

DALEX

Lung cancer case study

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Munich, 25.05.2018



Data set

	Gender	Smoking	No.mths.after.giving.up.smoking	Industrial.city	Chronic.bronchitis	Asthma	Pack.years.of.smoking	Age	
1	M	YES	48	NO	NO	NO		40	63
2	M	NO	0	NO	NO	NO		0	69
3	W	YES	0	NO	YES	NO		50	73
4	M	YES	0	NO	NO	NO		35	59
5	M	NO	0	NO	NO	NO		40	70
6	M	NO	0	NO	YES	NO		0	66
	Cancers.in.family	Live.more.than.3.y	Lung	Degree.of.efficiency.by.Zubord	Symptoms.pain	Symptoms.haemoptysis			
1	NO	0	Left	1	YES	NO			
2	NO	0	Left	0	NO	NO			
3	NO	1	Right	0	NO	NO			
4	NO	0	Left	0	NO	NO			
5	NO	0	Right	1	NO	NO			
6	NO	0	Right	0	NO	NO			
	Symptoms.breathlessness	Symptoms.cough	Symptoms.degradation.of.efficiency	weight.loss	Feature.T	Feature.N	Feature.M	Group	
1	YES	YES	NO	0	3	1	0	IIIA	
2	NO	NO	NO	0	2	1	0	IIB	
3	NO	NO	NO	0	2	0	0	IB	
4	NO	NO	NO	30	2	0	0	IB	
5	YES	NO	NO	0	2	2	0	IIIA	
6	NO	NO	NO	0	3	0	0	IIB	
	Initial.histopathological.diagnosis	Second.cancer	Tumour.volume						
1	Missing	NO	11.300351						
2	Missing	NO	11.831379						
3	Non-small cell carcinoma	NO	9.469623						
4	Non-small cell carcinoma	NO	10.868568						
5	Missing	NO	12.714395						
6	Missing	NO	9.711116						

Model

```
library(mlr)

classif_task <- makeClassifTask(id = "rf_model", data = data_model, target = "Live.more.than.3.y")
classif_lrn_rf <- makeLearner("classif.randomForest", predict.type = "prob")

classif_rf <- train(classif_lrn_rf, classif_task, subset=train_index)
```

Model and its explainer

```
library(mlr)

classif_task <- makeClassifTask(id = "rf_model", data = data_model, target = "Live.more.than.3.y")
classif_lrn_rf <- makeLearner("classif.randomForest", predict.type = "prob")

classif_rf <- train(classif_lrn_rf, classif_task, subset=train_index)

y_test <- as.numeric(as.character(modelTest$Live.more.than.3.y))

custom_predict_classif <- function(object, newdata) {
  pred <- predict(object, newdata=newdata)
  response <- pred$data[,3]
  return(response)
}

explainer_classif_rf <- DALEX::explain(classif_rf, data=modelTest, y=y_test,
                                     label= "rf", predict_function = custom_predict_classif)
```

