text{pyrexia} + 0.73426\,\text{respiratoryInfection} - 0.0316533,$
$0.78025\,\text{b45} + 0.1014\,\text{cNIpostRej} + 0.568179\,\text{igG} + 0.604308\,\text{dQ8 respiratoryInfection} +$
$0.367708\,\text{respiratoryInfection} + 0.0207857,$
$1.03565\,\text{b45} + 0.109425\,\text{cNIpostRej} + 0.668081\,\text{dQ11} - 0.144282\,\text{pyrexia} +$
$0.095222\,\text{inflammationdatefirst respiratoryInfection} + 0.0562085,$
$0.437914\,\text{coaglationnecrosis} + 0.160925\,\text{denovoDSA} + 0.857781\,\text{aBOI dQ7} +$
$0.0422824\,\text{infectionCount} + 0.017742\,\text{wBCpeakover5} - 0.230491,$
$0.272261\,(\text{antiHLAclass2} + \text{b44} + \text{respiratoryInfection})^2 +$
$0.134773\,\text{cNIpostRej} + 0.560952\,\text{coaglationnecrosis} - 0.0912743,$
$1.0184\,\text{b45} + 0.112483\,\text{cNIpostRej} + 0.128448\,\text{dR7} + 0.550008\,\text{dQ7 respiratoryInfection} +$
$0.382715\,\text{respiratoryInfection} + 0.0118079,$
$0.687486\,\text{b45} + 0.582753\,\text{igG} - 0.243442\,\text{banfptc respiratoryInfection} +$
$0.931684\,\text{respiratoryInfection} + 0.0186811\,\text{wBCpeakover5} - 0.0162246,$
$0.107238\,\text{cNIpostRej} + 0.38261\,\text{dP4} + 0.533415\,\text{igG} -$
$0.507364\,\text{pyrexia respiratoryInfection} + 0.783405\,\text{respiratoryInfection} + 0.0190104,$
$0.144026\,\text{cRPpostRej} + 0.697796\,\text{igG} - 0.279195\,\text{pyrexia} + 0.803934\,\text{respiratoryInfection} -$
$0.150043\,\text{banfptc upperRespiratoryInfection} - 0.0044763,$
$0.211025\,\text{cRPpostRej} + 0.746951\,\text{igG} + 0.35178\,\text{respiratoryInfection} +$
$0.614272\,\text{allergy}\,(\text{b57} + \text{respiratoryInfection}) - 0.0674773,$
$0.725424\,\text{b45} + 0.355932\,\text{banfah citobacterdiversus} + 0.375141\,\text{heartDisease} +$
$0.531073\,\text{igG} + 0.279096\,\text{respiratoryInfection} + 0.00903955,$
$0.0649199\,(\text{dSAandHLAclass2pre} + 1.41026)\,\text{inflammationdatefirst respiratoryInfection} +$
$0.801232\,\sqrt{\text{b45} + \text{igG}} + 0.00947821,\ -0.365294\,\text{pyrexia}^3 + 0.833729\,\text{b45} +$
$0.108362\,\text{cNIpostRej} + 0.429477\,\text{igG} + 0.716711\,\text{respiratoryInfection} + 0.0425017,$
$0.725461\,\text{b45} - 0.861711\,\text{gynecology} + 0.431875\,\text{igG} +$
$0.803109\,\text{respiratoryInfection} - 0.600133\,\sqrt{\text{pyrexia}} + 0.0586016,$
$\frac{0.771992\,\text{cNIpostRej}}{\text{wBCinUrine}} + 0.973729\,\text{igG} - 0.347974\,\text{aerobicGPC banfptc respiratoryInfection} +$
$0.813682\,\text{respiratoryInfection} + 0.0283415,$
$1.07165\,\text{b45} + 0.10072\,\text{cNIpostRej} - 0.883912\,\text{gynecology respiratoryInfection} -$
$0.621356\,\text{pyrexia respiratoryInfection} + 0.957981\,\text{respiratoryInfection} + 0.0129075,$
$1.29953\,\text{b45} + 0.103306\,\text{cNIpostRej} + 0.626868\,\text{cNIpostRej igG} -$
$0.626793\,\text{pyrexia respiratoryInfection} + 0.963496\,\text{respiratoryInfection} + 0.0165451,$
$0.973412\,(\text{antiHLAclass2} + \text{coaglationnecrosis} + \text{hBV})\,\text{respiratoryInfection}^2 +$
$0.975921\,\text{b45} + 0.0427329\,\text{cNIpostRej cRPpreRej} + 0.0251523,$
$1.08892\,\text{b45} + 0.112483\,\text{cNIpostRej} + 0.248157\,\text{dR52} - 0.194732\,\text{feverOnly hLAmm}$
$\text{respiratoryInfection} + 0.95361\,\text{respiratoryInfection} + 0.00550686,$
$0.467197\,\text{antiHLAclass1 banfi} + 0.150216\,\text{cRPpostRej} + 0.829645\,\text{igG} +$
$0.735384\,\text{allergy respiratoryInfection} + 0.250132\,\text{respiratoryInfection} - 0.0577155$

0.735384 allergy respiratoryInfection + 0.250132 respiratoryInfection − 0.0577155,
0.251098 b45 dSAandHSAclass1 + 0.627036 igG − 0.534126 pyrexia respiratoryInfection +
0.745489 respiratoryInfection + 0.019909 wBCpeakover5 − 0.0189583,
0.799788 b45 + 0.110451 cNIpostRej + 0.626941 igG + 0.0994798 inflammationdatefirst
respiratoryInfection − 0.0176722 banfci wBCpostKTx + 0.0583014,
0.951962 b45 − 0.453961 pyrexia + 0.0643909 hDperiod respiratoryInfection +
0.532333 respiratoryInfection + 0.14086 cNIpostRej surgery + 0.0480376,
1.06604 b45 − 0.727931 banfptcbm cNIpostRej + 0.120111 cNIpostRej −
0.591672 pyrexia respiratoryInfection + 0.754712 respiratoryInfection + 0.0347903,
0.131678 hLAmm cRPpostRej − 0.383545 cRPpostRej + 0.553192 igG −
0.464308 pyrexia respiratoryInfection + 0.716111 respiratoryInfection − 0.00502158,
0.209349 $(\text{antiHLAclass2} + \text{b63} + \text{respiratoryInfection})^2$ + 0.124381 cNIpostRej +
0.0469143 inflammationdatefirst respiratoryInfection − 0.0633306,
0.0104528 (cRPpostRej + dR7 + igG) hLAmm^2 + 0.546933 dQ7 respiratoryInfection +
0.347124 respiratoryInfection − 0.0631703, 0.141029 hLAmm cRPpostRej −
0.420701 cRPpostRej + 0.546494 igG − 0.475359 aerobicGNR respiratoryInfection +
0.724931 respiratoryInfection − 0.00684578,
0.00716823 respiratoryInfection $\text{inflammationdatefirst}^2$ + 0.908402 igG +
0.889286 gERD (b45 + igG + respiratoryInfection) + 0.0533678,
−0.0749584 feverOnly hLADRmm^2 + 0.230079 (cRPpostRej + igG + streptococcusaureus)
hLADRmm + 0.540263 respiratoryInfection − 0.0666121,
0.0429387 denovoDSA^2 + 0.107375 cNIpostRej + 0.901046 igG −
0.450607 banfi respiratoryInfection + 1.06803 respiratoryInfection − 0.00906658,
0.0369495 igG + 0.247065 respiratoryInfection + 0.0195631 wBCpeakover5 +
0.790804 antiHLAclass2 (b45 + respiratoryInfection + •igA) − 0.0197563,
−0.201618 polyp^2 + 0.770024 b44 + 0.110862 cNIpostRej + 0.566812 igG +
0.0940564 inflammationdatefirst respiratoryInfection + 0.0396384,
0.0164542 cNIpostRej^2 + 0.0405447 dQ7 + 0.338533 dR7 + 0.750276 igG +
0.0889382 inflammationdatefirst respiratoryInfection − 0.0324234,
1.08268 b45 + 0.101196 cNIpostRej + 0.41743 respiratoryInfection +
0.429194 antiHLAclass2 (igG + respiratoryInfection + •igA) + 0.0131826,
0.000490074 wBCpeakover5^2 + 0.74068 b45 + 0.457662 aBOI dQ7 −
0.348872 pyrexia + 0.647476 respiratoryInfection + 0.0285289,
0.0321517 cRPpostRej^2 + 0.558329 b45 + 0.635662 igG − 0.143541 pyrexia +
0.0888598 inflammationdatefirst respiratoryInfection + 0.0247895,
0.482156 b45 + 0.212701 cRPpostRej + 0.377429 igG +
0.892868 (b45 + coaglationnecrosis + dR53) respiratoryInfection − 0.0406508,
0.217717 cNIpostRej surgery^2 − 0.0913062 cNIpostRej + 0.632234 igG −
0.431302 pyrexia + 0.724302 respiratoryInfection + 0.0601535,
−0.245762 respiratoryInfection banfi^2 − 0.511083 b18 + 0.847384 b44 +
0.11248 cNIpostRej + 0.999437 respiratoryInfection + 0.048258,
0.000516503 wBCpeakover5^2 + 0.861595 b45 + 0.317689 dR7 +
0.0806424 inflammationdatefirst respiratoryInfection +
0.127689 respiratoryInfection − 0.0225054,
−0.0324884 hypertention^2 + 0.534359 antiHLAclass1 banfi + 0.105643 cNIpostRej +
0.812885 igG + 0.478081 respiratoryInfection + 0.0493168, 0.127466
$(\text{antiHLAclass1} + \text{dR18} + \text{heartDisease} + \text{hLADRmm} + \text{respiratoryInfection} + \bullet\text{igA} - 1)^2$ −
0.0370859, $1.81298 - \dfrac{3.47988}{\text{b45} + \text{candida} + 2\,\text{igG} - \text{polyp} + \text{respiratoryInfection} + 1.92224}$,
1.08928 b62 + 0.106582 cNIpostRej + 0.118767 dQ7 + 0.640433 igG −
0.307847 pyrexia + 0.654283 respiratoryInfection + 0.0116825,
0.194101 cRPpostRej + 0.261804 gERD + 0.632368 igG − 0.237767 nS

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0.194101 cRPpostRej + 0.261804 gERD + 0.032368 igG - 0.237767 hS -
 0.415239 pyrexia + 0.69204 respiratoryInfection - 0.0500124,
0.0825153 antiHLAclass2 + 0.932276 b45 - 0.137484 banfci + 0.116118 cNIpostRej +
 0.418363 igG + 0.908534 respiratoryInfection + 0.0109925,
0.107649 cNIpostRej + 0.315127 denovoDSA + 0.300562 dR15 - 0.292441 dSAandHSAclass2 +
 0.488859 igG + 0.463417 respiratoryInfection - 0.00254748,
0.620113 b45 + 0.128994 cNIpostRej + 0.362765 coaglationnecrosis +
 0.0845162 denovoDSA + 0.431548 igG + 0.523818 respiratoryInfection - 0.0234038,
0.200922 (igG^2 + cRPpostRej + dR53 + hLADRmm) hLADRmm -
 0.541486 hLADRmm + 0.514207 respiratoryInfection + 0.182074,
0.667161 b45 + 0.628438 cellInvasion igG + 0.622092 dQ7 respiratoryInfection +
 0.0567437 inflammationdatefirst respiratoryInfection + 0.0193616 wBCpeakover5 -
 0.0201033, 0.562008 (c4d + type2DM) (c3 - respiratoryInfection)^2 +
