CF program

User manual

(for working with RandomForest projects)

Changes:

Date	Chapter	Description
(program version)		
03.02.09		First release version.
(1.27)		
		Predicted values for oob-set compounds can now
		be viewed on the "Forest statistics" tab.
	1	Working with case set files was improved.
		Specified model can be deleted from the model list
27.02.09		(menu FOREST / DELETE FOREST)
(1.28)	6	New chapter was inserted.
		"Options" menu with various settings was added
		to the program.
	4	Loading of multiple models to the same forest list
		are allowed now
18.03.09	1	V randomization procedure was implemented
(1 29)	1	r randomization procedure was implemented.
11.06.00		Possibility of analysis of multi target models was
(2.00)		addad
(2.00)		Lach V (property) can have its own weight at model
		Each Y (property) can have its own weight at model
		Construction process.
		Menu Statistics has been removed.
		Menu "Rebuild forest" has been disabled.
		Visualization of model statistics and details has
		been changed and can be displayed for each Y
		(property) separately.
		Data-files can now contain missing values marked
		as NAN.
25.09.09		RF algorithm speed was significantly boosted
(2.03)		Some interface elements were optimized for
		working with numerous data
05.11.09		Two domain applicability measures were
(2.04)		implemented:
		1) based on variable importance values (in
		descriptor space considering their relative
		importance)
		2) based on each tree prediction (in space of
		models)
21.11.09		Multi-threads calculation was implemented, which
(2.05)		can speed up very intensive calculation steps
10.01.10		Improve statistics calculation.
(2.06)		Found memory leaks were eliminated
· · · · /		Structure of the manual was considerably revised.
		new chapters were added and obsolete ones were
		deleted.

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Important remarks are marked in such style.



Advices are marked in such style.

1. Creation of the first RandomForest project.

1.1. Load data file

To create RandomForest project choose menu FILE / NEW PROJECT / NEW RANDOM FOREST PROJECT

Select a file with source data in the dialog:

- rfd-file, this is own file format of CF program,
- dat-file, this is file format of MDA1 program from HiT-QSAR Software package,

- txt-file, plain text format, descriptors are in columns, cases (compounds) are in rows (see example below). First row and column contain descriptors names and molecules names correspondingly. If some values are missing then they should be represented as NAN textual value or leave empty. Such missed descriptor values automatically replaced with special NAN value. Descriptor values should be numerical only (restriction of the current version) else an error message will be displayed and file will not be opened. (Program does not check all possible errors in txt-file, so be careful and be sure that there are no errors in your data file).

	MTL.txt — Бло	окнот													x
Φ	айл Правка	Формат Вид	Справка												
Ī	H/b	lood H/fat	H/brain	H/liver	H/muscl	e	H/kidne	У	R/fat	R/brain	R/liver	R/muscle	2	R/kid	ne 🔺
mt	1_0001	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	30.08	3.76	
mt	1_0002	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	58.14	4.15	
mt	1_0003	-0.08	1.6	0.34	0.32	-0.16	-0.22	NAN	NAN	NAN	NAN	NAN	72.17	4.25	=
mt	1_0004	0.36	2.02	0.7	0.72	0.7	0.48	NAN	NAN	0.72	0.46	NAN	86.2	4.31	
mt	1_0005	-0.59	1.82	0.45	0.54	NAN	0.15	NAN	NAN	NAN	NAN	NAN	86.2	4.31	
mt	1_0006	0.78	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	86.2	4.31	
mt	1_0007	-0.39	1.94	0.58	0.65	0.46	0.3	NAN	NAN	NAN	NAN	NAN	86.2	4.31	
mt	1_0008	-0.37	2.01	0.64	0.69	0.58	0.4	NAN	NAN	NAN	NAN	NAN	86.2	4.31	
mt	1_0009	0.62	2.59	1.09	1.03	1.1	0.95	2.58	NAN	1.18	0.62	NAN	100.23	4.36	
mt	1_0010	0.11	2.44	1.01	1.03	1.03	0.86	NAN	NAN	NAN	NAN	NAN	100.23	4.36	
mt	1_0011	0.61	2.37	1.22	1.41	0.93	0.91	NAN	NAN	NAN	NAN	NAN	114.26	4.39	
mt	1_0012	NAN	NAN	NAN	NAN	NAN	NAN	2.65	NAN	1.27	0.64	NAN	114.26	4.39	
mt	1_0013	0.2	NAN	NAN	NAN	NAN	NAN	2.47	NAN	2.03	0.52	NAN	114.26	4.39	
mt]_0014	1.7	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	128.29	4.42	
mt	1_0015	1.92	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	142.32	4.45	
mt]_0016	-0.27	0.9	0.15	-0.22	-0.4	-0.4	NAN	NAN	NAN	NAN	NAN	42.09	4.68	
mt	1_0017	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	70.15	4.68	
mt	1_0018	-0.07	2.25	0.86	0.89	0.7	0.67	NAN	NAN	NAN	NAN	NAN	84.18	4.68	
mt	1_0019	0.24	2.42	1.03	1.03	1.02	0.86	2.37	NAN	0.9	0.01	NAN	84.18	4.68	
mt	1_0020	0.61	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	98.21	4.68	
mt	1_0021	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	98.21	4.68	
mt	1_0022	-0.73	0.16	NAN	-0.35	-0.19	NAN	0.31	NAN	-0.24	-0.2	NAN	28.06	4.68	
mt	1_0023	-0.36	NAN	NAN	NAN	NAN	NAN	0.69	NAN	-0.32	-0.26	NAN	42.09	4.68	
mt	1_0024	0.19	NAN	NAN	NAN	NAN	NAN	1.34	-0.37	-0.03	-0.14	-0.04	54.1	5.41	
mt	1_0025	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	68.13	5.24	
mt	1_0026	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	68.13	5.24	
mt	1_0027	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	68.13	5.24	
mt	1_0028	NAN	NAN	NAN	NAN	NAN	NAN	1.86	NAN	0.49	0.31	NAN	68.13	5.24	
mt	1_0029	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	82.16	5.14	
mt	1_0030	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	82.16	5.14	
mt	1_0031	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	94.17	5.54	
mt	1_0032	1.61	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	66.11	6.01	
mt	1_0033	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	1.3	NAN	108.2	5.41	-
•															► a
<u> </u>															

If txt-file has been chosen to create new project following dialog window would be displayed. One should select appropriate settings to load txt-file. If variables (descriptors) names are absent in the first line of the file (uncheck corresponding box) program will give names automatically (Var1, Var2 etc). Analogous procedure will be executed if case names are absent.