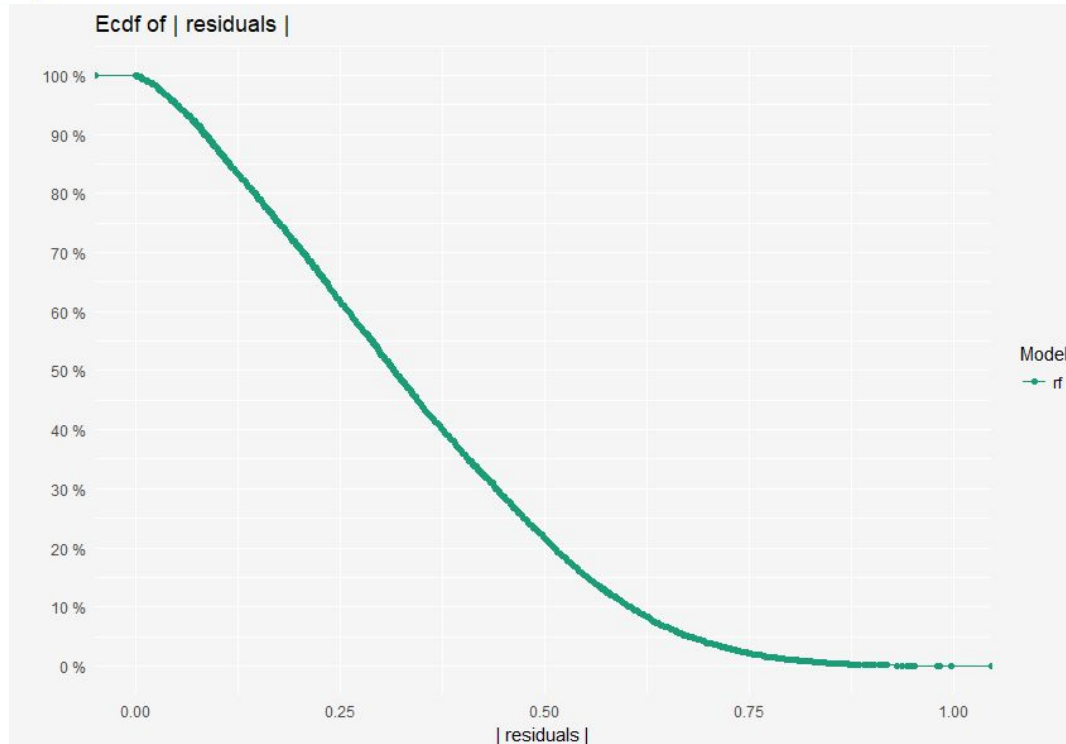
Interpretability with DALEX

Model performance

```
library(DALEX)  
mp_classif_rf <- model_performance(explainer_classif_rf)  
plot(mp_classif_rf)
```

Model performance

```
library(DALEX)  
mp_classif_rf <- model_performance(explainer_classif_rf)  
plot(mp_classif_rf)
```



Feature importance

```
vi_classif_rf <- variable_importance(explainer_classif_rf, loss_function = loss_root_mean_square)
vi_classif_rf
```

	variable	dropout_loss	label
1	_baseline_	0.5538452	rf
2	Tumour.volume	0.4593264	rf
3	Age	0.4484891	rf
4	Initial.histopathological.diagnosis	0.4254442	rf
5	Years.of.smoking	0.4241094	rf
6	Group	0.4232901	rf
7	Gender	0.4194648	rf
8	Feature.T	0.4109437	rf
9	Degree.of.efficiency.by.Zubord	0.4086999	rf
10	Lung	0.4063517	rf
11	No.mths.after.giving.up.smoking	0.4049651	rf
12	Feature.N	0.4043632	rf
13	Symptoms.cough	0.4024710	rf
14	Symptoms.degradation.of.efficiency	0.4014890	rf
15	Symptoms.pain	0.4009991	rf
16	Smoking	0.4004038	rf
17	Symptoms.haemoptysis	0.3975389	rf
18	Cancers.in.family	0.3971816	rf
19	Symptoms.breathlessness	0.3969818	rf
20	Industrial.city	0.3964980	rf
21	weight.loss	0.3960647	rf
22	Chronic.bronchitis	0.3937310	rf

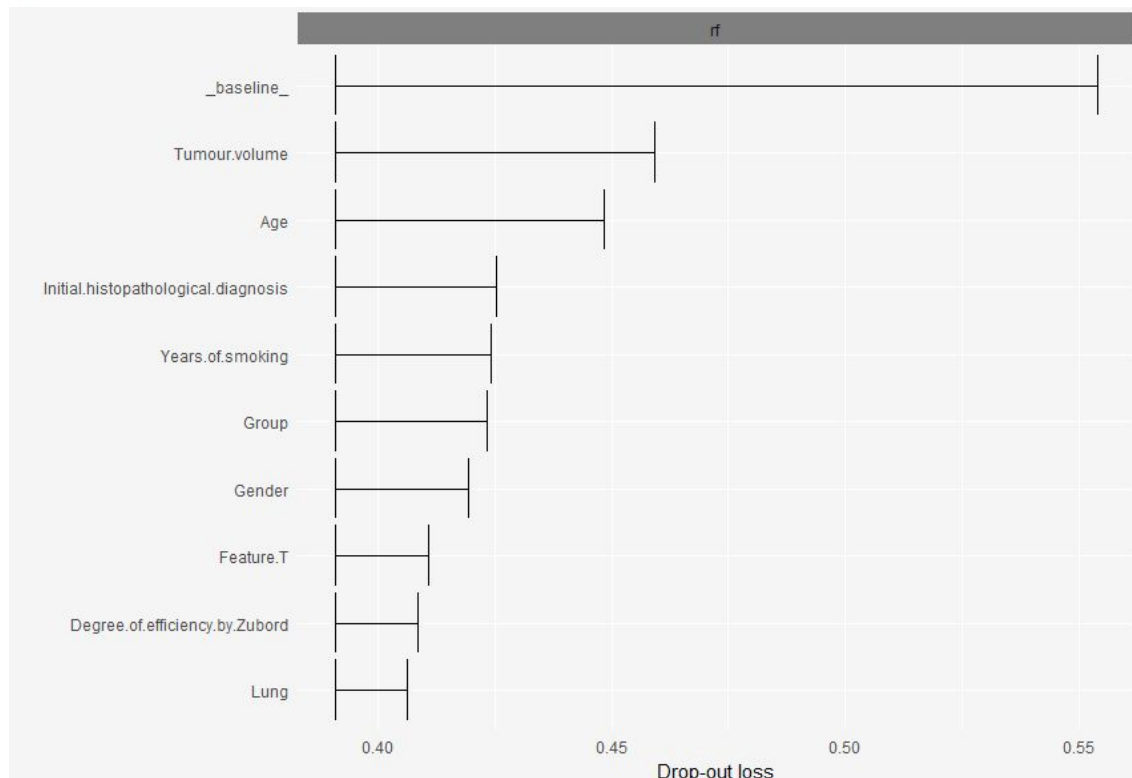
Feature importance

```
vi_classif_rf <- variable_importance(explainer_classif_rf, loss_function = loss_root_mean_square)  
plot(vi_classif_rf)
```