 0.161798 cRPpostRej + 0.241002 twinpeak - 0.0875204,
0.0405264 denovoDSA^2 - 1.48242 banfct dP18 + 0.940114 igG -
 0.0469971 maxWBC respiratoryInfection + 1.27594 respiratoryInfection - 0.0211666,
-0.183897 banfi respiratoryInfection^2 + 0.115243 inflammationdatefirst
  respiratoryInfection + 0.104718 cNIpostRej + 0.236395 dSAandHSAclass1 +
 0.827748 igG + 0.032459, 0.677307 dR7 respiratoryInfection^3 +
 0.0836213 inflammationdatefirst respiratoryInfection +
 0.0847348 cNIpostRej + 0.83177 igG - 0.128652 pyrexia + 0.0479715,
0.228277 b61 cRPpostRej^2 + 0.0999957 cNIpostRej + 0.903613 igG -
 0.610231 aerobicGPC respiratoryInfection + 0.811055 respiratoryInfection + 0.0191034,
0.111621 hLADRmm ((dQ7 + respiratoryInfection + type2DM)^2 +
    cRPpostRej + respiratoryInfection - 1.5869) + 0.0699466,
0.114383 (cRPpostRej + igG + streptococcusaureus) hLADRmm^2 -
 0.271408 feverOnly respiratoryInfection^2 + 0.73893 respiratoryInfection - 0.0538509,
0.924664 b45 - 0.11408 banfct + 0.109343 cNIpostRej + 0.459054 igG -
 0.535933 pyrexia respiratoryInfection + 0.851438 respiratoryInfection + 0.0516822,
0.87924 b45 + 0.130703 cNIpostRej - 0.218983 enterococcusfaecalis + 0.383378 igG +
 0.813683 respiratoryInfection - 0.534706 pyrexia rMale + 0.0387961,
1.05306 b45 + 0.131829 cNIpostRej - 0.231839 enterococcusfaecalis - 0.39953 pyrexia +
 0.782054 respiratoryInfection + 0.791556 antiHLAclass2 •igA + 0.0576075,
0.818392 b45 + 0.105625 cNIpostRej + 0.480619 igG - 0.331959 polyp -
 0.046466 maxWBC respiratoryInfection + 1.3345 respiratoryInfection + 0.0299695,
0.245823 (coaglationnecrosis + dQ7 + respiratoryInfection)^2 + 0.767167 b45 +
 0.0629629 hLAmm + 0.0222092 wBCpeakover5 - 0.280793, 0.190069 antiHLAclass1 +
 0.618495 b45 + 0.362241 igG - 0.460411 banfi respiratoryInfection +
 1.01141 respiratoryInfection + 0.0207847 wBCpeakover5 - 0.0312543,
1.01562 b45 + 0.120684 cNIpostRej + 0.159735 dR7 - 0.57552 banfi pyrexia +
 0.627811 pyrexia + 0.825579 respiratoryInfection + 0.00582248,
1.07387 b45 + 0.11558 cNIpostRej + 0.181898 dR15 - 0.371878 pyrexia +
 0.21717 dR53 respiratoryInfection + 0.668775 respiratoryInfection + 0.0231591,
0.760352 b45 + 0.0181372 hDperiod + 0.40836 igG - 0.476556 pyrexia respiratoryInfection +
 0.737593 respiratoryInfection + 0.118796 type2DM - 0.108256,
0.111708 cNIpostRej + 0.128974 denovoDSA + 0.0439434 dQ8 + 0.660622 igG +
 0.75179 respiratoryInfection - 0.645329 aerobicGPC upperRespiratoryInfection -
 0.0232497, 0.135388 cRPpostRej + 0.0613714 denovoDSA +
 0.236501 dR7 + 0.0389856 dSAandHLAclass1pre + 0.606467 igG +
 0.0822643 inflammationdatefirst respiratoryInfection - 0.107583,
0.750512 b45 + 0.144727 cRPpostRej - 0.218872 dP13 + 0.135476 dQ7 -
 0.459073 banfi respiratoryInfection + 1.04363 respiratoryInfection - 0.0698588
```

```
 0.459075 banfi respiratoryInfection + 1.04565 respiratoryInfection - 0.0098588,
0.107988 cNIpostRej + 0.116707 denovoDSA + 0.548493 igG -
 0.0440596 maxWBC respiratoryInfection + 1.15661 respiratoryInfection +
 0.0301399 sABC1q - 0.0108501, 0.733078 b45 + 0.129481 cNIpostRej +
 0.105618 denovoDSA + 0.0493893 dQ8 + 0.767939 respiratoryInfection -
 0.492429 aerobicGPC upperRespiratoryInfection - 0.0187353,
0.223553 antiHLAclass1 + 0.057057 dQ5 + 0.813092 aBOI igG - 0.373492 pyrexia +
 0.682069 respiratoryInfection + 0.0199579 wBCpeakover5 - 0.0132699,
0.0156958 cNIpostRej^2 + 0.976134 b45 + 0.199342 dR15 - 0.864407 gynecology -
 0.490584 pyrexia + 0.840081 respiratoryInfection + 0.0126221,
1.62601 - 3.21584 / (b45 + candida + 3 igG +
    antiHLAclass2 respiratoryInfection + respiratoryInfection + 1.9767),
0.261893 (2 b45 + coaglationnecrosis + dR53 + respiratoryInfection)^2 +
 0.12298 cNIpostRej - 0.00475347, 0.00124222 cRPpostRej hLAmm^3 + 0.682649 b45 +
 0.0726185 cNIpostRej - 0.0353869 banfi maxWBC respiratoryInfection +
 1.14526 respiratoryInfection - 0.00354623, 0.00266779 cRPpostRej hLAmm^3 -
 0.0170019 hLAmm + 0.358883 c3 - 0.0371994 banfi maxWBC respiratoryInfection +
 1.16525 respiratoryInfection - 0.00774233,
-0.319708 feverOnly respiratoryInfection^3 + 0.833582 respiratoryInfection +
 1.07645 b45 + 0.103988 cNIpostRej + 0.0924798 dR18 hDperiod type2DM + 0.0108479,
0.00228701 hLAmm^3 + 0.0901822 cNIpostRej + 0.846293 b45 igG -
 0.0353142 banfi maxWBC respiratoryInfection + 1.12618 respiratoryInfection -
 0.0661788, 3.32373 interstitialHemorrhage type2DM cRPpostRej +
 0.13046 cRPpostRej + 0.0708083 denovoDSA +
 0.0854955 inflammationdatefirst (b45 + igG + respiratoryInfection) - 0.0742596,
0.363201 hLAmm pyrexia respiratoryInfection^2 - 1.62404 pyrexia respiratoryInfection +
 0.821178 respiratoryInfection + 0.964992 b45 + 0.0207266 wBCpeakover5 - 0.00644534,
0.0358476 cRPpostRej^2 + 0.886621 b45 +
 0.243742 (dQ4 + Sqrt[antiHLAclass2] + Sqrt[hDperiod]) respiratoryInfection + 0.00294265,
0.747312 b45 + 0.072334 cNIpostRej + 0.615187 igG + 0.724726 dR15 respiratoryInfection +
 0.0857304 inflammationdatefirst respiratoryInfection +
 0.0081016 wBCpeakover5 - 0.0103848, 0.909801 b45 + 0.112743 cNIpostRej +
 0.238705 dR15 + 0.380624 igG + 0.371131 dR53 respiratoryInfection +
 0.0799768 inflammationdatefirst respiratoryInfection - 0.00546579,
-0.261501 respiratoryInfection banfi^2 + 1.0549 b45 + 0.113373 cNIpostRej -
 (0.00214952 respiratoryInfection)/hDperiod + 1.10415 respiratoryInfection + 0.0402808,
0.832554 b45 + 0.109874 cNIpostRej + 0.437081 igG -
 0.0986237 pyrexia + 0.417403 dQ7 respiratoryInfection +
 0.070319 inflammationdatefirst respiratoryInfection + 0.0411441,
1.0585 b45 + 0.100028 cNIpostRej + 0.122893 dR15 + 0.479663 cNIpostRej dR51 -
 0.457682 banfi respiratoryInfection + 1.08813 respiratoryInfection + 0.0254743,
1.04896 b45 - 0.064904 dQ4 + 0.279508 dR15 + 0.573484 dR53 respiratoryInfection +
 0.0668628 inflammationdatefirst respiratoryInfection +
 0.0204046 wBCpeakover5 - 0.02487, 1.11851 b45 + 0.1294 cNIpostRej +
 0.318805 dR53 - 0.0762175 pyrexia + 0.523556 bTF respiratoryInfection +
 0.0855926 inflammationdatefirst respiratoryInfection - 0.00987899,
1.05009 b45 + 0.112805 cNIpostRej - 0.109371 pyrexia + 0.552211 dR53
   respiratoryInfection + 0.0768059 inflammationdatefirst respiratoryInfection +
 0.00721502 thrombusformation + 0.0446098, 1.06048 b45 + 0.111253 cNIpostRej +
 0.71171 coaglationnecrosis + 0.612142 dQ8 respiratoryInfection -
 0.0238649 maxWBC respiratoryInfection + 0.657368 respiratoryInfection + 0.0329182
```

0.0238649 maxWBC respiratoryInfection + 0.657368 respiratoryInfection + 0.0329182,
0.133654 antiHLAclass1 denovoDSA + 0.230172 gERD + 0.844639 c3 igG − 0.421361 pyrexia +
0.700234 respiratoryInfection + 0.0206382 wBCpeakover5 − 0.0402075,
1.07473 b45 + 0.103717 cNIpostRej + 0.868989 c3 dR52 − 0.00152896 infarctionhemohorrage −
0.0458707 maxWBC respiratoryInfection + 1.35599 respiratoryInfection + 0.012339,
0.940554 b45 + 28.661 igG − 0.446851 igG rage + 0.80937 (dQ7 + pastheart)
respiratoryInfection + 0.168665 respiratoryInfection + 0.0282116,
0.626345 b13 − 0.438273 pyrexia + 0.816063 respiratoryInfection +
0.149752 cNIpostRej (cGN + surgery) (surgery + type2DM) + 0.0403218,
0.69105 b45 + 0.361446 candida + 0.499713 banfah citobacterdiversus +
0.456971 heartDisease + 0.616753 igG +
0.999426 coaglationnecrosis respiratoryInfection + 0.000573723,
0.682635 b45 + 0.474559 candida + 0.580348 igG − 0.267768 pyrexia +
0.318707 banfah dQ7 respiratoryInfection + 0.494749 respiratoryInfection + 0.027191,
0.885726 b45 + 0.121088 cNIpostRej + 0.289313 coaglationnecrosis + 0.348691 dR15 +
0.471932 igG + 0.093083 inflammationdatefirst $\sqrt{\text{respiratoryInfection}}$ − 0.0200391,
0.564294 igG^4 + 0.787397 b45 + 0.106674 cNIpostRej −
0.248778 banfi^2 respiratoryInfection + 1.0347 respiratoryInfection + 0.0200091,
0.0595145 dSAandHSAclass1^2 − 0.257358 dP13 + 0.827655 igG − 0.306819 pyrexia −
0.200091 banfptc respiratoryInfection + 0.972091 respiratoryInfection + 0.0278182,
0.000641314 wBCpeakover5^2 + 0.737475 b45 − 0.293141 enterococcusfaecalis +
0.458564 igG − 0.262353 banfi pyrexia + 0.776203 respiratoryInfection + 0.0306779,
0.907631 b45^2 + 0.125563 dR7 − 0.605831 pyrexia respiratoryInfection +