🏟 CF		
File Options About		
	 Select delimiter Does the first row contain var names Does the first column contain case names Select a sing-delimiter Delimiter Tabi Space Comma Semicolumn Other 	

After successful loading of source data it will be displayed on "Data" tab.

There is no possibility to edit data.

🏺 CF - D	:\CF_example\MTL.txt									×
File Fo	rest Prediction Options About									
1 🗋 💋	· 🔚 🛯 🛦 🛦 🕾 🖂 🖊									
Lictoff	vente Trance Forest Statistics Va	riabla impo	rtanca (Da	ita						
		nable impo								
				_mtl_00	_mtl_00	_mtl_00	mtl_00	_mtl_00	_mtl_00	<u>mtl_(</u>
		1	2	3	4	5	6	7	8	9 🔺
1	H/blood	NAN	NAN	-0.08	0.36	-0.59	0.78	-0.39	-0.37	0
2	H/fat	NAN	NAN	1.6	2.02	1.82	NAN	1.94	2.01	2
3	H/brain	NAN	NAN	0.34	0.7	0.45	NAN	0.58	0.64	1
4	H/liver	NAN	NAN	0.32	0.72	0.54	NAN	0.65	0.69	1
5	H/muscle	NAN	NAN	-0.16	0.7	NAN	NAN	0.46	0.58	1
6	H/kidney	NAN	NAN	-0.22	0.48	0.15	NAN	0.3	0.4	0
7	R/fat	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	2 ≡
8	R/brain	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	N
9	R/liver	NAN	NAN	NAN	0.72	NAN	NAN	NAN	NAN	1
10	R/muscle	NAN	NAN	NAN	0.46	NAN	NAN	NAN	NAN	0
11	R/kidney	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	N
12	MW	30.08	58.14	72.17	86.2	86.2	86.2	86.2	86.2	1
13	AMW	3.76	4.15	4.25	4.31	4.31	4.31	4.31	4.31	4
14	Sv	3.79	6.99	8.59	10.18	10.18	10.18	10.18	10.18	1:
15	Se	7.66	13.44	16.33	19.21	19.21	19.21	19.21	19.21	2
16	Sp	4.27	7.79	9.55	11.31	11.31	11.31	11.31	11.31	1
17	Ss	4	7	8.5	10	10.75	10.67	10.33	10.33	1:
18	Mv	0.47	0.5	0.51	0.51	0.51	0.51	0.51	0.51	0
19	Me	0.96	0.96	0.96	0.96	0.96	0.96	0.96	0.96	0
20	Мр	0.53	0.56	0.56	0.57	0.57	0.57	0.57	0.57	0
21	Ms	2	1.75	1.7	1.67	1.79	1.78	1.72	1.72	1
22	nAT	8	14	17	20	20	20	20	20	2
23	nSK	2	4	5	6	6	6	6	6	7
24	nBT	7	13	16	19	19	19	19	19	2 -
 ■ 	·									•
									_	

1.2. Build RF model

1.2.1. Variables tab

To grow forest (build model) choose menu FOREST / GROW FOREST.

🏺 CF - I	D:\CF_example		rowth options			-	×	D		23
File F	orest Predict	· nee g								
10 2	> 🔲 🛛 🛋	Variables	Cases Forest							
] 🛄 🖛		#	Variable name	Set	Туре	_	Set	UH.		
Listof	forests Trees	1	H/blood	Х	Continious		I			
		2	H/fat	Х	Continious		Y	0	. mtl_00	mtl_
		3	H/brain	Х	Continious		×		8	9 🔺
1	H/blood	4	H/liver	Х	Continious				-0.37	0
2	H/fat	5	H/muscle	Х	Continious		Excluded (-)		2.01	2
3	H/brain	6	H/kidney	Х	Continious				0.64	1
4	H/liver	7	R/fat	Х	Continious				0.69	1
5	H/muscle	8	R/brain	Х	Continious	=	Select by names		0.58	1
6	H/kidney	9	R/liver	Х	Continious				0.4	0
7	R/fat	10	R/muscle	Х	Continious		Truce		NAN	2 =
8	R/brain	11	R/kidney	Х	Continious		туре		NAN	N
9	R/liver	12	MW	Х	Continious		Continious		NAN	1
10	R/muscle	13	AMW	Х	Continious				NAN	0
11	R/kidney	14	Sv	Х	Continious		Rank		NAN	N
12	MW	15	Se	Х	Continious		blowing		86.2	1
13	AMW	16	Sp	Х	Continious		Nominai		4.31	4
14	Sv	17	Ss	Х	Continious				10.18	1
15	Se	18	Mv	Х	Continious				19.21	2
16	Sp	19	Ме	Х	Continious		Y weights		11.31	1
17	Ss	20	Мр	Х	Continious				10.33	1
18	Mv	21	Ms	Х	Continious				0.51	0
19	Me	22	nAT	Х	Continious				0.96	0
20	Мр	23	nSK	Х	Continious				0.57	0
21	Ms	24	nBT	Х	Continious				1.72	1
22	nAT	25	nBO	Х	Continious	Ŧ			20	2
23	nSK			·····					6	7
24	nBT								19	2 -
<	11				ж		Cancel			- P-

The following window will appear. Select variables which will be used for model construction on "Variables" tab. Variables can be dependent (Y, several Y's are allowed), independent (X) and excluded (which will not take part in model construction). Also variables type should be chosen. Y variable can possess all three types (but each Y should have identical variable type), X variables can be continuous type only (restriction of the current program version). To do these operation simply select variable(s) in the list and click on the appropriate button.



Buttons Y, X and Excluded have keyboard shortcuts - y, x and space correspondingly.

One can select variables in the list by its names. Click on the "Select by names" button and input variables names (one variable name per line).