Feature importance

```
vi_classif_rf <- variable_importance(explainer_classif_rf, loss_function = loss_root_mean_square)  
plot(vi_classif_rf)
```

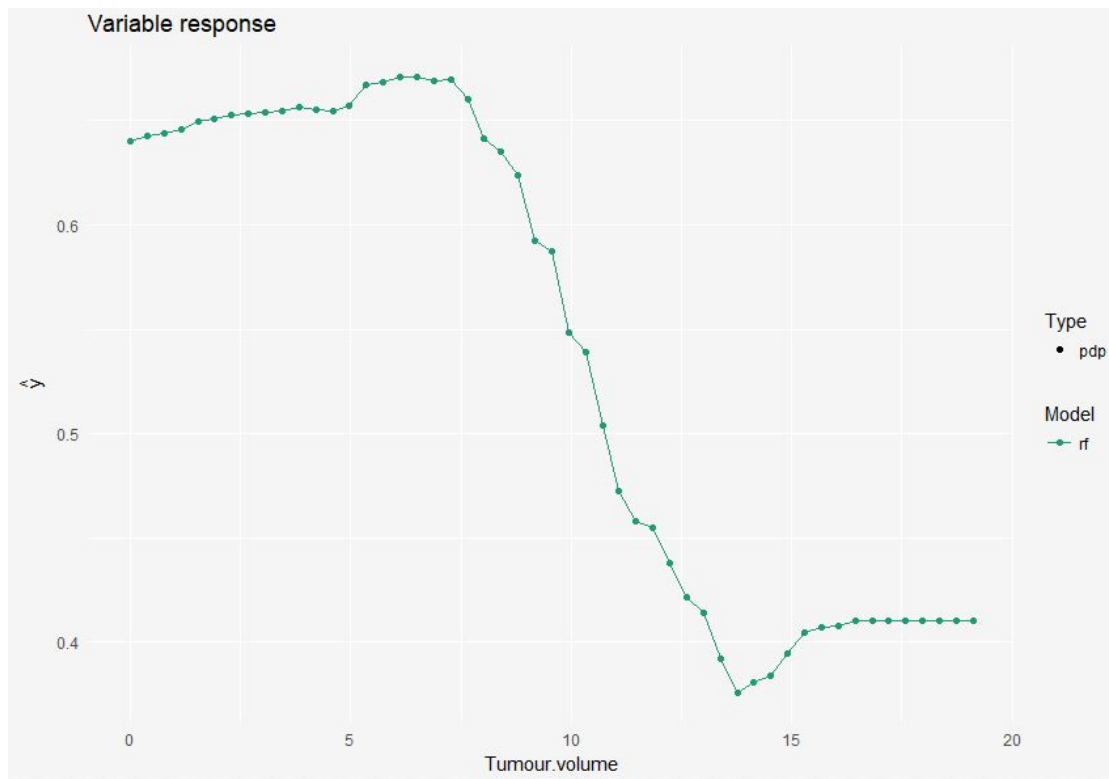


Variable response

```
pdp_classif_rf <- variable_response(explainer_classif_rf, variable = "Tumour.volume", type = "pdp")  
plot(pdp_classif_rf)
```

Variable response

```
pdp_classif_rf <- variable_response(explainer_classif_rf, variable = "Tumour.volume", type = "pdp")  
plot(pdp_classif_rf)
```