0.842921 respiratoryInfection + 0.0200103 wBCpeakover5 − $\frac{0.00188393}{\text{hDperiod}}$ − 0.00825217,
0.0555628 $(\text{antiHLAclass1} + \text{respiratoryInfection} + \text{type2DM})^4$ +
0.0946748 anemia + 0.0997382 cNIpostRej + 0.322998 igG − 0.00762138,
0.000505701 wBCpeakover5^2 + 0.68359 b63 − 0.641017 enterobacteraerogenes + 0.56875 igG +
1.08978 respiratoryInfection − 0.0852048 respiratoryInfection uTI + 0.00564782,
0.00900176 $\text{pRAclass2pre aBOI}^2$ + 0.96406 b45 + 0.0859835 banfah − 0.421871 pyrexia +
0.698681 respiratoryInfection + 0.0213303 wBCpeakover5 − 0.049712,
0.00491479 cRPpostRej^3 + 0.0595978 cNIpostRej + 0.122155 denovoDSA +
0.881707 aBOI igG − 0.318957 pyrexia + 0.644977 respiratoryInfection − 0.0247754,
−0.808201 gynecology $\text{respiratoryInfection}^2$ + 0.828322 respiratoryInfection +
0.940334 b45 + 0.0774181 banfah − 0.500779 pyrexia + 0.0205392 wBCpeakover5 − 0.0201216,
0.142746 cRPpostRej + 0.335172 respiratoryInfection +
0.581168 $\sqrt{\text{b13} + \text{igG} + \text{dQ8 respiratoryInfection}}$ − 0.0637518, 0.647433 b45 +
0.688285 igG − 0.726642 $\left(\text{b45} + \text{igG} + \text{pastanemia} + \sqrt{\text{pyrexia}}\right)$ respiratoryInfection +
0.98908 respiratoryInfection + 0.00842473, 0.281875 (dSAandHLAclass2pre + 0.244303)
(dQ7 + dSAandHLAclass2pre + inflammationdatefirst) respiratoryInfection +
0.80519 $\sqrt{\text{b45} + \text{igG}}$ + 0.00995596, 0.761676 b45 + 0.158118 dR15 +
0.38868 igG − 0.407374 pyrexia + 0.724331 respiratoryInfection +
0.018578 wBCpeakover5 − $\frac{0.00168618}{\text{hDperiod}}$ + 0.00878099,
0.754636 b45 + 0.137403 banfah − 0.112887 banfct + 0.591429 igG − 0.451777 pyrexia +
0.765028 respiratoryInfection + 0.0210685 wBCpeakover5 − 0.0483015,
0.691785 b45 + 0.134318 cNIpostRej + 0.0545488 denovoDSA + 0.201878 dQ7 +
0.180983 hLADRmm − 0.220164 pyrexia + 0.561572 respiratoryInfection − 0.232852,
0.240531 antiHLAclass1 + 0.152932 cRPpostRej + 0.295832 gERD + 0.636096 igG −
0.178613 pastanemia − 0.330045 pyrexia + 0.574312 respiratoryInfection − 0.0550192,
0.384287 b61 + 0.106597 banfah + 0.765183 igG − 0.319526 polyp − 0.373892 pyrexia +

```
 0.642841 respiratoryInfection + 0.0235021 wBCpeakover5 - 0.0499691,
2.25555 - 3.79088 / (b45^2 + candida + igG + antiHLAclass2 respiratoryInfection +
    coaglationnecrosis respiratoryInfection + 1.70567),
-1.63465 pyrexia respiratoryInfection cRPpostRej + 0.107888 cRPpostRej +
 0.84845 b45 dP4 + 0.00910988 hDperiod + 0.704491 igG +
 0.698189 respiratoryInfection - 0.0822203,
0.988534 dR7 igG^2 + 1.01894 b45 - 0.145587 pyrexia - 0.392808 banfi respiratoryInfection +
 1.1204 respiratoryInfection - 0.0608061 upperRespiratoryInfection + 0.0114663,
0.852335 b45 + 0.108063 cNIpostRej - 0.137328 denovoDSA igG + 0.720068 igG -
 0.719023 Sqrt[pyrexia] respiratoryInfection + 0.868196 respiratoryInfection + 0.0156785,
0.110859 cNIpostRej + 0.156237 denovoDSA - 0.288498 denovoDSA igG + 1.0892 igG -
 0.617727 Sqrt[pyrexia] respiratoryInfection + 0.740416 respiratoryInfection - 0.0388584,
0.0164194 denovoDSA^2 + 0.380824 dSAclass1number igG -
 0.546996 pyrexia respiratoryInfection + 0.73909 respiratoryInfection +
 0.0190747 wBCpeakover5 - 0.0017096/hDperiod + 0.00253675,
0.708531 b45 - 0.197657 dP18 + 0.488105 igG - 0.602771 pyrexia respiratoryInfection +
 0.821029 respiratoryInfection + 0.0196998 wBCpeakover5 - 0.00190932/hDperiod + 0.0102273,
1.03319 b45 + 0.245907 c3 + 0.12885 cNIpostRej + 0.38795 coaglationnecrosis +
 0.216103 dQ6 - 0.308827 feverOnly respiratoryInfection +
 0.831192 respiratoryInfection - 0.0479741,
0.0331691 (b45 + c3 + cRPpostRej + dQ7 + dR15 + hLADRmm + 2 respiratoryInfection)^2 -
 0.142195, -0.692241 upperRespiratoryInfection aerobicGPC +
 0.0252199 aerobicGPC + 0.693739 b45 + 0.105365 cNIpostRej + 0.694906 igG +
 0.0448982 mMFpostRej + 0.859465 respiratoryInfection - 0.111821,
0.243641 (2 b45 + coaglationnecrosis + dQ6 + respiratoryInfection)^2 +
 0.129551 cNIpostRej + 0.115868 respiratoryInfection - 0.019084,
-0.157501 aerobicGPC + 0.312524 coaglationnecrosis + 0.191428 cRPpostRej +
 0.131318 dSAandHSAclass1 + 0.54527 igG + 0.488362 respiratoryInfection +
 0.153639 Sqrt[dQ7] - 0.0811309, 0.00866876 respiratoryInfection hDperiod^2 +
 0.989266 b45 + 0.949077 dR15 igG - 0.634785 pyrexia respiratoryInfection +
 0.625164 respiratoryInfection + 0.0200944 wBCpeakover5 - 0.0294546,
0.933516 dR15^2 igG^2 + 0.973829 b45 - 0.630435 pyrexia respiratoryInfection +
 0.88472 respiratoryInfection + 0.0191362 wBCpeakover5 - 0.00196524/hDperiod - 0.0098258,
0.880796 b45 + 0.110948 cNIpostRej + 0.504355 coaglationnecrosis +
 0.153628 dR15 + 0.438353 igG + 0.306999 dQ7 mMFatRej respiratoryInfection +
 0.17916 respiratoryInfection - 0.00683247,
0.807157 b45 + 0.12339 cNIpostRej + 0.466367 igG -
 0.372422 aerobicGPC respiratoryInfection - 0.3499 feverOnly respiratoryInfection +
 1.14713 respiratoryInfection - 0.0321518 uTI + 0.0793209,
1.30627 b45 + 0.109989 cNIpostRej + 0.292598 coaglationnecrosis -
 0.278303 enterobacteraerogenes + 0.620898 cNIpostRej igG -
 0.357039 feverOnly respiratoryInfection + 0.918085 respiratoryInfection + 0.0132293,
0.0601878 dSAandHSAclass1^2 + 0.000500349 wBCpeakover5^2 + 0.703296 igG -
 0.747597 aerobicGNR (anemia + dSAandHLAclass1pre) respiratoryInfection +
 0.737528 respiratoryInfection + 0.00589983,
-0.0644628 anemia + 0.488095 antiHLAclass1 banfi - 0.12845 denovoDSA igG + 1.08534 igG -
 0.306402 pyrexia + 0.559371 respiratoryInfection + 0.0182622 wBCpeakover5 + 0.0161102,
-0.00243833 banfptc^4 + 0.133939 cNIpostRej surgery^2 + 0.733449 b45 +
 0.413661 igG - 0.402172 pyrexia + 0.784865 respiratoryInfection + 0.0597202
```

```
  0.413661 igG - 0.402172 pyrexia + 0.784865 respiratoryInfection + 0.0597202,
 0.776945 b45 + 0.114696 cNIpostRej + 0.607721 igG +
  1.31387 respiratoryInfection - 0.343708 respiratoryInfection
   (aerobicGPC + cNIpostRej + feverOnly + igG + respiratoryInfection) + 0.0154823,
 0.727571 candida + 0.693079 igG - 0.267146 pyrexia + 0.502597 respiratoryInfection +
  0.177387 dR7 (denovoDSA + 2 igG + respiratoryInfection) + 0.0211302,
 -0.200621 respiratoryInfection banfi^2 + 0.311061 antiHLAclass1 banfi +
  0.47046 b45 + 0.124732 cNIpostRej + 0.526388 igG + 0.941928 respiratoryInfection -
  0.0323454 uTI + 0.076169, -0.0425276 respiratoryInfection banfi^4 +
  0.469614 antiHLAclass1 banfi - 0.0212122 hypertention^2 +
  0.101081 cNIpostRej + 0.73304 igG + 0.691592 respiratoryInfection + 0.047187,
 0.163443 cGN^2 + 0.0837862 cMV^2 + 1.12152 b45 + 0.133482 cNIpostRej +
  0.161437 dQ6 - 0.564916 pyrexia respiratoryInfection +
  0.743854 respiratoryInfection - 0.0513556}, 0.7)
```

□ **Created standalone model is expressed as ALLPHENOTYPE, created function as ALLCREATEDMODEL.**

(Predicted values are calculated with ALLCREATEDMODEL @@@ ALLTRAININGDATA)

◆ **5. The Optimized Model created from 4373 Selected Models (expressed as ALLCREATEDMODEL) is as follows.**

```
Function[{rMale, rage, infectionCount, feverOnly, pyrexia, inflammation, virusInfection,
  cMV, anemia, heartDisease, respiratoryInfection, upperRespiratoryInfection,
  upperDigestivetract, diarrhea, uTI, wBCinUrine, wBCpeakover10, urology, skin,
  woundInfection, herpesZoster, orthopedics, ascites, surgery, aerobicGPC, aerobicGNR,
  candida, staphylococcusaureus, streptococcusaureus, enterobacteraerogenes,
  enterobactereclacue, enterococcusfaecalis, citobacterdiversus, pseudomonas,
  inflammationdatefirst, infectiondatelast, asthma, pastanemia, infarctionhemohorrage,
  calcification, digestiveorgan, appendicitis, polyp, ulcer, gERD, pastheart,
  kidney, pastliverbilialy, hBV, hCV, stone, hypothyroidism, gynecology, ocular,
  allergy, hypertention, type2DM, bTF, timeoftransplantation, regraft, aBOI, hLAABmm,
  hLADRmm, hLAmm, pRAclass1pre, pRAclass2pre, pRAclass1after, pRAclass2after,
  mFImax, twinpeak, dSAclass1, dSAclass1number, dSAclass2, dSAclass2number, preDSA,
  denovoDSA, antiHLAclass1, hSAclass1number, antiHLAclass2, hSAclass2number,
  dSAandHSAclass2, dSAandHSAclass1, dSAandHLAclass2pre, dSAandHLAclass1pre, a23,
  a25, a26, a32, a34, a66, b13, b18, b27, b35, b37, b38, b42, b44, b45, b47, b49,
  b50, b51, b52, b53, b54, b55, b56, b57, b58, b59, b61, b62, b63, b7, b71, b73, b75,