🏺 CF - I	D:\CF_example				D		23
File Fo	orest Predict	👳 Tree gi	rowth op	lions			
		Variables	Cases	Forest			
] 🛄 🔤		#	Variabl	e name Set Turne Set			
List of f	forests Trees	1	H/bloo	d X Continious			
		2	H/fat	Y	0	mtl 00	mtl (
		3	H/br	Select by names		8	9 🔺
1	H/blood	4	НЛім	Input names. Each name on the separate line		-0.37	0
2	H/fat	5	H/mu	Excluded (-)		2.01	2
3	H/brain	6	H/kic	My A	I	0.64	1
4	H/liver	7	R/fat			0.69	1
5	H/muscle	8	R/br	elect by names		0.58	1
6	H/kidney	9	R/live			0.4	0
7	R/fat	10	R/mu			NAN	2 ≡
8	R/brain	11	R/kic	ype		NAN	N
9	R/liver	12	MVV	Continious		NAN	1
10	R/muscle	13	AMV			NAN	0
11	R/kidney	14	Sv	Rank		NAN	N
12	MW	15	Se	Nominal		86.2	1
13	AMW	16	Sp	Teomina		4.31	4
14	Sv	17	Ss		<u> </u>	10.18	1:
15	Se	18	M⊻			19.21	2
16	Sp	19	Me	Y weights		11.31	1
17	Ss	20	Мр	*		10.33	1:
18	Mv	21	Ms			0.51	0
19	Me	22	nAT	OK		0.96	0
20	Mp	23	nSK			0.57	0
21	Ms	24	nBT	A Contanious		1.72	1
22	nAT	25	nBO	X Continious 🚽		20	2
23	nSK				J	6	7
24	nBT			OK Capael		19	2 -
				Caliber			
					9		11

After button OK clicked specified variables would be selected (and you can set all of them as excluded for example).

🏺 CF - I	D:\CF_example		muth entires	-		_	_	×	h		×
File Fo	orest Predict	🚽 nee g	rowin options								
	•	Variables	Cases Forest								
		±	Variable name		Set	Tune		Set			
List of f	forests Trees	1	H/blood		X	Continious					
		2	H/fat		х	Continious		Υ	0	. mtl_00	mtl_(
		3	H/brain		х	Continious		v l		8	9 🔺
1	H/blood	4	H/liver		х	Continious				-0.37	0
2	H/fat	5	H/muscle		х	Continious		Excluded (-)		2.01	2
3	H/brain	6	H/kidney		х	Continious				0.64	1
4	H/liver	7	R/fat		х	Continious				0.69	1
5	H/muscle	8	R/brain		х	Continious	Ξ	Select by names		0.58	1
6	H/kidney	9	R/liver		х	Continious				0.4	0
7	R/fat	10	R/muscle		х	Continious		Tune		NAN	2 ≡
8	R/brain	11	R/kidney		х	Continious		туре		NAN	N
9	R/liver	12	MW		х	Continious		Continious		NAN	1
10	R/muscle	13	AMW		х	Continious				NAN	0
11	R/kidney	14	Sv		X	Continious		Rank		NAN	N
12	MW	15	Se		х	Continious		Nominal		86.2	1
13	AMW	16	Sp		х	Continious				4.31	4
14	Sv	17	Ss		х	Continious				10.18	1.
15	Se	18	Mv		X	Continious				19.21	2
16	Sp	19	Me		Х	Continious		Y weights		11.31	1
17	Ss	20	Мр		х	Continious				10.33	1
18	Mv	21	Ms		Х	Continious				0.51	0
19	Me	22	nAT		Х	Continious				0.96	0
20	Мр	23	nSK		х	Continious				0.57	0
21	Ms	24	nBT		х	Continious				1.72	1
22	nAT	25	nBO		х	Continious	Ŧ			20	2
23	nSK									6	7
24	n⊎1′				0	K		Cancel		19	2 -
								Carloon			'
					_		_				11

If you choose several Y's then "Y weights..." button will be enabled and weights for each Y (property) will be able to be assigned. All positive numbers are allowed.

							57			-
File Forest Predi	t 🏺 Tree g	rowth options								
	Variables	Cases Fores	st							
	1 +	Voriable name		Set	Tupo		Set			
List of forests Tre	* 1	Hiblood	8	V	Continious		Sei			
	2	H/fat		Ý	Continious	Ē	Y	0	mtl 00	mtl (
	3	H/brain		Ý	Continious				8	9 🔺
1 H/blood	4	Hiver		Ý	Continious		X		-0.37	0
2 H/fat	5	H/muscle		Ý	Continious		Excluded (-)		2.01	2
3 H/brain	6	Hikdney		Y	Continious				0.64	1
4 H/liver	7	R/fat	Properties weights						0.69	1
5 H/muscle	8	R/brain	Property Weight			=	Select by names		0.58	1
6 H/kidney	9	R/liver	H/blood 1		<u>n</u>				0.4	Ō
7 R/fat	10	R/muscle							NAN	2 ≡
8 R/brain	11	R/kidney					Туре		NAN	N
9 R/liver	12	MW	H/brain I				Continious		NAN	1
10 R/muscle	13	AMW	H/liver I						NAN	0
11 R/kidney	14	Sv	H/muscle 1				Rank		NAN	N
12 MW	15	Se	H/kidney 1			۳			86.2	1
13 AMW	16	Sp	R/fat 1				Nominal		4.31	4
14 Sv	17	Ss	R/brain 1		-				10.18	1
15 Se	18	Mv	ОК						19.21	2
16 Sp	19	Ме					V weights		11.31	1
17 Ss	20	Мр		Х	Continious		r noighto		10.33	1.
18 Mv	21	Ms		х	Continious				0.51	0
19 Me	22	nAT		х	Continious				0.96	0
20 Mp	23	nSK		х	Continious				0.57	0
21 Ms		nBT		х	Continious				1.72	1
22 nAT		nBO		х	Continious	-			20	2
23 nSK									6	7
24 nBT									19	2 -
					ок		Cancel			•
						_				4

1.2.2. Cases tab

Select appropriate set of each case (compound) on the "Cases" tab. Possible values are training (working) set, test set or excluded set.