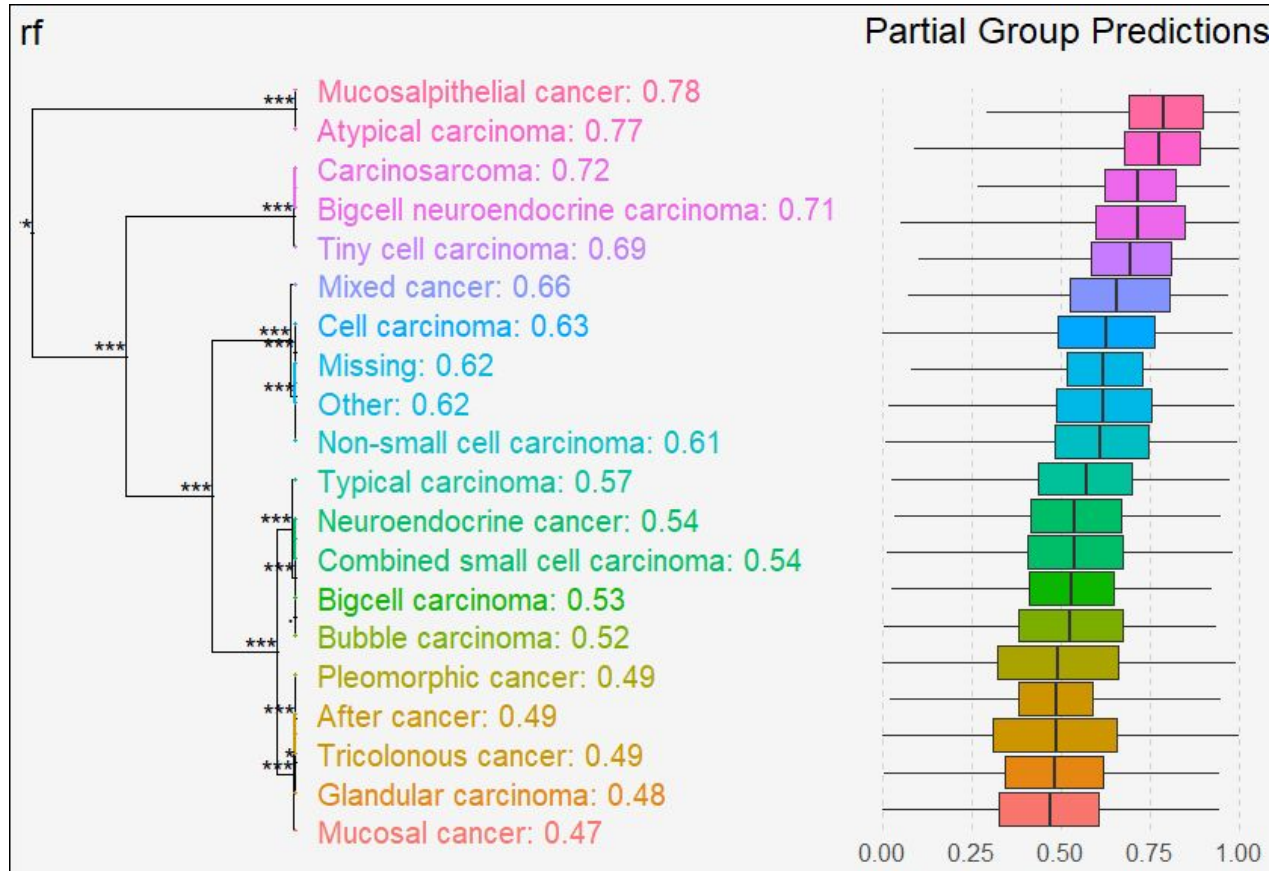


Merging Path Plot

```
svd_rf <- single_variable(explainer_classif_rf,  
                           variable = "Initial.histopathological.diagnosis", type = "factor")  
plot(svd_rf)
```