  b77, b78, b8, b82, cw17, cw6, cw9, dP10, dP11, dP13, dP14, dP15, dP17, dP18, dP19,
  dP20, dP3, dP4, dP5, dP6, dP9, dQ11, dQ2, dQ4, dQ5, dQ6, dQ7, dQ8, dQ9, dR1, dR10,
  dR103, dR11, dR12, dR13, dR14, dR15, dR16, dR17, dR18, dR4, dR51, dR52, dR53, dR7,
  dR8, dR9, pregnancyhistory, birthhistory, naturalAbortion, artificialAbortion,
  hDperiod, cGN, igA, nS, hypoplastickidney, malignantHypertention, banfi, banf t ,
  banf g , banf v , banfci, banfct, banfcv, banfcg, banfptc, banfptcbm, banfah,
  banfaah, interstitialHemorrhage, cellInvasion, lymphinvasion, thrombusformation,
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coaglationnecrosis, •igA, igM, igG, sABC1q, c3, c4d, c5b, bulbarsclerosis, cRPpreRej,
cRPpostRej, wBCpeakover5, maxCRP, wBCpreRej, wBCpostKTx, wBCpeakover9postRej,
maxWBC, mMFpostRej, mMFatRej, cNIpostRej, graftLoss}, MedianAverage[
{0.0386245 + 0.846161 igG + 0.0864108 inflammationdatefirst respiratoryInfection,
 0.047619 + 0.952381 antiHLAclass2 (b13 + respiratoryInfection + •igA), 0.0294566 +
  0.102799 banfptc cNIpostRej + 0.700582 igG + 0.595647 respiratoryInfection, 0.0183323 +
  0.981668 b45 + 0.473839 dR15 + 0.0898571 inflammationdatefirst respiratoryInfection,
 0.0714286 + 0.928571 b45 + 0.928571 antiHLAclass2 (respiratoryInfection + •igA),
 0.00933915 + 0.377234 cRPpreRej heartDisease + 0.875869 igG +
  0.0860939 inflammationdatefirst respiratoryInfection, 0.0540541 + 0.945946 b45 +
  0.954567 respiratoryInfection - 0.215517 feverOnly hLAmm respiratoryInfection,
 0.0501855 - 0.408121 pyrexia + 0.740964 Sqrt[igG + respiratoryInfection],
 0.0423573 + 0.957643 b45 +
  0.662983 (allergy + antiHLAclass2 + coaglationnecrosis) respiratoryInfection,
 0.0261538 + 0.484615 (b45 + heartDisease + respiratoryInfection) (c4d + type2DM),
 0.03961 + 0.96039 Sqrt[cw9] + 0.845325 igG + 0.086299 inflammationdatefirst
    respiratoryInfection, 0.0714286 + 0.928571 b45 + 0.928571 coaglationnecrosis +
  0.928571 dQ8^2 respiratoryInfection, -0.070139 + 0.169835 cRPpostRej +
  0.584882 respiratoryInfection + 0.0763346 dSAandHLAclass1pre wBCpeakover5^2,
 -0.0815212 + 0.230325 antiHLAclass2 + 0.968762 b13 + 0.140044 cNIpostRej +
  0.652431 respiratoryInfection, 0.0319886 + 0.476686 c3 + 0.108982 cNIpostRej -
  0.382261 pyrexia + 0.773915 respiratoryInfection, -0.0121421 + 0.991371 b45 +
  0.0151127 hDperiod - 0.406121 pyrexia + 0.738206 respiratoryInfection,
 0.0520871 + 0.734346 (c3 + respiratoryInfection) Sqrt[dQ7 + type2DM],
 0.034055 + 1.05955 b45 + 0.1115 cNIpostRej + 0.938582 respiratoryInfection -
  0.619749 pyrexia respiratoryInfection, 0.00990099 + 0.19802 dSAandHSAclass1 +
  0.613861 igG + 0.732673 respiratoryInfection - 0.49505 pyrexia respiratoryInfection,
 0.0515464 + 0.948454 b45 - 0.453608 pyrexia + 0.829897 respiratoryInfection -
  0.881443 enterococcusfaecalis respiratoryInfection,
 -0.0170889 + 0.107137 cNIpostRej + 0.149575 denovoDSA + 0.674084 respiratoryInfection -
  0.460302 pyrexia respiratoryInfection, 0.0436082 + 0.722878 b45 +
  0.467027 igG - 1.87848 cRPpostRej pyrexia + 0.745217 respiratoryInfection,
 0.0207191 - 0.420537 cRPpostRej + 0.154488 cRPpostRej hLAmm - 0.339971 pyrexia +
  0.671579 respiratoryInfection, 0.0321031 + 0.967897 b45 + 0.270728 dR15 +
  0.742922 respiratoryInfection - 0.516684 pyrexia respiratoryInfection,
 -0.0152629 + 0.978578 a34 + 0.781149 antiHLAclass2 igG + 0.537258 respiratoryInfection +
  0.0183426 wBCpeakover5, -0.00202429 + 1.00202 b45 + 0.331984 dR15 +
  0.746964 candida heartDisease + 0.510121 respiratoryInfection,
 0.0629092 + 0.937091 a34 + 0.724466 igG - 0.41974 Sqrt[pyrexia] +
  0.637874 respiratoryInfection, -0.0316737 + 0.00268283 cRPpostRej hLAmm^3 +
  1.1325 respiratoryInfection - 0.0371912 banfi maxWBC respiratoryInfection,
 0.0527375 + 0.947263 b45 - 0.450061 pyrexia + 0.827228 respiratoryInfection +
  0.138538 cNIpostRej hLADRmm staphylococcusaureus,
 0.0455227 + 0.407512 cRPpreRej heartDisease + 0.881272 igG - 0.00964699 maxCRP +
  0.0889581 inflammationdatefirst respiratoryInfection, -3.14018 × 10^-17 + 1. b45 +
  1. banf t igG + 0.333333 respiratoryInfection + 0.666667 dQ8 respiratoryInfection,
 0.0316843 + 1.22285 b45 + 0.695688 cNIpostRej igG + 0.932553 respiratoryInfection -
  0.642825 pyrexia respiratoryInfection, 0.0327787 + 1.05972 b45 + 0.110183 cNIpostRej +
  0.986025 respiratoryInfection - 0.203539 feverOnly hLAmm respiratoryInfection,
 0.0428659 + 0.129718 aerobicGPC banfptc cNIpostRej + 0.732689 igG -
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 0.35344 pyrexia + 0.699841 respiratoryInfection,
-0.0247295 + 0.766924 respiratoryInfection - 0.544973 pyrexia respiratoryInfection +
 0.0200706 wBCpeakover5 + 0.246959 dSAandHLAclass1pre wBCpeakover5,
0.04187 + 1.05644 b45 + 0.117101 cNIpostRej + 0.542785 dQ7 respiratoryInfection +
 0.0642324 inflammationdatefirst respiratoryInfection,
0.00752967 + 0.856936 igG + 0.0890798 respiratoryInfection +
 0.0793806 inflammationdatefirst respiratoryInfection + 0.99247 heartDisease •igA,
-2.19813 × 10^-16 + 1. b45 + 0.333333 respiratoryInfection +
 0.666667 dQ7 respiratoryInfection + 0.666667 surgery •igA,
0.0277778 + 0.972222 b45 + 0.972222 dSAandHLAclass1pre lymphinvasion +
 0.812222 respiratoryInfection - 0.56 pyrexia respiratoryInfection,
-0.0017267 + 1.09953 b45 + 0.116497 cNIpostRej + 0.332016 diarrhea dR53 hLADRmm +
 0.506966 respiratoryInfection, 0.0667386 + 1.10919 b45 + 0.111745 cNIpostRej +
 0.224436 cNIpostRej dQ7 + 0.0947478 inflammationdatefirst respiratoryInfection,
0.00314436 + 0.230783 b45 denovoDSA + 1.10543 respiratoryInfection -
 0.520377 banfi respiratoryInfection + 0.0203774 wBCpeakover5,
0.0957356 + 0.904264 b45 - 0.415752 pyrexia + 0.14593 hDperiod respiratoryInfection +
 0.123495 cNIpostRej surgery, 0.0540541 + 0.945946 b45 + 1.26553 respiratoryInfection -
 0.587629 banfi respiratoryInfection - 0.262887 birthhistory respiratoryInfection,
-0.00487959 + 0.137865 cRPpostRej + 0.614756 igG +
 0.85227 antiHLAclass1 respiratoryInfection + 0.771984 respiratoryInfection type2DM,
0.0309519 + 1.04936 b45 + 0.0956724 cNIpostRej +
 0.913069 (0.0830896 + antiHLAclass2 + coaglationnecrosis) respiratoryInfection,
0.0414329 + 1.03661 b45 + 0.0929635 cNIpostRej +
 0.96926 (b45 + coaglationnecrosis + dQ8) respiratoryInfection,
-0.0195495 + 0.244673 respiratoryInfection + 0.0196082 wBCpeakover5 +
 0.802765 antiHLAclass2 (b45 + respiratoryInfection + •igA), 0.0297991 + 0.709937 b45 +
 0.00788768 cRPpostRej^3 + 0.43284 igG + 0.869517 dQ7 respiratoryInfection,
0.0141712 + 0.11118 cNIpostRej + 0.244221 dSAandHSAclass1 + 0.840791 igG^2 +
 0.0952402 inflammationdatefirst respiratoryInfection, 0.0598289 + 1.02837 b45 +
 0.105059 cNIpostRej + 1.03177 coaglationnecrosis + 0.936351 dQ8^2 respiratoryInfection,
-0.0531389 + 0.157304 cRPpostRej + 0.8932 igG + 0.994314 respiratoryInfection -
 0.249023 banfi^2 respiratoryInfection, -0.0499232 + 0.622529 antiHLAclass1 banfi +
 0.0779311 cNIpostRej + 0.850547 igG + 0.00428319 infectionCount^2, -0.07591 +
 0.0169932 cNIpostRej^2 + 0.252596 (antiHLAclass1 + respiratoryInfection + type2DM)^2,
0.027027 + 0.972973 b45 + 0.252973 respiratoryInfection +
 0.56 (antiHLAclass2 + bTF + interstitialHemorrhage) respiratoryInfection,
0.0604642 + 1.03919 b45 + 0.118704 cNIpostRej - 0.320413 pyrexia +
 4.32239 respiratoryInfection / wBCinUrine, 0.0563376 + 0.94176 a26 + 0.670104 igG +
 0.806883 antiHLAclass2 respiratoryInfection + 0.00047561 wBCpeakover5^2,
-0.0346477 + 0.128421 cNIpostRej + 0.130538 denovoDSA + 0.196768 Sqrt[dSAclass1number] +
 0.0863025 inflammationdatefirst respiratoryInfection, 0.0479384 + 1.04814 b45 +
 0.114448 cNIpostRej + 8.94186 respiratoryInfection / maxWBC - 0.0923429 upperDigestivetract,
0.0293039 + 0.931512 b45 + 0.621008 respiratoryInfection (b18 + dQ9 + type2DM) +
 0.0195922 wBCpeakover5, -0.0217582 + 0.904588 b45 + 0.0380337 cRPpostRej^2 +
 0.495661 respiratoryInfection + 0.51359 dR53 type2DM, 0.0314417 - 0.118482 igG +
 0.465874 (heartDisease + igG + respiratoryInfection) (c4d + type2DM), 0.0711524 +
 1.02626 b45 + 0.116042 cNIpostRej - 0.192344 pyrexia + 1.50389 respiratoryInfection / mMFpostRej,