🏺 CF - D	:\CF_example		a		×	
File Fo	orest Predict	👳 Tree gro	owth options			
100		Variables	Cases Forest			
		#	Variable name	Set	Set	
List of fe	orests Trees	1	mtl_0001	ws 4	· Tasisis a du X	
		2	mtl_0002	ws		0 mtl_00 mtl_(
		3	mtl_0003	ws	test set	8 9 🔺
1	H/blood	4	mtl_0004	ws		-0.37 0
2	H/fat	5	mtl_0005	WS	External test (t)	2.01 2
3	H/brain	6	mtl_0006	WS	Excluded (-)	0.64 1
4	H/liver	7	mtl_0007	WS		0.69 1
5	H/muscle	8	mtl_0008	WS	Internal test	0.58 1
6	H/kidney	9	mtl_0009	WS		0.4 0
7	R/fat	10	mtl_0010	WS		NAN 2
8	R/brain	11	mtl_0011	WS	Select by names	NAN N
9	R/liver	12	mtl_0012	WS		NAN 1
10	R/muscle	13	mtl_0013	WS		NAN 0
11	R/kidney	14	mtl_0014	WS	Landard	NAN N
12	MVV	15	mtl_0015	WS	Load set	664ws 339ts 110ts2.rfs
13	AMW	16	mtl_0016	WS	Save set	dr amar ifr
14	Sv	17	mtl_0017	WS		di_anesins
15	Se	18	mtl_0018	WS	ws count = 199	278ws_69ts_random.rfs
16	Sp	19	mtl_0019	WS	ts count = 0	alpha1a.rfs
17	Ss	20	mtl_0020	ws	exc count = 0	4361ws_2181ts.rfs
18	Mv	21	mtl_0021	ws	tsint count = 0	dragon 4361ws 2181ts.rfs
19	Me	22	mtl_0022	ws		-11 224-4
20	Mp	23	mtl_0023	ws		all_32ts.ms
21	Ms	24	mtl_0024	ws ,	Class weights	all_28ts.rfs
22	nAT	, EL OCADUA				1.rfs
23	nSK	F:\QSAK\A	Apna-1A\Project\Models\alpha1a.ifs			all.rfs
24	nBT			OK	Canaal	
	-					►

The program allows to define up to 10 separate test sets. To set a case to the wanted test set (second for example) one should specify corresponding number in "test set number" field (in our case it is 2) and then select the case and click "External test" button.

Buttons Training, External test и Excluded have keyboard shortcuts – w, t and space correspondingly.

It is possible to load and save case sets. Case sets saves simultaneously in two formats:

- rfs, internal format of CF program (it supports multiple test sets);
- wsf, format of MDA1 program from HiT-QSAR Software package for backward compatibility purpose (it supports only one test set, all test sets (if more than one) are saved as one entire test set).

Program keeps 10 latest loaded and saved set-files. To view list of them click by right mouse button on "Load set..." button. Latest used files will be on the top of the list.

Full path to selected set file in popup menu are displayed in the status bar just under the list of cases. If opened set file was not find in its location the respective message would be appeared in the status bar.

Statistics of compound numbers in each set are displayed below:

- ws number of compounds in the training set;
- ts number of compounds in all test sets;
- exc number of compounds in the excluded set.

If one Y variable selected and it has ranked or nominal type ("Variables" tab) then button "Class weights..." will be enabled. Click it and following window will appear where one can define weights of each compound class. Case weights can be integers only. This window is analogous to previously described "Y weights..." dialog from "Variable" tab.

It is recommended to leave all values equal to 1 because testing of this option is in progress now.

Function of "Select by names" button is absolutely analogous to the same button on "Variables" tab.

1.2.3. Forest tab

Model building settings are defined on "Forest" tab.

🏺 CF - D:\CF_example	Tree growth options		1 23
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🗋 🥟 🖬 🌆	Variables Cases Forest		
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	Ordinary mode		1
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4	. 1 1 1	8	9 1
		-0.37	
2 Нлат		2.01	
3 H/brain		0.64	1
4 H/liver		0.69	1
5 H/muscle		0.58	1
b H/kidney		0.4	
/ R/fat	Preset mode (statistics only)	NAN	2 -
8 R/brain	Number of forests	NAN	N
9 R/liver	. of each type 📃 🔽 trees in each forest variables in each forest	NAN	1
10 R/muscle		NAN	U
11 R/kidney		NAN	N
12 MVV		86.2	1
13 AMVV	- Browse	4.31	4
14 SV		10.18	1.
15 Se	v v	19.21	2
16 Sp		11.31	1
17 Ss	OOB set mode (global option) Y randomization	10.33	1.
18 Mv	🗌 🕞 Bootstran (classical)	0.51	0
19 Me		0.96	0
20 Mp	67 🚖	0.57	0
21 Ms	. C o training / oob 100	1.72	1
22 nAT	. 67% / 33%	20	2
23 nSK		6	7
24 nBT	Old Consol	19	2 -
			•
	1		1

Here "Ordinary mode" » is described only. "Preset mode" will be described below in a separate chapter.

It should be input in the table:

- Trees - the number of trees in the Random Forest model;

- Vars – the number of variables (descriptors) which will be used for splitting in each node of trees. If one input this value which will be greater then available descriptors number this value will be reduced automatically at the calculation step.

- **Min parent** and **Min child** – it is a minimum number of cases (compounds) in the parent or child nodes. It can not be greater then 1/3 from the number of training set compounds. Otherwise warning message will appear and this model will not be constructed.

In the original algorithm there are no such restriction parameters. All trees are growing for their maximum size. So we recommend to use 1 as a value of "Min child" and "Min parent" fields for classification tasks. For regression task to greater numbers can be assigned for these values to increase calculation speed (for example Min parent = 5), usually it has no influence on model quality

- Models – it is the number of models which will be constructed according to specified settings.

When all fields in one row are filled with non-zero values another row is appeared. This new row one can fill with new settings. Thus a queue (package) of tasks is formed. Press Ctrl+Del to delete selected row in the table.



In the case of very big datasets (thousands of cases and variables) models construction consumes considerable memory size. So be careful when you choose forest growth settings. And be sure that you have enough memory to complete all your needed operations.

A method of training set formation of each tree is specified in the **OOB set mode options** dialog:

- **Bootstrap** – it as a classical mode of formation of training and out-of-bag sets for each tree construction (with replacement).