Merging Path Plot



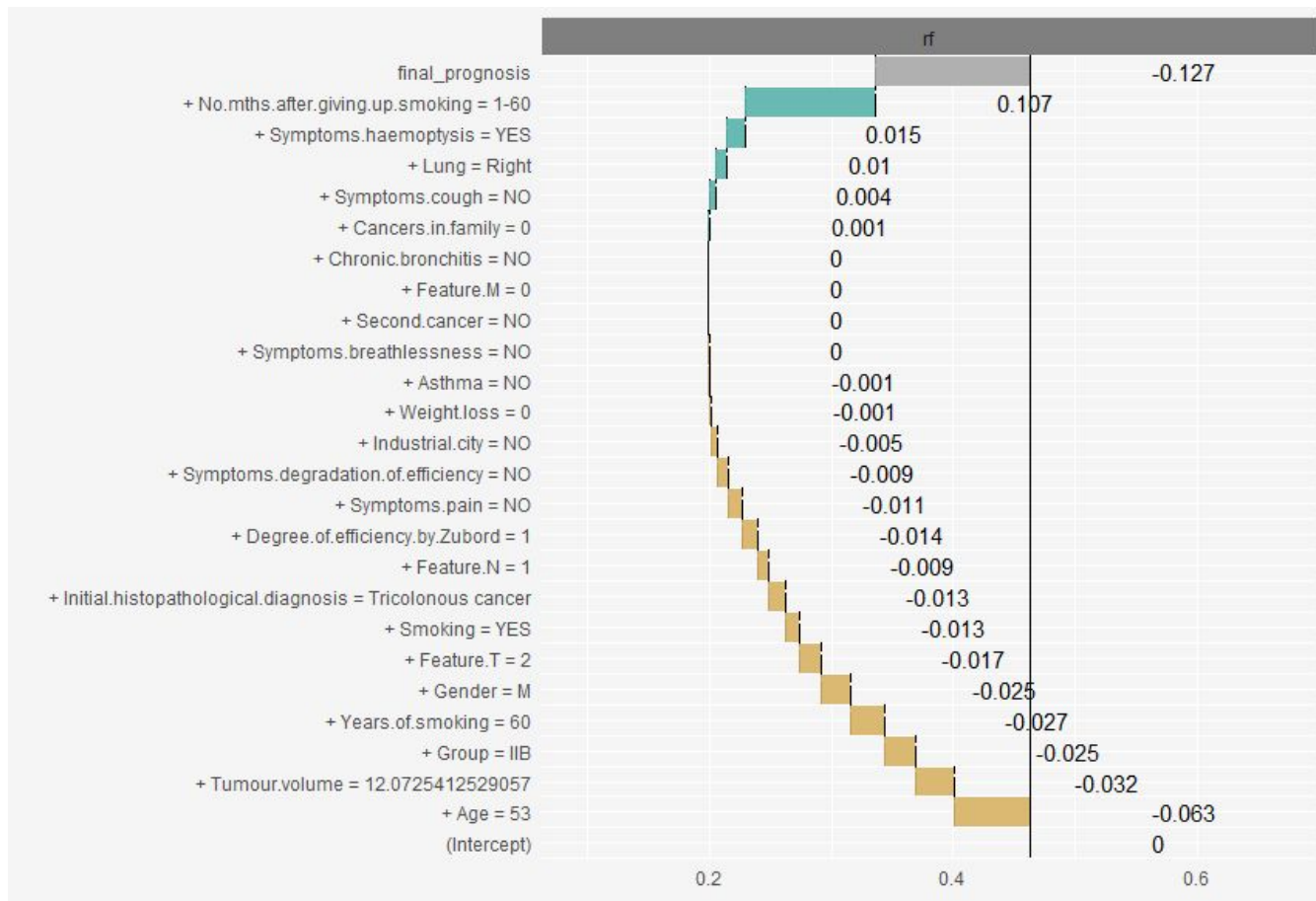
breakDown

```
2 Gender Smoking No.mths.after.giving.up.smoking Industrial.city Chronic.bronchitis Asthma Years.of.smoking Age
2 M YES 1-60 NO NO NO 60 53
2 Cancers.in.family Lung Degree.of.efficiency.by.Zubord Symptoms.pain Symptoms.haemoptysis
2 0 Right 1 NO YES
2 Symptoms.breathlessness Symptoms.cough Symptoms.degradation.of.efficiency weight.loss Feature.T Feature.N
2 NO NO NO 0 2 1
2 Feature.M Group Initial.histopathological.diagnosis Second.cancer Tumour.volume
2 0 IIB Tricolonus cancer NO 12.07254
```

```
library(breakDown)
library(DALEX)
```

```
breakDownExplain <- prediction_breakdown(explainer_classif_rf, modelTest[1,])
plot(breakDownExplain)
```