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0.0474897 + 1.04556 b45 + 0.110835 cNIpostRej - 0.833755 gynecology -
 0.512187 pyrexia + 0.881975 respiratoryInfection, -0.0261993 + 0.116307 cNIpostRej +
 0.157197 denovoDSA + 0.845017 igG - 0.32073 pyrexia + 0.663393 respiratoryInfection,
0.022188 + 0.10607 cNIpostRej + 0.240122 dSAandHSAclass1 + 0.835877 igG -
 0.366787 pyrexia + 0.756135 respiratoryInfection, -0.0977902 + 0.163902 cRPpostRej +
 0.234866 (antiHLAclass1 + dR15 + igG + respiratoryInfection)^2, 0.0460485 + 1.05066 a34 +
 0.102094 cNIpostRej + 0.716647 igG - 0.34778 pyrexia + 0.680237 respiratoryInfection,
-0.00091083 + 1.00091 b45 + 0.773386 candida - 0.656071 dR12 + 0.62788 dR53 +
 0.338647 respiratoryInfection, 0.0429716 + 0.922827 b44 - 0.00195133/hDperiod -
 0.461858 pyrexia + 0.783759 respiratoryInfection + 0.0182303 wBCpeakover5,
0.0659294 + 0.348418 cRPpostRej - 0.186116 feverOnly + 0.581689 igG +
 0.729044 respiratoryInfection - 0.0615758 uTI, 0.0106217 + 0.102653 cNIpostRej +
 0.343362 gERD + 0.968209 igG - 0.449501 pyrexia + 0.765433 respiratoryInfection,
0.0820046 + 0.699797 b44 - 0.00195602/hDperiod + 0.440927 igG - 0.428367 pyrexia +
 0.735711 respiratoryInfection, 0.0237396 + 0.0836221 banfptc cNIpostRej + 0.85404 igG +
 0.797772 respiratoryInfection - 0.302692 aerobicGPC banfptc respiratoryInfection,
-0.00174626 + 0.945387 cellInvasion igG + 0.615057 antiHLAclass2 respiratoryInfection +
 0.0551365 inflammationdatefirst respiratoryInfection +
 0.0187863 wBCpeakover5, -0.0436571 +
 0.129543 hLADRmm (cNIpostRej + denovoDSA + dQ7 + igG + 2 respiratoryInfection),
-0.000641318 + 0.776557 respiratoryInfection - 0.522106 pyrexia respiratoryInfection +
 0.253803 dSAandHLAclass1pre wBCpeakover5 + 0.000508318 wBCpeakover5^2,
0.00690778 + 0.817571 b45 + 0.100961 cRPpostRej + 0.690701 dQ7 respiratoryInfection +
 0.00413708 inflammationdatefirst^2 respiratoryInfection, 0.0441539 +
 0.462058 (coaglationnecrosis + cRPpostRej + dQ7) Sqrt[b62 + igG + respiratoryInfection],
-0.0659972 + 0.764388 b45 + 0.12339 dQ7 hLAABmm + 0.541288 respiratoryInfection +
 0.00518719 cRPpostRej^2 wBCinUrine, 0.0309519 + 1.04936 b45 + 0.0956724 cNIpostRej +
 0.913069 (0.0830896 + antiHLAclass2 + coaglationnecrosis) respiratoryInfection^2,
-0.0199699 + 0.704012 b45 + 0.117231 cNIpostRej + 0.277214 dR7 +
 0.551531 igG + 0.0969292 inflammationdatefirst respiratoryInfection,
0.0202076 + 1.0848 b45 + 0.110852 cNIpostRej + 0.530302 igG +
 0.783471 respiratoryInfection - 0.507277 pyrexia respiratoryInfection,
-0.0685274 + 0.140839 cRPpostRej + 0.167579 dSAandHSAclass1 + 0.84154 igG +
 1.17652 respiratoryInfection - 0.528689 banfi respiratoryInfection,
0.0137918 + 0.949309 b45 - 0.00201454/hDperiod + 0.862527 respiratoryInfection -
 0.632566 pyrexia respiratoryInfection + 0.0196156 wBCpeakover5,
0.00451313 + 0.68146 b45 + 0.628054 igG +
 0.0836558 respiratoryInfection (c4d + igG + inflammationdatefirst + wBCpreRej),
0.0331933 + 1.06507 b45 + 0.11705 cNIpostRej + 0.906253 respiratoryInfection -
 0.056097 banfi^4 respiratoryInfection, 0.032986 + 1.066 b45 + 0.117916 cNIpostRej +
 12.901 respiratoryInfection - 0.859317 (14 + pyrexia) respiratoryInfection,
-0.038208 + 0.147765 antiHLAclass2 + 0.99881 b45 + 0.129086 cNIpostRej -
 1.72197 cRPpostRej pyrexia + 0.822253 respiratoryInfection,
0.0226072 + 0.715165 candida + 0.193768 denovoDSA dR7 + 0.802574 igG -
 0.279183 pyrexia + 0.524456 respiratoryInfection,
-0.00992005 + 1.06491 b45 + 0.130763 cNIpostRej + 0.109566 dQ7 +
 0.286732 dR51 + 0.0926177 inflammationdatefirst respiratoryInfection,
0.0385383 + 0.49955 antiHLAclass1 banfi + 0.095362 cNIpostRej +
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 0.775627 igG - 0.267758 pyrexia + 0.527915 respiratoryInfection,
-0.00152164 + 0.937777 b44 + 0.0974427 hDperiod igG - 0.385033 pyrexia +
 0.692449 respiratoryInfection + 0.0188001 wBCpeakover5, 0.0297991 + 0.709937 b45 +
 0.00788768 cRPpostRej^3 + 0.43284 igG + 0.869517 dQ7 respiratoryInfection^2,
-0.0176024 + 1.12341 b45 + 0.126036 cNIpostRej + 0.254934 dR15 +
 0.166999 dR53 + 0.0960752 inflammationdatefirst respiratoryInfection,
0.0640059 + 1.14047 b45 - 0.0239694 banfah + 0.10656 cNIpostRej +
 0.907627 respiratoryInfection - 1.05087 upperRespiratoryInfection wBCpreRej,
0.0185964 + 0.107461 cNIpostRej + 0.836518 igG + 0.317483 respiratoryInfection +
 0.00523935 inflammationdatefirst^2 respiratoryInfection^2,
-0.0714687 + 0.876863 b45 + 0.150369 dSAclass2 + 0.784794 respiratoryInfection -
 0.58097 pyrexia respiratoryInfection + 0.0221186 wBCpeakover5,
-0.0912313 + 0.296104 antiHLAclass1 + 0.191998 cRPpostRej + 0.701519 igG +
 0.318217 respiratoryInfection + 0.680734 allergy respiratoryInfection,
-0.101846 + 0.353115 igG + 0.228084 (antiHLAclass1 + respiratoryInfection + type2DM)^2 +
 0.0214927 wBCpeakover5, 0.00849362 + 0.830772 b45 + 0.11714 cNIpostRej +
 0.518147 igG + 0.0502691 (7 + inflammationdatefirst) respiratoryInfection,
0.0357499 + 0.836865 b45 + 0.110026 cNIpostRej + 0.439505 igG +
 0.703232 respiratoryInfection - 0.0137384 pyrexia wBCpeakover9postRej,
-0.06767 + 0.901413 b45 + 0.242528 (coaglationnecrosis + dQ7 + respiratoryInfection)^2 +
 0.0224965 wBCpeakover5, -0.0427875 + 0.520996 b45 + 0.162413 cRPpostRej +
 0.478874 igG - 0.285202 feverOnly pyrexia + 0.70142 respiratoryInfection,
-0.0178535 + 0.150203 cRPpostRej - 0.0019662/hDperiod + 0.616334 igG +
 0.774841 respiratoryInfection - 0.532563 pyrexia respiratoryInfection,
0.0698006 + 0.636794 b45 - 0.00726273 pRAclass1pre +
 0.555807 (c3 + respiratoryInfection) (dQ7 + type2DM),
-0.0762541 + 0.227334 antiHLAclass1 + 0.186089 cRPpostRej + 0.653323 igG +
 1.21034 respiratoryInfection - 0.0457655 maxWBC respiratoryInfection,
-0.0149752 + 0.708301 b45 + 0.538704 igG + 1.30825 respiratoryInfection -
 0.0489432 maxWBC respiratoryInfection + 0.0186609 wBCpeakover5,
-0.0316533 + 0.817236 b45 + 0.123334 cRPpostRej + 0.482742 banfg igG - 0.369618 pyrexia +
 0.73426 respiratoryInfection, 0.0207857 + 0.78025 b45 + 0.1014 cNIpostRej +
 0.568179 igG + 0.367708 respiratoryInfection + 0.604308 dQ8 respiratoryInfection,
0.0562085 + 1.03565 b45 + 0.109425 cNIpostRej + 0.668081 dQ11 -
 0.144282 pyrexia + 0.095222 inflammationdatefirst respiratoryInfection,
-0.230491 + 0.437914 coaglationnecrosis + 0.160925 denovoDSA +
 0.857781 aBOI dQ7 + 0.0422824 infectionCount + 0.017742 wBCpeakover5,
-0.0912743 + 0.134773 cNIpostRej + 0.560952 coaglationnecrosis +
 0.272261 (antiHLAclass2 + b44 + respiratoryInfection)^2,
0.0118079 + 1.0184 b45 + 0.112483 cNIpostRej + 0.128448 dR7 +
 0.382715 respiratoryInfection + 0.550008 dQ7 respiratoryInfection,
-0.0162246 + 0.687486 b45 + 0.582753 igG + 0.931684 respiratoryInfection -
 0.243442 banfptc respiratoryInfection + 0.0186811 wBCpeakover5,
0.0190104 + 0.107238 cNIpostRej + 0.38261 dP4 + 0.533415 igG +
 0.783405 respiratoryInfection - 0.507364 pyrexia respiratoryInfection,
-0.0044763 + 0.144026 cRPpostRej + 0.697796 igG - 0.279195 pyrexia +
 0.803934 respiratoryInfection - 0.150043 banfptc upperRespiratoryInfection,
-0.0674773 + 0.211025 cRPpostRej + 0.746951 igG + 0.35178 respiratoryInfection +
 0.614272 allergy (b57 + respiratoryInfection),
0.00903955 + 0.725424 b45 + 0.355932 banfah citobacterdiversus + 0.375141 heartDisease +
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0.531073 igG + 0.279096 respiratoryInfection, 0.00947821 + 0.801232 $\sqrt{\text{b45} + \text{igG}}$ +
0.0649199 (1.41026 + dSAandHLAclass2pre) inflammationdatefirst respiratoryInfection,
0.0425017 + 0.833729 b45 + 0.108362 cNIpostRej + 0.429477 igG − 0.365294 pyrexia^3 +
0.716711 respiratoryInfection, 0.0586016 + 0.725461 b45 − 0.861711 gynecology +
0.431875 igG − 0.600133 $\sqrt{\text{pyrexia}}$ + 0.803109 respiratoryInfection,
0.0283415 + 0.973729 igG + 0.813682 respiratoryInfection −
0.347974 aerobicGPC banfptc respiratoryInfection + $\frac{0.771992\ \text{cNIpostRej}}{\text{wBCinUrine}}$,
0.0129075 + 1.07165 b45 + 0.10072 cNIpostRej + 0.957981 respiratoryInfection −
0.883912 gynecology respiratoryInfection − 0.621356 pyrexia respiratoryInfection,
0.0165451 + 1.29953 b45 + 0.103306 cNIpostRej + 0.626868 cNIpostRej igG +