- Custom – user can specify parts of cases of training and out-of-bag sets (without replacement).



Experience is shown that models which constructed in the second (custom) mode have not appreciable changes in their quality. In addition there is only little difference in model construction time. So we recommend to choose the first (classical) mode (bootstrap).

Each model can be constructed with randomized Y values (**Y randomization**). To define part of Y values which will be shuffled at model building one should check "**Mix**" field and choose corresponding value from the range 0-100. If 100% value was chosen it would be Y scrambling procedure. This procedure is used to prove that obtained model isn't random.

1.2.4. Possible warning messages

After OK button is pressed, if there are descriptors with constant and/or missing values among X's then a list with those descriptors names will be appeared in separate windows. All these descriptors will be removed from the model construction process.

🏺 CF - I	D:\CF_example\MTL.txt									23
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		🏺 frmDelete	dItems				6	7	8	9 🔺
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3	H/brain						NAN	0.58	0.64	1
4	H/liver	nl				*	NAN	0.65	0.69	1
5	H/muscle	nP					NAN	0.46	0.58	1
6	H/kidney						NAN	0.3	0.4	0
7	R/fat						NAN	NAN	NAN	2 =
8	R/brain						NAN	NAN	NAN	N
9	R/liver						NAN	NAN	NAN	1
10	R/muscle						NAN	NAN	NAN	0
11	R/kidney						NAN	NAN	NAN	N
12	MVV						86.2	86.2	86.2	1
13	AMW						4.31	4.31	4.31	4
14	Sv						10.18	10.18	10.18	1
15	Se						19.21	19.21	19.21	2
16	Sp						11.31	11.31	11.31	1
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20	Мр						0.57	0.57	0.57	0
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22	nAT	8	14	17	20	20	20	20	20	2
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3	H/brain	and will t	be excluded I	rom training	set			0.58	0.64	1	Ш
4	H/liver		4					0.65	0.69	1	Ш
5	H/muscle	mti_000	2				Â	0.46	0.58	1	
6	H/kidney	mt[_001	7					0.3	0.4	0	
7	R/fat	mtl_002	1					NAN	NAN	2	2
8	R/brain	mtl 002	6				Ξ	NAN	NAN	N	Ш
9	R/liver	mt[_002	7					NAN	NAN	1	Ш
10	R/muscle	mtL_002	9 N	NAN	NAN	0	Ш				
11	R/kidney	mt_003	1	NAN	NAN	N	Ш				
12	MVV	mt[_003	9					86.2	86.2	1	Ш
13	AMVV	mtl_004	U 1					4.31	4.31	4 –	4
14	Sv	mtl_009	4					10.18	10.18	1.	
15	Se	mtl_009	7					19.21	19.21	2	
16	Sp	mtl 010	o 0					11.31	11.31	1	
17	Ss	mt[_010	3				-	10.33	10.33	1	
18	Mv			2				0.51	0.51	0	
19	Me			0	K			0.96	0.96	0	
20	Мр							0.57	0.57	0	
21	Ms	2	1.75	1.7	1.67	1.79	1.78	1.72	1.72	1	
22	nAT	8	14	17	20	20	20	20	20	2	
23	nSK	2	4	5	6	6	6	6	6	7	
24	nBT	7	13	16	19	19	19	19	19	2	-
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Progress of model construction is displayed in the bottom of main window. After that statistics of obtained model is calculated for each case set.

2. View model results

2.1. General statistics

General obtained results can be looked on Forest list tab. Statistics for each property are displayed.

Ist of forests Trees Forest Statistics Variable importance Data Trees count Vars count Min parent Min child Property Risk estimate (ws) Risk estimate (oob) R2 (ws) R2 (oob) 100 31 1	Image: Second statistic s	Forest Prediction Options About Image: Statistics Variable importance Data Trees count Vars count Min parent Min child Property Risk estimate (ws) Risk estimate (oob) R2 (ws) R2 (oob) 100 31 1 1 Holood 0.4999 0.673 0.828 0.523 H/rat 0.1463 0.2588 0.915 0.458 H/rat 0.1463 0.2581 0.889 0.138 H/rat 0.1174 0.2681 0.889 0.138 H/rat 0.2067 0.4208 0.888 0.504 H/kidney 0.2076 0.4457 0.892 0.52 R/rat 0.2348 0.3152 0.888 0.514 River 0.2099 0.4398 0.852 0.528 R/rat 0.2348 0.3152 0.888 0.514 R/ratin 0.2148 0.3969 0.834 0.315 R/ratin 0.2148 0.3926 0.528 0.528 R/ratin 0.2032 0.4561<	CF	- D:\CF_examp	le\MTL.txt							
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R/brain 0.2148 0.3969 0.834 0.315 R/liver 0.299 0.4398 0.852 0.528	R/brain0.21480.39690.8340.315R/liver0.2990.43980.8520.528R/muscle0.30320.45610.8640.563R/kidney0.09390.24450.9330.573	R/brain 0.2148 0.3969 0.834 0.315 R/liver 0.299 0.4398 0.852 0.528 R/muscle 0.3032 0.4561 0.864 0.563 R/kidney 0.0939 0.2445 0.933 0.573						R/fat	0.2348	0.3152	0.888	0.514
R/liver 0.299 0.4398 0.852 0.528	R/liver0.2990.43980.8520.528R/muscle0.30320.45610.8640.563R/kidney0.09390.24450.9330.573	R/iver 0.299 0.4398 0.852 0.528 R/iver 0.3032 0.4561 0.864 0.563 R/kidney 0.0939 0.2445 0.933 0.573						R/brain	0.2148	0.3969	0.834	0.315
	R/muscle 0.3032 0.4561 0.864 0.563 R/kidney 0.0939 0.2445 0.933 0.573	R/muscle 0.3032 0.4561 0.864 0.563 R/kidney 0.0939 0.2445 0.933 0.573						R/liver	0.299	0.4398	0.852	0.528
R/muscle 0.3032 0.4561 0.864 0.563	R/kidney 0.0939 0.2445 0.933 0.573	Rıkidney 0.0939 0.2445 0.933 0.573						R/muscle	0.3032	0.4561	0.864	0.563
R/kidney 0.0939 0.2445 0.933 0.573								R/kidney	0.0939	0.2445	0.933	0.573

All data from this table can be copied by right mouse button click. A case set is shown into the brackets after the value name in the column caption (**ws**-training set, **oob**-out-of-bag set, **ts**-first test set, **ts2**-second test set and so on).