breakDown

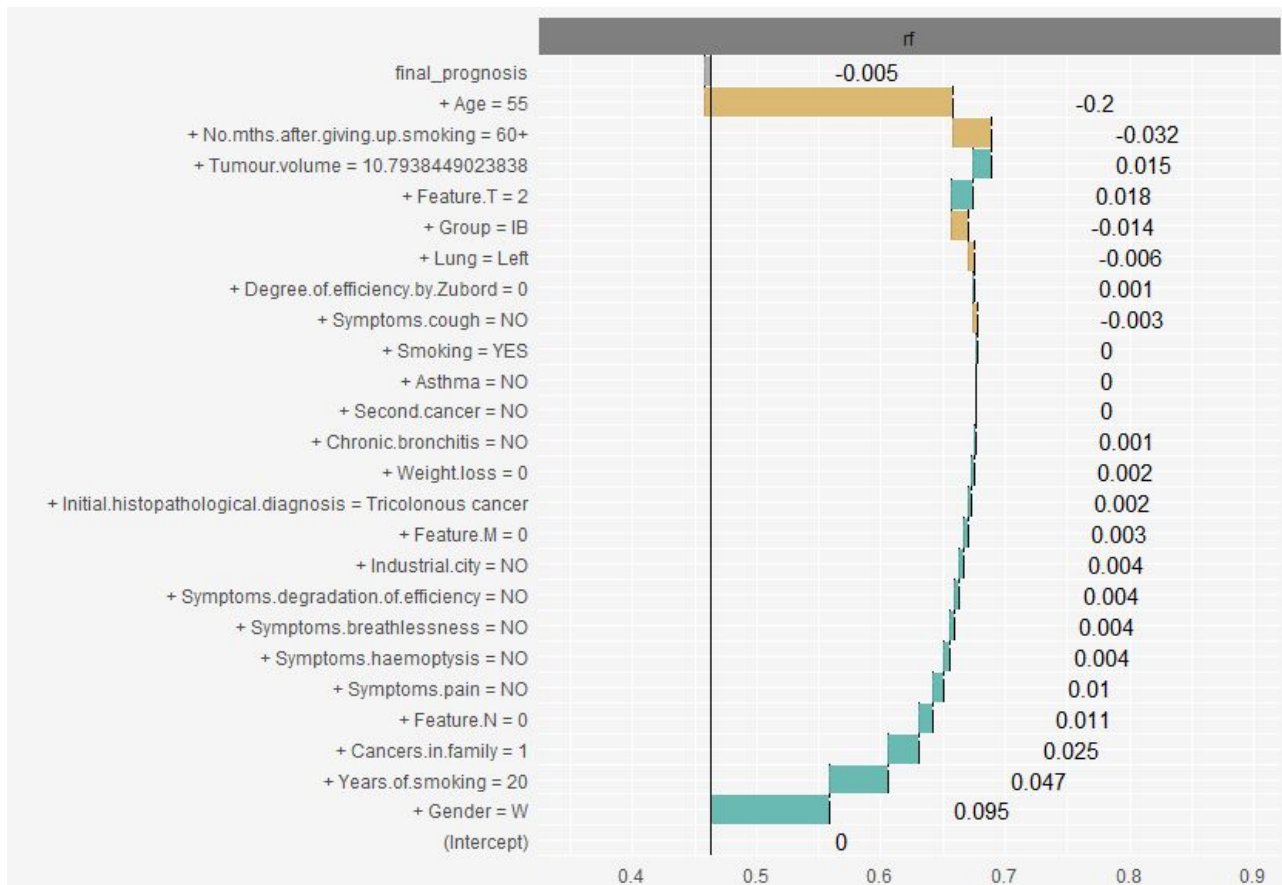


breakDown

```
44.1 Gender Smoking No.mths.after.giving.up.smoking Industrial.city Chronic.bronchitis Asthma Years.of.smoking
44.1 W YES 60+ NO NO NO 20
44.1 Age Cancers.in.family Lung Degree.of.efficiency.by.Zubord Symptoms.pain Symptoms.haemoptysis
44.1 55 1 Left 0 NO NO
44.1 Symptoms.breathlessness Symptoms.cough Symptoms.degradation.of.efficiency weight.loss Feature.T Feature.N
44.1 NO NO NO 0 2 0
44.1 Feature.M Group Initial.histopathological.diagnosis Second.cancer Tumour.volume
44.1 0 IB Tricolonus cancer NO 10.79384
```

```
breakDownExplain <- prediction_breakdown(explainer_classif_rf, modelTest[27,])
plot(breakDownExplain)
```

breakDown



Acknowledgements

We acknowledge the financial support from the NCN Opus grant
2016/21/B/ST6/02176.