0.963496 respiratoryInfection − 0.626793 pyrexia respiratoryInfection,
0.0251523 + 0.975921 b45 + 0.0427329 cNIpostRej cRPpreRej +
0.973412 (antiHLAclass2 + coaglationnecrosis + hBV) $\text{respiratoryInfection}^2$,
0.00550686 + 1.08892 b45 + 0.112483 cNIpostRej + 0.248157 dR52 +
0.95361 respiratoryInfection − 0.194732 feverOnly hLAmm respiratoryInfection,
− 0.0577155 + 0.467197 antiHLAclass1 banfi + 0.150216 cRPpostRej + 0.829645 igG +
0.250132 respiratoryInfection + 0.735384 allergy respiratoryInfection, − 0.0189583 +
0.251098 b45 dSAandHSAclass1 + 0.627036 igG + 0.745489 respiratoryInfection −
0.534126 pyrexia respiratoryInfection + 0.019909 wBCpeakover5,
0.0583014 + 0.799788 b45 + 0.110451 cNIpostRej + 0.626941 igG +
0.0994798 inflammationdatefirst respiratoryInfection − 0.0176722 banfci wBCpostKTx,
0.0480376 + 0.951962 b45 − 0.453961 pyrexia + 0.532333 respiratoryInfection +
0.0643909 hDperiod respiratoryInfection + 0.14086 cNIpostRej surgery,
0.0347903 + 1.06604 b45 + 0.120111 cNIpostRej − 0.727931 banfptcbm cNIpostRej +
0.754712 respiratoryInfection − 0.591672 pyrexia respiratoryInfection,
− 0.00502158 − 0.383545 cRPpostRej + 0.131678 cRPpostRej hLAmm + 0.553192 igG +
0.716111 respiratoryInfection − 0.464308 pyrexia respiratoryInfection,
− 0.0633306 + 0.124381 cNIpostRej + 0.0469143 inflammationdatefirst
respiratoryInfection + 0.209349 $(\text{antiHLAclass2} + \text{b63} + \text{respiratoryInfection})^2$,
− 0.0631703 + 0.0104528 hLAmm^2 (cRPpostRej + dR7 + igG) +
0.347124 respiratoryInfection + 0.546933 dQ7 respiratoryInfection,
− 0.00684578 − 0.420701 cRPpostRej + 0.141029 cRPpostRej hLAmm + 0.546494 igG +
0.724931 respiratoryInfection − 0.475359 aerobicGNR respiratoryInfection,
0.0533678 + 0.908402 igG + 0.00716823 $\text{inflammationdatefirst}^2$ respiratoryInfection +
0.889286 gERD (b45 + igG + respiratoryInfection),
− 0.0666121 − 0.0749584 feverOnly hLADRmm^2 + 0.540263 respiratoryInfection +
0.230079 hLADRmm (cRPpostRej + igG + streptococcusaureus),
− 0.00906658 + 0.107375 cNIpostRej + 0.0429387 denovoDSA^2 + 0.901046 igG +
1.06803 respiratoryInfection − 0.450607 banfi respiratoryInfection,
− 0.0197563 + 0.0369495 igG + 0.247065 respiratoryInfection + 0.0195631 wBCpeakover5 +
0.790804 antiHLAclass2 (b45 + respiratoryInfection + •igA),
0.0396384 + 0.770024 b44 + 0.110862 cNIpostRej + 0.566812 igG −
0.201618 polyp^2 + 0.0940564 inflammationdatefirst respiratoryInfection,
− 0.0324234 + 0.0164542 cNIpostRej^2 + 0.0405447 dQ7 + 0.338533 dR7 +
0.750276 igG + 0.0889382 inflammationdatefirst respiratoryInfection,
0.0131826 + 1.08268 b45 + 0.101196 cNIpostRej + 0.41743 respiratoryInfection +
0.429194 antiHLAclass2 (igG + respiratoryInfection + •igA),
0.0285289 + 0.74068 b45 + 0.457662 aBOI dQ7 − 0.348872 pyrexia +
0.647476 respiratoryInfection + 0.000490074 wBCpeakover5^2,

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0.0247895 + 0.558329 b45 + 0.0321517 cRPpostRej^2 + 0.635662 igG -
 0.143541 pyrexia + 0.0888598 inflammationdatefirst respiratoryInfection,
-0.0406508 + 0.482156 b45 + 0.212701 cRPpostRej + 0.377429 igG +
 0.892868 (b45 + coaglationnecrosis + dR53) respiratoryInfection,
0.0601535 - 0.0913062 cNIpostRej + 0.632234 igG - 0.431302 pyrexia +
 0.724302 respiratoryInfection + 0.217717 cNIpostRej surgery^2,
0.048258 - 0.511083 b18 + 0.847384 b44 + 0.11248 cNIpostRej +
 0.999437 respiratoryInfection - 0.245762 banfi^2 respiratoryInfection,
-0.0225054 + 0.861595 b45 + 0.317689 dR7 + 0.127689 respiratoryInfection +
 0.0806424 inflammationdatefirst respiratoryInfection + 0.000516503 wBCpeakover5^2,
0.0493168 + 0.534359 antiHLAclass1 banfi + 0.105643 cNIpostRej - 0.0324884
  hypertention^2 + 0.812885 igG + 0.478081 respiratoryInfection, -0.0370859 + 0.127466
  (-1 + antiHLAclass1 + dR18 + heartDisease + hLADRmm + respiratoryInfection + •igA)^2,
1.81298 - 3.47988/(1.92224 + b45 + candida + 2 igG - polyp + respiratoryInfection),
0.0116825 + 1.08928 b62 + 0.106582 cNIpostRej + 0.118767 dQ7 +
 0.640433 igG - 0.307847 pyrexia + 0.654283 respiratoryInfection,
-0.0500124 + 0.194101 cRPpostRej + 0.261804 gERD + 0.632368 igG -
 0.237767 nS - 0.415239 pyrexia + 0.69204 respiratoryInfection,
0.0109925 + 0.0825153 antiHLAclass2 + 0.932276 b45 - 0.137484 banfci +
 0.116118 cNIpostRej + 0.418363 igG + 0.908534 respiratoryInfection,
-0.00254748 + 0.107649 cNIpostRej + 0.315127 denovoDSA + 0.300562 dR15 -
 0.292441 dSAandHSAclass2 + 0.488859 igG + 0.463417 respiratoryInfection,
-0.0234038 + 0.620113 b45 + 0.128994 cNIpostRej + 0.362765 coaglationnecrosis +
 0.0845162 denovoDSA + 0.431548 igG + 0.523818 respiratoryInfection,
0.182074 - 0.541486 hLADRmm + 0.200922 hLADRmm (cRPpostRej + dR53 + hLADRmm + igG^2) +
 0.514207 respiratoryInfection, -0.0201033 + 0.667161 b45 +
 0.628438 cellInvasion igG + 0.622092 dQ7 respiratoryInfection +
 0.0567437 inflammationdatefirst respiratoryInfection + 0.0193616 wBCpeakover5,
-0.0875204 + 0.161798 cRPpostRej + 0.241002 twinpeak +
 0.562008 (c3 - respiratoryInfection)^2 (c4d + type2DM),
-0.0211666 + 0.0405264 denovoDSA^2 - 1.48242 banfct dP18 + 0.940114 igG +
 1.27594 respiratoryInfection - 0.0469971 maxWBC respiratoryInfection,
0.032459 + 0.104718 cNIpostRej + 0.236395 dSAandHSAclass1 + 0.827748 igG + 0.115243
  inflammationdatefirst respiratoryInfection - 0.183897 banfi respiratoryInfection^2,
0.0479715 + 0.0847348 cNIpostRej + 0.83177 igG - 0.128652 pyrexia + 0.0836213
  inflammationdatefirst respiratoryInfection + 0.677307 dR7 respiratoryInfection^3,
0.0191034 + 0.0999957 cNIpostRej + 0.228277 b61 cRPpostRej^2 + 0.903613 igG +
 0.811055 respiratoryInfection - 0.610231 aerobicGPC respiratoryInfection,
0.0699466 + 0.111621 hLADRmm (-1.5869 + cRPpostRej +
    respiratoryInfection + (dQ7 + respiratoryInfection + type2DM)^2),
-0.0538509 + 0.73893 respiratoryInfection - 0.271408 feverOnly respiratoryInfection^2 +
 0.114383 hLADRmm^2 (cRPpostRej + igG + streptococcusaureus),
0.0516822 + 0.924664 b45 - 0.11408 banfct + 0.109343 cNIpostRej + 0.459054 igG +
 0.851438 respiratoryInfection - 0.535933 pyrexia respiratoryInfection,
0.0387961 + 0.87924 b45 + 0.130703 cNIpostRej - 0.218983 enterococcusfaecalis +
 0.383378 igG + 0.813683 respiratoryInfection - 0.534706 pyrexia rMale,
0.0576075 + 1.05306 b45 + 0.131829 cNIpostRej - 0.231839 enterococcusfaecalis -
 0.39953 pyrexia + 0.782054 respiratoryInfection + 0.791556 antiHLAclass2 •igA,
0.0299695 + 0.818392 b45 + 0.105625 cNIpostRej + 0.480619 igG - 0.331959 polyp +
 1.3345 respiratoryInfection - 0.046466 maxWBC respiratoryInfection,
```

```
-0.280793 + 0.767167 b45 + 0.0629629 hLAmm +
 0.245823 (coaglationnecrosis + dQ7 + respiratoryInfection)^2 + 0.0222092 wBCpeakover5,
-0.0312543 + 0.190069 antiHLAclass1 + 0.618495 b45 + 0.362241 igG +
 1.01141 respiratoryInfection - 0.460411 banfi respiratoryInfection +
 0.0207847 wBCpeakover5, 0.00582248 + 1.01562 b45 + 0.120684 cNIpostRej + 0.159735 dR7 +
 0.627811 pyrexia - 0.57552 banfi pyrexia + 0.825579 respiratoryInfection,
0.0231591 + 1.07387 b45 + 0.11558 cNIpostRej + 0.181898 dR15 - 0.371878 pyrexia +
 0.668775 respiratoryInfection + 0.21717 dR53 respiratoryInfection,
-0.108256 + 0.760352 b45 + 0.0181372 hDperiod + 0.40836 igG + 0.737593
  respiratoryInfection - 0.476556 pyrexia respiratoryInfection + 0.118796 type2DM,
-0.0232497 + 0.111708 cNIpostRej + 0.128974 denovoDSA + 0.0439434 dQ8 + 0.660622 igG +
 0.75179 respiratoryInfection - 0.645329 aerobicGPC upperRespiratoryInfection,
-0.107583 + 0.135388 cRPpostRej + 0.0613714 denovoDSA + 0.236501 dR7 +
 0.0389856 dSAandHLAclass1pre + 0.606467 igG +
 0.0822643 inflammationdatefirst respiratoryInfection,
-0.0698588 + 0.750512 b45 + 0.144727 cRPpostRej - 0.218872 dP13 + 0.135476 dQ7 +
 1.04363 respiratoryInfection - 0.459073 banfi respiratoryInfection,
-0.0108501 + 0.107988 cNIpostRej + 0.116707 denovoDSA + 0.548493 igG + 1.15661
  respiratoryInfection - 0.0440596 maxWBC respiratoryInfection + 0.0301399 sABC1q,
-0.0187353 + 0.733078 b45 + 0.129481 cNIpostRej + 0.105618 denovoDSA + 0.0493893 dQ8 +
 0.767939 respiratoryInfection - 0.492429 aerobicGPC upperRespiratoryInfection,
-0.0132699 + 0.223553 antiHLAclass1 + 0.057057 dQ5 + 0.813092 aBOI igG -