Risk estimate value is a **misclassification error** for classification models and **mean square error** for regression ones. Values of **coefficients of determination** (R2) are calculated only for regression models. R^2 for out-of-bag (OOB) and test sets are calculated by the formula 1-PRESS/SS.

New obtaining models are added to the end of the models list until the list will not be cleared. To clear the models list choose menu FOREST / CLEAR FOREST LIST. To delete selected model from the list choose menu FOREST / DELETE FOREST

2.2. View single trees composing RF model

To do that select model in the list by left-click and switch to Trees tab. Each tree in the list can be selected and viewed. Due to of a little importance of such information only general information is displayed.



2.3. Detailed statistics and results

To do that make double click on the model in the list or select model in the list by left-click and switch to Forest Statistics tab.

The following information are displayed:

- 1) compound name
- 2) set to which compound belongs
- 3) observed values of investigated properties
- 4) predicted values of investigated properties
 - for regression models it is a mean of all single tree predictions;
 - for classification models it is a class having majority of votes (one tree-one vote).

5) is compound inside (sing "+") or outside (sing "-") of domain of applicability (several domain of applicability measures were implemented and will discussed separately)

Additional regression model specific information:

1) standard deviation (StdDev) – it is calculated from set of predicted values by each tree

Additional classification model specific information:

- 1) number of each class predictions (in separate columns)
- 2) misclassification matrix (on the bottom of the window)

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List of	forests Trees F	Forest S	Statistics Variable	importance Data]				
Proper	ty all		▼ Set all		 DA in sigma uni 	its 3 Rec:	alc		
#	Compound name	Set	Observed (H/blo	Predicted (H/bloo	Pred. StdDev (H/blood)	Observed (H/f	Predicted (H/f	Pred. StdDev	7 (H/I
	mtl_0011	oob	0.61	0.875	0.58	2.37	2.386	0.505	
	mtl_0101	oob	-1.099	0.42	0.267	-	1.753	0.475	
	mtl_0102	doo	-0.249	0.284	0.24	-	1.71	0.417	
	mtl_0104	doo	0.87	0.652	0.663	-	2.164	0.622	
	mtl_0106	doo	-0.359	0.432	0.488	-	1.913	0.478	
	mtl_0107	oob	-0.589	0.564	0.586	-	1.976	0.647	
	mtl_0108	oob	-1.519	0.544	0.45	-	1.994	0.503	
	mtl_0012	oob	-	0.898	0.559	-	2.455	0.473	
	mtl_0117	oob	-	0.329	0.339	-	1.434	0.559	
	mtl_0118	oob	-	0.231	0.258	-	1.471	0.575	
	mtl_0119	doo	-	0.678	0.42	-	1.941	0.578	
	mtl_0120	doo	-0.079	0.421	0.343	-	1.834	0.484	Ψ.
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There is a possibility to filter results by property and/or set. Selecting certain property from the list allows to see detailed model property corresponding specified property (see figure below).

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List of f	forests Trees	Forest S	Statistics Variat	ole importance 🛛	Data				
Proper	ty H/blood		▼ Set al	I	▼ DA in	sigma units	s 3	Recalc	
#	Compound name	Set	Observed (H/blo	Predicted (H/k	olo Pred. StdDe	v (H/blo			
	mtl_0011	doo	0.61	0.875	0.58				
	mtl_0101	oob	-1.099	0.42	0.267				
	mtl_0102	oob	-0.249	0.284	0.24				
	mtl_0104	doo	0.87	0.652	0.663				
	mtl_0106	oob	-0.359	0.432	0.488				
	mtl_0107	oob	-0.589	0.564	0.586				
	mtl_0108	oob	-1.519	0.544	0.45				
	mtl_0012	oob	-	0.898	0.559				
	mtl_0117	oob	-	0.329	0.339				
	mtl_0118	oob	-	0.231	0.258				
	mtl_0119	oob	-	0.678	0.42				
	mtl_0120	oob	-0.079	0.421	0.343				
I	mtl 0013	oob	0.2	0.833	0.566				Ψ.
Set			-			WS	OOB		
	,				R2	0.838	0.757		
					R2 test	0.645	0.534		
					MSE	0.501	0.657		
<u> </u>					RMSE	0.708	0.811		
<u> </u>									
<u> </u>									

For regression models following measures are calculated:

1) R² – determination coefficient (reliable for training set only)

2) R²test – coefficient is calculated as 1-PRESS/SS (reliable for OOB, test and external sets)

3) MSE – mean standard error

4) RMSE - root mean square error

For classification models following measures are calculated:

1) Misclassification error – ratio of number of erroneous predictions to the whole number of predictions

When domain of applicability was calculated corresponding values based on set of compounds inside of domain of applicability are displayed.

3. Model (forest) routines.

Unlimited number of trees can be added to the selected forest. To make this choose menu FOREST / ADD TREES TO FOREST and specify the desired number of trees.

3.1. Variable importance calculation

To calculate variable importances choose menu FOREST / CALC VAR IMPORTANCE.

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File	Forest Pre	ediction	Option	ns About							
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Listo	of forests	Frees	Forest S	tatistics V	ariable impor	tance Data					
#	Trees cour	nt Van	rs count	Min parent	Min child	Property	Risk estimate (ws)	Risk estimate (oob)	R2 (ws)	R2 (oob)	
-	100	31		1	1						
						H/blood	0.5011	0.657	0.838	0.534	
						H/fat	0.1244	0.2528	0.921	0.471	
						H/brain	0.1841	0.4506	0.901	0.431	
						HЛiver	0.1038	0.2544	0.921	0.181	
				6		H/muscle	0.218	0.4944	0.894	0.417	
				- V	ariable impor	tance calculatio	on options		0.898	0.411	
				S	elect calculatio	n type(s)			0.895	0.543	
					Sum coefficie	ents for each des	croptor		0.845	0.293	
									0.855	0.519	
					 Permutation (mode num	ber of iterations = 1	Ξ	0.873	0.557	
									0.928	0.444	
						OK					
					_						

User has to define calculation type of variable importances (selection of both simultaneously are allowed).

Sum coefficients for each descriptor – it is a very fast and very rough estimate (temporarily disabled).

> We do not recommend to choose this mode due to very low adequacy of obtaining results. Due to this option is disabled now.

Permutation mode – it is a more time-consuming process (especially for very large sets of compounds). But obtaining results are highly adequate. This calculation based on estimation of influence of randomization of each descriptor values on out-of-bag prediction ability of the forest. The greater statistic values for out-of-bag set decrease the greater importance of the descriptor. Due to

randomness of permutation process it is more reliable to make several iterative calculation and average of obtained result.

Numbers of iterations is a fully arbitrary parameter. However we can give an advice – the more compounds in the training set the less number of iterations is needed. For huge data sets (about 1000 compounds and more) one iteration can be enough.

To view results of calculation switch to Variable importance tab.

Variables importance for each property is calculated separately.

3.2. Domain of applicability calculation

To calculate domain of applicability measures choose FOREST / CALC DOMAIN APPLICABILITY

🏺 CI	F - D:\CF_exa	mple\MTL.tx	t							23
File	Forest Pr	ediction 0	ptions Abou	t						
In	29 🔲 🗌	***								
					1 1					
LIST	of forests	Trees Fore	st Statistics	Variable impor	tance Data					
#	Trees cou	nt Vars co	unt 🛛 Min pare	ent Min child	Property	Risk estimate (ws)	Risk estimate (oob)	R2 (ws)	R2 (oob)	
	100	31	1	1						
					H/blood	0.5011	0.657	0.838	0.534	- 1
					H/fat	0.1244	0.2528	0.921	0.471	- 1
					H/brain	0.1841	0.4506	0.901	0.431	- 1
			_		H/liver	0.1038	0.2544	0.921	0.181	- 1
			🛛 🌳 C	hoose DA type (calculation	6		0.894	0.417	- 1
								0.898	0.411	- 1
				hoose domain app	olicability calcula	tion type		0.895	0.543	- 1
O.845 0.293										
O based on variable importance									- 1	
			· · · · · · · · · · · · · · · · · · ·					0.873	0.557	- 1
				based on proxir	nities			0.928	0.444	- 1
										- 1
					0	к				- 1
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				_	_					- 1
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										- 1
		,								111

In the opened dialog you can select desired domain applicability measure.

Measure **based on trees prediction** calculated by creation minimum-cost-tree. Distance s between pairs of training set compounds in models space are considered. That is each model has T number of predictions made by each tree in the model (T - total number of trees). Each prediction is considered as a separate dimension. Thus Euclidean distance can be calculated.

Measure **based on variable importance** is calculated by creation minimum-cost-tree. Euclidean distances between pairs of training set compounds in descriptors space are calculated, but additionally variables importance are considered. So the more important variable is the lesser variability of descriptor value is allowed. This procedure is more time-consuming than previous one. Measure **based on proximities** is under testing and disabled now.

In all calculations of domain applicability only training set compounds having observed values are considered.

To change domain applicability ranges one should change the number in the field "DA in sigma units" (Forest statistics tab), which represents the coefficient k in the following equation (this coefficient can be a real non-negative number).

DA limit = mean distance value + k × standard deviation distance value

After "Recalc" button clicked DA limit will be recalculated and all corresponding statistics too.

CF - D:\CF_example\saves\1.rf							x
File Forest Prediction About							
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List of forests Trees Forest Statistics Variable importa	ance Data						
Property log(IGC50-1) Set 1s2	- DA	in sian	na unite	3	Pacalo		
		an sign			(ecale		 _
# Compound name Set Observed (log(IGC50 P	Predicted (log(IGC50	DA	Pred. St	dDev (log(l	GC50		
tp1086_ethyl_p ts2 1.67 0	0.724	+	0.468				
tp1087_a-chloro ts2 1.73 U	U.467	+	0.54				
tp1088_4-ntrop ts2 1.81 1	1.045	+	0.709				
tp1089_phenylp ts2 2.02 0	0.319	+	0.413				
tp1090_4-cnioro ts2 2.11 1	0.00		1.159				
tp1091_1-bronio ts2 2.31 0	1.30	- T	0.392				
tp1092_1_4-dic ts2 2.33	1.344		1 201				
tp/084_3 budro ts2	0.757		0.433				
tp0985 4-bydro ts2 -0.969	-0.757	- T	0.400				
tp0986_4-mparots20.505	-0.330	- T	0.53				
tp0987 Benzam ts2 -0.000 -	-0.322	• •	0.387				=
tp0988 Resorci ts2 -0.869 -	-0.392	+	0.796				
tp0989 4-aceta ts2 -0.819 0	0.051	+	0.779				
1 0000 AL A A 0 0770	~		0.500				-
Set		V	VS	OOB	TS	TS2	
	R2	C).989	0.9	0.912	0.81	- 1
	R2test	C).974	0.807	0.828	0.729	
	MSE	C	0.0293	0.215	0.192	0.293	_
	RMSE	C	0.171	0.464	0.438	0.541	- 1
	R2 (DA)	C).989	0.9	0.923	0.805	
	R2test (DA)	C).974	0.807	0.848	0.723	
	MSE (DA)	C	0.0293	0.215	0.159	0.282	
	RMSE (DA)	0	0.171	0.464	0.399	0.531	
	DA Coverage	1		1	0.962	0.973	
1							
DA calculation complete							1

4. "Preset mode" of model construction.