 0.373492 pyrexia + 0.682069 respiratoryInfection + 0.0199579 wBCpeakover5,
0.0126221 + 0.976134 b45 + 0.0156958 cNIpostRej^2 + 0.199342 dR15 -
 0.864407 gynecology - 0.490584 pyrexia + 0.840081 respiratoryInfection,
1.62601 - 3.21584 / (1.9767 + b45 + candida + 3 igG + respiratoryInfection +
    antiHLAclass2 respiratoryInfection), -0.00475347 + 0.12298 cNIpostRej +
 0.261893 (2 b45 + coaglationnecrosis + dR53 + respiratoryInfection)^2,
-0.00354623 + 0.682649 b45 + 0.0726185 cNIpostRej + 0.00124222 cRPpostRej hLAmm^3 +
 1.14526 respiratoryInfection - 0.0353869 banfi maxWBC respiratoryInfection,
-0.00774233 + 0.358883 c3 - 0.0170019 hLAmm + 0.00266779 cRPpostRej hLAmm^3 +
 1.16525 respiratoryInfection - 0.0371994 banfi maxWBC respiratoryInfection,
0.0108479 + 1.07645 b45 + 0.103988 cNIpostRej + 0.833582 respiratoryInfection -
 0.319708 feverOnly respiratoryInfection^3 + 0.0924798 dR18 hDperiod type2DM,
-0.0661788 + 0.0901822 cNIpostRej + 0.00228701 hLAmm^3 + 0.846293 b45 igG +
 1.12618 respiratoryInfection - 0.0353142 banfi maxWBC respiratoryInfection,
-0.0742596 + 0.13046 cRPpostRej + 0.0708083 denovoDSA +
 0.0854955 inflammationdatefirst (b45 + igG + respiratoryInfection) +
 3.32373 cRPpostRej interstitialHemorrhage type2DM,
-0.00644534 + 0.964992 b45 + 0.821178 respiratoryInfection -
 1.62404 pyrexia respiratoryInfection + 0.363201 hLAmm pyrexia respiratoryInfection^2 +
 0.0207266 wBCpeakover5, 0.00294265 + 0.886621 b45 + 0.0358476 cRPpostRej^2 +
 0.243742 (Sqrt[antiHLAclass2] + dQ4 + Sqrt[hDperiod]) respiratoryInfection, -0.0103848 +
 0.747312 b45 + 0.072334 cNIpostRej + 0.615187 igG + 0.724726 dR15 respiratoryInfection +
 0.0857304 inflammationdatefirst respiratoryInfection + 0.0081016 wBCpeakover5,
-0.00546579 + 0.909801 b45 + 0.112743 cNIpostRej + 0.238705 dR15 +
 0.380624 igG + 0.371131 dR53 respiratoryInfection +
 0.0799768 inflammationdatefirst respiratoryInfection,
0.0402808 + 1.0549 b45 + 0.113373 cNIpostRej + 1.10415 respiratoryInfection -
```

$$0.261501\ \text{banfi}^2\ \text{respiratoryInfection} - \frac{0.00214952\ \text{respiratoryInfection}}{\text{hDperiod}},$$

$$0.0411441 + 0.832554\ \text{b45} + 0.109874\ \text{cNIpostRej} + 0.437081\ \text{igG} - 0.0986237\ \text{pyrexia} + 0.417403\ \text{dQ7 respiratoryInfection} + 0.070319\ \text{inflammationdatefirst respiratoryInfection},$$

$$0.0254743 + 1.0585\ \text{b45} + 0.100028\ \text{cNIpostRej} + 0.122893\ \text{dR15} + 0.479663\ \text{cNIpostRej dR51} + 1.08813\ \text{respiratoryInfection} - 0.457682\ \text{banfi respiratoryInfection}, -0.02487 + 1.04896\ \text{b45} - 0.064904\ \text{dQ4} + 0.279508\ \text{dR15} + 0.573484\ \text{dR53 respiratoryInfection} + 0.0668628\ \text{inflammationdatefirst respiratoryInfection} + 0.0204046\ \text{wBCpeakover5},$$

$$-0.00987899 + 1.11851\ \text{b45} + 0.1294\ \text{cNIpostRej} + 0.318805\ \text{dR53} - 0.0762175\ \text{pyrexia} + 0.523556\ \text{bTF respiratoryInfection} + 0.0855926\ \text{inflammationdatefirst respiratoryInfection}, 0.0446098 + 1.05009\ \text{b45} + 0.112805\ \text{cNIpostRej} - 0.109371\ \text{pyrexia} + 0.552211\ \text{dR53 respiratoryInfection} + 0.0768059\ \text{inflammationdatefirst respiratoryInfection} + 0.00721502\ \text{thrombusformation},$$

$$0.0329182 + 1.06048\ \text{b45} + 0.111253\ \text{cNIpostRej} + 0.71171\ \text{coaglationnecrosis} + 0.657368\ \text{respiratoryInfection} + 0.612142\ \text{dQ8 respiratoryInfection} - 0.0238649\ \text{maxWBC respiratoryInfection},$$

$$-0.0402075 + 0.133654\ \text{antiHLAclass1 denovoDSA} + 0.230172\ \text{gERD} + 0.844639\ \text{c3 igG} - 0.421361\ \text{pyrexia} + 0.700234\ \text{respiratoryInfection} + 0.0206382\ \text{wBCpeakover5},$$

$$0.012339 + 1.07473\ \text{b45} + 0.103717\ \text{cNIpostRej} + 0.868989\ \text{c3 dR52} - 0.00152896\ \text{infarctionhemohorrage} + 1.35599\ \text{respiratoryInfection} - 0.0458707\ \text{maxWBC respiratoryInfection},$$

$$0.0282116 + 0.940554\ \text{b45} + 28.661\ \text{igG} - 0.446851\ \text{igG rage} + 0.168665\ \text{respiratoryInfection} + 0.80937\ (\text{dQ7} + \text{pastheart})\ \text{respiratoryInfection},$$

$$0.0403218 + 0.626345\ \text{b13} - 0.438273\ \text{pyrexia} + 0.816063\ \text{respiratoryInfection} + 0.149752\ \text{cNIpostRej}\ (\text{cGN} + \text{surgery})\ (\text{surgery} + \text{type2DM}), 0.000573723 + 0.69105\ \text{b45} + 0.361446\ \text{candida} + 0.499713\ \text{banfah citobacterdiversus} + 0.456971\ \text{heartDisease} + 0.616753\ \text{igG} + 0.999426\ \text{coaglationnecrosis respiratoryInfection},$$

$$0.027191 + 0.682635\ \text{b45} + 0.474559\ \text{candida} + 0.580348\ \text{igG} - 0.267768\ \text{pyrexia} + 0.494749\ \text{respiratoryInfection} + 0.318707\ \text{banfah dQ7 respiratoryInfection},$$

$$-0.0200391 + 0.885726\ \text{b45} + 0.121088\ \text{cNIpostRej} + 0.289313\ \text{coaglationnecrosis} + 0.348691\ \text{dR15} + 0.471932\ \text{igG} + 0.093083\ \text{inflammationdatefirst}\ \sqrt{\text{respiratoryInfection}},$$

$$0.0200091 + 0.787397\ \text{b45} + 0.106674\ \text{cNIpostRej} + 0.564294\ \text{igG}^4 + 1.0347\ \text{respiratoryInfection} - 0.248778\ \text{banfi}^2\ \text{respiratoryInfection},$$

$$0.0278182 - 0.257358\ \text{dP13} + 0.0595145\ \text{dSAandHSAclass1}^2 + 0.827655\ \text{igG} - 0.306819\ \text{pyrexia} + 0.972091\ \text{respiratoryInfection} - 0.200091\ \text{banfptc respiratoryInfection},$$

$$0.0306779 + 0.737475\ \text{b45} - 0.293141\ \text{enterococcusfaecalis} + 0.458564\ \text{igG} - 0.262353\ \text{banfi pyrexia} + 0.776203\ \text{respiratoryInfection} + 0.000641314\ \text{wBCpeakover5}^2,$$

$$-0.00825217 + 0.907631\ \text{b45}^2 + 0.125563\ \text{dR7} - \frac{0.00188393}{\text{hDperiod}} + 0.842921\ \text{respiratoryInfection} - 0.605831\ \text{pyrexia respiratoryInfection} + 0.0200103\ \text{wBCpeakover5},$$

$$-0.00762138 + 0.0946748\ \text{anemia} + 0.0997382\ \text{cNIpostRej} + 0.322998\ \text{igG} + 0.0555628\ (\text{antiHLAclass1} + \text{respiratoryInfection} + \text{type2DM})^4, 0.00564782 + 0.68359\ \text{b63} - 0.641017\ \text{enterobacteraerogenes} + 0.56875\ \text{igG} + 1.08978\ \text{respiratoryInfection} - 0.0852048\ \text{respiratoryInfection uTI} + 0.000505701\ \text{wBCpeakover5}^2,$$

$$-0.049712 + 0.96406\ \text{b45} + 0.0859835\ \text{banfah} + 0.00900176\ \text{aBOI}^2\ \text{pRAclass2pre} - 0.421871\ \text{pyrexia} + 0.698681\ \text{respiratoryInfection} + 0.0213303\ \text{wBCpeakover5},$$

$$-0.0247754 + 0.0595978\ \text{cNIpostRej} + 0.00491479\ \text{cRPpostRej}^3 + 0.122155\ \text{denovoDSA} + 0.881707\ \text{aBOI igG} - 0.318957\ \text{pyrexia} + 0.644977\ \text{respiratoryInfection},$$

$$-0.0201216 + 0.940334\ \text{b45} + 0.0774181\ \text{banfah} - 0.500779\ \text{pyrexia} + 0.828322\ \text{respiratoryInfection} - 0.808201\ \text{gynecology respiratoryInfection}^2 +$$

```
 0.0205392 wBCpeakover5, -0.0637518 + 0.142746 cRPpostRej +
 0.335172 respiratoryInfection + 0.581168 Sqrt[b13 + igG + dQ8 respiratoryInfection],
0.00842473 + 0.647433 b45 + 0.688285 igG + 0.98908 respiratoryInfection -
 0.726642 (b45 + igG + pastanemia + Sqrt[pyrexia]) respiratoryInfection,
0.00995596 + 0.80519 Sqrt[b45 + igG] + 0.281875 (0.244303 + dSAandHLAclass2pre)
   (dQ7 + dSAandHLAclass2pre + inflammationdatefirst) respiratoryInfection,
0.00878099 + 0.761676 b45 + 0.158118 dR15 - 0.00168618/hDperiod + 0.38868 igG -
 0.407374 pyrexia + 0.724331 respiratoryInfection + 0.018578 wBCpeakover5,
-0.0483015 + 0.754636 b45 + 0.137403 banfah - 0.112887 banfct + 0.591429 igG -
 0.451777 pyrexia + 0.765028 respiratoryInfection + 0.0210685 wBCpeakover5,
-0.232852 + 0.691785 b45 + 0.134318 cNIpostRej + 0.0545488 denovoDSA +
 0.201878 dQ7 + 0.180983 hLADRmm - 0.220164 pyrexia + 0.561572 respiratoryInfection,
-0.0550192 + 0.240531 antiHLAclass1 + 0.152932 cRPpostRej + 0.295832 gERD +
 0.636096 igG - 0.178613 pastanemia - 0.330045 pyrexia + 0.574312 respiratoryInfection,
-0.0499691 + 0.384287 b61 + 0.106597 banfah + 0.765183 igG - 0.319526 polyp -
 0.373892 pyrexia + 0.642841 respiratoryInfection + 0.0235021 wBCpeakover5,
2.25555 - 3.79088 / (1.70567 + b45^2 + candida + igG + antiHLAclass2 respiratoryInfection +