🔗 Tree growth options					
\varTheta DT - F:\Delphi\Projects\DTProj Variables Cases Forest				-	
File Tree Forest Prediction Statistics					
Select forest grow mode					
List of function in the second of the second					
List of forests Irees Forest Statisti Trees Vars Min parent Min child Models					
		_lit_188	lit_194	lit_196	lit_1
		9	10	11	
1 Ranked_pKi, nM_6.3_7.2_8		4	4	4	
2 S_A(lip)/D_E_E_E/1_2a,1_		0	2	0	
3 S_A(chg)/C_C_C_E/1_3a,2		0	2	0	
4 <u>S_A(lip)/D_E_E_E/1_2s,1_</u>		0	1	0	
5 S_A(Iip)/D_D_E_E/1_3a,2_		0	0	0	
6 S_A(ip)/C_D_E_E/2_3a,2 (* Preset niode (statistics only)	Dessible surshau sé	0	16	0	
7 S_A(type)/C.AR_H_N.AM_O of each type 10 Torests 10 trees in each forest	variables in each forest	1	0	1	
		1	1	1	
9 S_A(chg)/A_E_E_F/1_2S,3 Log file 10	10 🔼	4	0	4	
10 S_A(chg)/C_E_E_F/1_2S,3 F:\Delphi\Projects\DTProject_Tex 200	25	26	U	22	
11 S_A(cng)/A_C_C_E/1_45,2	100	U 47	1	U 45	
	200	17	U	15	
13 <u>S_A(III)/A_B_B_B/I_3S,Z_4</u>	500	2	2	2	
14 <u>S_A(iip)/C_D_D_0/T_45,2</u>		2 C	0	2	
15 5_A(clig)/C_C_E_F/1_25,3		17	0	15	
17 S A(cho)(A C C E/1 4e 2		1	1	10	
18 S A(lin)(C C C G(1 3s 2		1	1	1	
19 S A(chq)/C C E E(1, 2s 2		40	28	56	
20 S A(ch0)/A C E E/1 3S1 (C Bostetren (cleasicel)		2	4	2	-
21 S A(fyne)/CAR CAR H N		6	6	- 6	
		1	1	1	
23 S A(d a)/ 11 1/1 3s 2 4s C training (app		. 137	111	119	
24 S A(cha)/C C E E/1 2s.1		14	22	22	
					>
File was opened	K Cancel				
					14

This option is needed to collect statistics of huge number of models on the base of predefined settings (possibility of saving of individual models is absent in this mode). This procedure is useful to investigate forest behavior in a wide range of setup variables (number of trees and number of descriptors).

There should be defined:

- number of models of each type;
- possible number of trees and descriptors for splitting (one value per line);
- log-file name, where all results are saved.

In this mode "Min parent" and "Min child" parameters equal 1 and cannot be changed.

Data is saved in the log-file as soon as it is produced. So there is no risk to lost data.

5. Model (files) routines.

5.1. Saving model

One can save model in a file by choosing FILE / SAVE PROJECT. Model saves into several separate files:

1) .rf file - has a plain text format and contains general information, which can be useful for user

2) .t file – has a binary file format and contains all trees composing the model

3) .bin - has a binary file format and contains all data concerning the model and all statistics for training, OOB and test sets (information and statistics of external set doesn't save in the file)
4) .imp - has a binary file format and contains information concerning variable importances (if they are calculated of course)

All these files are needed for model opening and should be stored in the same directory.

If the source file of the data set is not an rfd-file then at saving one should specify rfd-file name (which will be contain a data set) and then rf-file name (which will be contain model information).

Rfd-file has an associated rfn-file of the same name. Both of them are store source data and needed to successful data loading.



If rfd-file was created once try to use only it to create new projects for the same data set. This can keep free space on HDD. Otherwise each time new rfd-dile will be created.

5.2. Opening model(s)

To open model use standard menu FILE / OPEN PROJECT

To open model it is necessary that data file (rfd-file) is in its initial directory (where it has been saved first time) or in the same directory with rf-file.

one can freely move models on the computer, if place of corresponding rfd-file will be initial
 one can copy model to USB stick and transfer it to another computer, but it is necessary to copy all model files and associated rfd/rfn-files into the same directory

One could add saved models to the current forest list if they have identical associated data-file (rfd-file).

1) if one try to open model file and data-file name will be identical to already opened model then the new model will be added to the list.

2) if one model has been already opened than one can select menu FILE / ADD MODELS TO THE CURRENT LIST to proceed. In opened dialog only models having according associated data-file will be displayed. Selection of multiple files is allowed.

6. Prediction of compounds properties which are in an external data-file.

To make prediction of compounds in an external data-file select the desired model in the model list and choose menu PREDICTION / PREDICT DATA FROM FILE.

If the open file has a variable with the same name as a target property then this file will be recognized as an external test set and the corresponding statistics will be calculated.

After prediction process was complete new set named "ext1" will be added to the list of model sets on Forest statistics tab. There one can select this set from the list, or select certain property to look for detailed statistics. As results of external data prediction don't save to model file one can find it useful to copy and paste this information in external editor.

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File Forest Prediction	n Options	About						
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List of forests Trees	Forest Stat	istics Variable	importance	Data				
Property H/blood	-	Set all			in sigma unit	s 3 I	Recalc	
# Compound name	Set C	- bserved (H/blo	Predicted (H	I/blo Pred. Sto	Dev (H/blo			
mtl_0001	ext1 -		0.89	1.11				
mtl_0002	ext1 -	•	1.158	1.206				
mtl_0011	ext1 0	0.61	0.752	0.466				
mtl_0101	ext1 -	1.099	0.31	0.356				
mtl_0102	ext1 -	0.249	0.316	0.362				
mtl_0103	ext1 -		0.374	0.423				
mtl_0104	ext1 0).87	0.568	0.576				
mtl_0105	ext1 -	•	0.364	0.421				
mtl_0106	ext1 -	0.359	0.467	0.514				
mtl_0107	ext1 -	0.589	0.467	0.514				
mtl_0108	ext1 -	1.519	0.469	0.514				
mtl_0109	ext1 -	•	1.395	0.582				
mtl 0110	evt1 -		1 385	0.551			\frown	
Set	-				WS	OOB	EXT1	
, 		1 1		R2	0.84	0.738	0.84	
				R2 test	0.643	0.506	0.643	
				MSE	0.503	0.697	0.503	
				RMSE	0.71	0.835	0.71	
<u> </u>				<u> </u>				
								1.

To copy data from various lists and tables one can often use right-mouse clicking and chosing appropriate item in popup menu.

Current program version is displayed in window which is call via menu ABOUT.

8. Afterword.

Do not hesitate to contact us if you found mistakes, faults, unusual program behavior or program failure or had any questions or ideas to improve program algorithm or interface! Any advices are welcome and will be taking in consideration at next version development!

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