    coaglationnecrosis respiratoryInfection),
-0.0822203 + 0.107888 cRPpostRej + 0.84845 b45 dP4 + 0.00910988 hDperiod + 0.704491 igG +
 0.698189 respiratoryInfection - 1.63465 cRPpostRej pyrexia respiratoryInfection,
0.0114663 + 1.01894 b45 + 0.988534 dR7 igG^2 - 0.145587 pyrexia +
 1.1204 respiratoryInfection - 0.392808 banfi respiratoryInfection -
 0.0608061 upperRespiratoryInfection,
0.0156785 + 0.852335 b45 + 0.108063 cNIpostRej + 0.720068 igG - 0.137328 denovoDSA igG +
 0.868196 respiratoryInfection - 0.719023 Sqrt[pyrexia] respiratoryInfection,
-0.0388584 + 0.110859 cNIpostRej + 0.156237 denovoDSA + 1.0892 igG -
 0.288498 denovoDSA igG + 0.740416 respiratoryInfection -
 0.617727 Sqrt[pyrexia] respiratoryInfection, 0.00253675 + 0.0164194 denovoDSA^2 -
 0.0017096/hDperiod + 0.380824 dSAclass1number igG + 0.73909 respiratoryInfection -
 0.546996 pyrexia respiratoryInfection + 0.0190747 wBCpeakover5,
0.0102273 + 0.708531 b45 - 0.197657 dP18 - 0.00190932/hDperiod + 0.488105 igG +
 0.821029 respiratoryInfection - 0.602771 pyrexia respiratoryInfection +
 0.0196998 wBCpeakover5, -0.0479741 + 1.03319 b45 + 0.245907 c3 +
 0.12885 cNIpostRej + 0.38795 coaglationnecrosis + 0.216103 dQ6 +
 0.831192 respiratoryInfection - 0.308827 feverOnly respiratoryInfection, -0.142195 +
 0.0331691 (b45 + c3 + cRPpostRej + dQ7 + dR15 + hLADRmm + 2 respiratoryInfection)^2,
-0.111821 + 0.0252199 aerobicGPC + 0.693739 b45 + 0.105365 cNIpostRej +
 0.694906 igG + 0.0448982 mMFpostRej + 0.859465 respiratoryInfection -
 0.692241 aerobicGPC upperRespiratoryInfection,
-0.019084 + 0.129551 cNIpostRej + 0.115868 respiratoryInfection +
 0.243641 (2 b45 + coaglationnecrosis + dQ6 + respiratoryInfection)^2,
-0.0811309 - 0.157501 aerobicGPC + 0.312524 coaglationnecrosis +
 0.191428 cRPpostRej + 0.153639 Sqrt[dQ7] + 0.131318 dSAandHSAclass1 + 0.54527 igG +
 0.488362 respiratoryInfection, -0.0294546 + 0.989266 b45 + 0.949077 dR15 igG +
 0.625164 respiratoryInfection + 0.00866876 hDperiod^2 respiratoryInfection -
 0.634785 pyrexia respiratoryInfection + 0.0200944 wBCpeakover5,
```

$$-0.0098258 + 0.973829\,\text{b45} - \frac{0.00196524}{\text{hDperiod}} + 0.933516\,\text{dR15}^2\,\text{igG}^2 +$$
$$0.88472\,\text{respiratoryInfection} - 0.630435\,\text{pyrexia respiratoryInfection} +$$
$$0.0191362\,\text{wBCpeakover5},\ -0.00683247 + 0.880796\,\text{b45} + 0.110948\,\text{cNIpostRej} +$$
$$0.504355\,\text{coaglationnecrosis} + 0.153628\,\text{dR15} + 0.438353\,\text{igG} +$$
$$0.17916\,\text{respiratoryInfection} + 0.306999\,\text{dQ7 mMFatRej respiratoryInfection},$$
$$0.0793209 + 0.807157\,\text{b45} + 0.12339\,\text{cNIpostRej} + 0.466367\,\text{igG} +$$
$$1.14713\,\text{respiratoryInfection} - 0.372422\,\text{aerobicGPC respiratoryInfection} -$$
$$0.3499\,\text{feverOnly respiratoryInfection} - 0.0321518\,\text{uTI},$$
$$0.0132293 + 1.30627\,\text{b45} + 0.109989\,\text{cNIpostRej} + 0.292598\,\text{coaglationnecrosis} -$$
$$0.278303\,\text{enterobacteraerogenes} + 0.620898\,\text{cNIpostRej igG} +$$
$$0.918085\,\text{respiratoryInfection} - 0.357039\,\text{feverOnly respiratoryInfection},$$
$$0.00589983 + 0.0601878\,\text{dSAandHSAclass1}^2 + 0.703296\,\text{igG} + 0.737528\,\text{respiratoryInfection} -$$
$$0.747597\,\text{aerobicGNR}\,(\text{anemia} + \text{dSAandHLAclass1pre})\,\text{respiratoryInfection} +$$
$$0.000500349\,\text{wBCpeakover5}^2,\ 0.0161102 - 0.0644628\,\text{anemia} +$$
$$0.488095\,\text{antiHLAclass1 banfi} + 1.08534\,\text{igG} - 0.12845\,\text{denovoDSA igG} -$$
$$0.306402\,\text{pyrexia} + 0.559371\,\text{respiratoryInfection} + 0.0182622\,\text{wBCpeakover5},$$
$$0.0597202 + 0.733449\,\text{b45} - 0.00243833\,\text{banfptc}^4 + 0.413661\,\text{igG} - 0.402172\,\text{pyrexia} +$$
$$0.784865\,\text{respiratoryInfection} + 0.133939\,\text{cNIpostRej surgery}^2,$$
$$0.0154823 + 0.776945\,\text{b45} + 0.114696\,\text{cNIpostRej} + 0.607721\,\text{igG} +$$
$$1.31387\,\text{respiratoryInfection} - 0.343708\,\text{respiratoryInfection}$$
$$(\text{aerobicGPC} + \text{cNIpostRej} + \text{feverOnly} + \text{igG} + \text{respiratoryInfection}),$$
$$0.0211302 + 0.727571\,\text{candida} + 0.693079\,\text{igG} - 0.267146\,\text{pyrexia} + 0.502597$$
$$\text{respiratoryInfection} + 0.177387\,\text{dR7}\,(\text{denovoDSA} + 2\,\text{igG} + \text{respiratoryInfection}),$$
$$0.076169 + 0.47046\,\text{b45} + 0.311061\,\text{antiHLAclass1 banfi} + 0.124732\,\text{cNIpostRej} +$$
$$0.526388\,\text{igG} + 0.941928\,\text{respiratoryInfection} -$$
$$0.200621\,\text{banfi}^2\,\text{respiratoryInfection} - 0.0323454\,\text{uTI},$$
$$0.047187 + 0.469614\,\text{antiHLAclass1 banfi} + 0.101081\,\text{cNIpostRej} - 0.0212122\,\text{hypertention}^2 +$$
$$0.73304\,\text{igG} + 0.691592\,\text{respiratoryInfection} - 0.0425276\,\text{banfi}^4\,\text{respiratoryInfection},$$
$$-0.0513556 + 1.12152\,\text{b45} + 0.163443\,\text{cGN}^2 + 0.0837862\,\text{cMV}^2 +$$
$$0.133482\,\text{cNIpostRej} + 0.161437\,\text{dQ6} + 0.743854\,\text{respiratoryInfection} -$$
$$0.564916\,\text{pyrexia respiratoryInfection}\},\ 0.7]]$$

◆ 6. Comparison Between Predicted values (Red) and Observed ones (Blue) with all Original Dataset using the Optimized Model Created from all 4373 Selected Models in 51 Cross Validations

◆ 7. Classification Performance with Optimized Model

■ Confusion Matrix

	Observed as 1	Observed as 0	Total
Predicted as 1	11	0	11
Predicted as 0	0	40	40
Total	11	40	51

◇1. Sample size: 51 Number of explanatory variables 211

◇ 2. Accuracy(正確度) 100.%

◇ 3. Precision(精度=陽性的中率)
100.%、 Negative Predictive Value(陰性的中率) 100.%

◇ 4. Recall(再現率=感度) 100.%、 Specificity(特異度) 100.%

◇ 5. F1-measure(F1値) 1.、 C-statistic(C統計量) 1. (100. %)

◇6. AUC of ROC curve: 1.

◆ The data in the analysis was exported in the home directory with the following name:
BuildModelOptimizedResultfromLOONo1Date2020714225421.xlsx

◆ **The Raw Result using Optimized Model created from all Selected Models in Leave-One-Out Cross Validation is expressed as TRIPLEBAGOM with {predicted value, rounded value, observed value}.**

◆ 8. Receiver Operating Characteristics Analysis

◆ **ROC curve**

◆ **AUC of ROC curve: 1.**

◆ **Effect of THRESHOLD between positive and negative**

◆ **9. Estimated values and Observed values**

	The 1st case	The 2nd case	The 3rd case	The 4th case	The 5th ca
Predicted	-0.0631753	0.856842	-0.0226995	0.251186	0.0385306
Observed	0	1	0	0	0
Right/Wrong	right	right	right	right	right

◆ **9. Training Data File**
with Predicted values and Observed values

◆ The data in the analysis was exported in the home directory in 2 files with the following names:
{BuildModelAllDataOptimzedModelNo1Date2020714225421.xlsx,
BuildModelAllDataOptimzedModelNo2Date2020714225422.xlsx}

◇ The ANALYZED Training Data with PREDICTED, ROUNDED and OBSERVED Target Values are expressed as ALLJOINEDDATA and ALLJOINEDITEMS.

Starting time: date 2020.7.13 time 20.49.33

Ending time : date 2020.7.14 time 2.25.43

Consumed time for caliculation: 5 hr 36 min 9 sec

◆ The end of the whole analysis

ardata7.xlsx, a dataset for the analysis

In[•]:= **DataIn[]**

The file name: ardata7 Its dimensions: {51, 212}

Out[•]= {{{1, RMale}, {2, Rage}, {3, InfectionCount}, {4, FeverOnly},
{5, Pyrexia}, {6, Inflammation}, {7, VirusInfection}, {8, CMV},
{9, anemia}, {10, HeartDisease}, {11, RespiratoryInfection},
{12, UpperRespiratoryInfection}, {13, UpperDigestivetract}, {14, Diarrhea},
{15, UTI}, {16, WBCinUrine}, {17, WBCpeakover10}, {18, urology},
{19, Skin}, {20, WoundInfection}, {21, HerpesZoster}, {22, Orthopedics},
{23, Ascites}, {24, Surgery}, {25, AerobicGPC}, {26, AerobicGNR},
{27, candida}, {28, staphylococcusaureus}, {29, streptococcusaureus},
{30, enterobacteraerogenes}, {31, enterobactereclacue},
{32, enterococcusfaecalis}, {33, citobacterdiversus}, {34, pseudomonas},
{35, inflammationdatefirst}, {36, infectiondatelast}, {37, asthma},
{38, pastanemia}, {39, infarctionhemohorrage}, {40, calcification},
{41, digestiveorgan}, {42, appendicitis}, {43, polyp}, {44, ulcer},
{45, GERD}, {46, pastheart}, {47, kidney}, {48, pastliverbilialy},
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