Group model report

1. Group variables:

biomarkers = ['sysbp','diabp','pulse','wbc','mcv','plt','bun','glu','crea','cho','tg','hdl','ldl','crp','hbalc','ua','htc','hgb','cysc']

chronic disease = ['hibpe','diabe','cancre','lunge','hearte','stroke','psyche','arthre','dyslipe','livere','kidneye','digeste','asthmae','memrye']

self-reported functional limitation = ['dressa','batha','eata','beda','toilta','urina','moneya','medsa','shopa','mealsa','housewka','joga','walk1kma','walk100a','chaira','climsa','stoopa','lifta','dimea','armsa']

cognition/depression = ['cesd10','shlta','slfmem','imrc','dlrc','ser7','orient','draw'] #exclude tr20

2. Variable types:

	Data Type
sysbp	Numeric
diabp	Numeric
pulse	Numeric
wbc	Numeric
mcv	Numeric
plt	Numeric
bun	Numeric
glu	Numeric
crea	Numeric
cho	Numeric
tg	Numeric
hdl	Numeric
ldl	Numeric
crp	Numeric
hbalc	Numeric
ua	Numeric
htc	Numeric
hgb	Numeric
cysc	Numeric
hibpe	Categorical
diabe	Categorical
cancre	Categorical
lunge	Categorical
hearte	Categorical
stroke	Categorical
psyche	Categorical
arthre	Categorical
dyslipe	Categorical
livere	Categorical
kidneye	Categorical
digeste	Categorical
asthmae	Categorical
memrye	Categorical
dressa	Categorical
batha	Categorical
eata	Categorical
beda	Categorical
toilta	Categorical
urina	Categorical
moneya	Categorical
medsa	Categorical
shopa	Categorical
mealsa	Categorical
housewka	Categorical
joga	Categorical
walk1kma	Categorical
walk100a	Categorical
chaira	Categorical
climsa	Categorical
stoopa	Categorical
lifta	Categorical
dimea	Categorical
armsa	Categorical
cesd10	Numeric
shlta	Categorical
slfmem	Categorical
imrc	Numeric
dlrc	Numeric
ser7	Numeric
orient	Numeric
draw	Categorical

With 2 ordinal variable:

'shlta' : ['Very Poor','Poor','Fair','Good','Very good'];

'slfmem' : ['Poor','Fair','Good','Very Good','Excellent']

3. Data filtering

2011+2015 with no age missing & 40<=age<=85, sample_size=19695

Missing rate:

cysc ~13.1%

dlrc ~ 7.2%

imrc ~6.9%

After drop nan value from cysc, dlrc, imrc, sample_size = 15834

4. Feature engineering & normalization

For all the numerical feature, implementing with mean value

For all the categorical feature, implementing with most frequent category

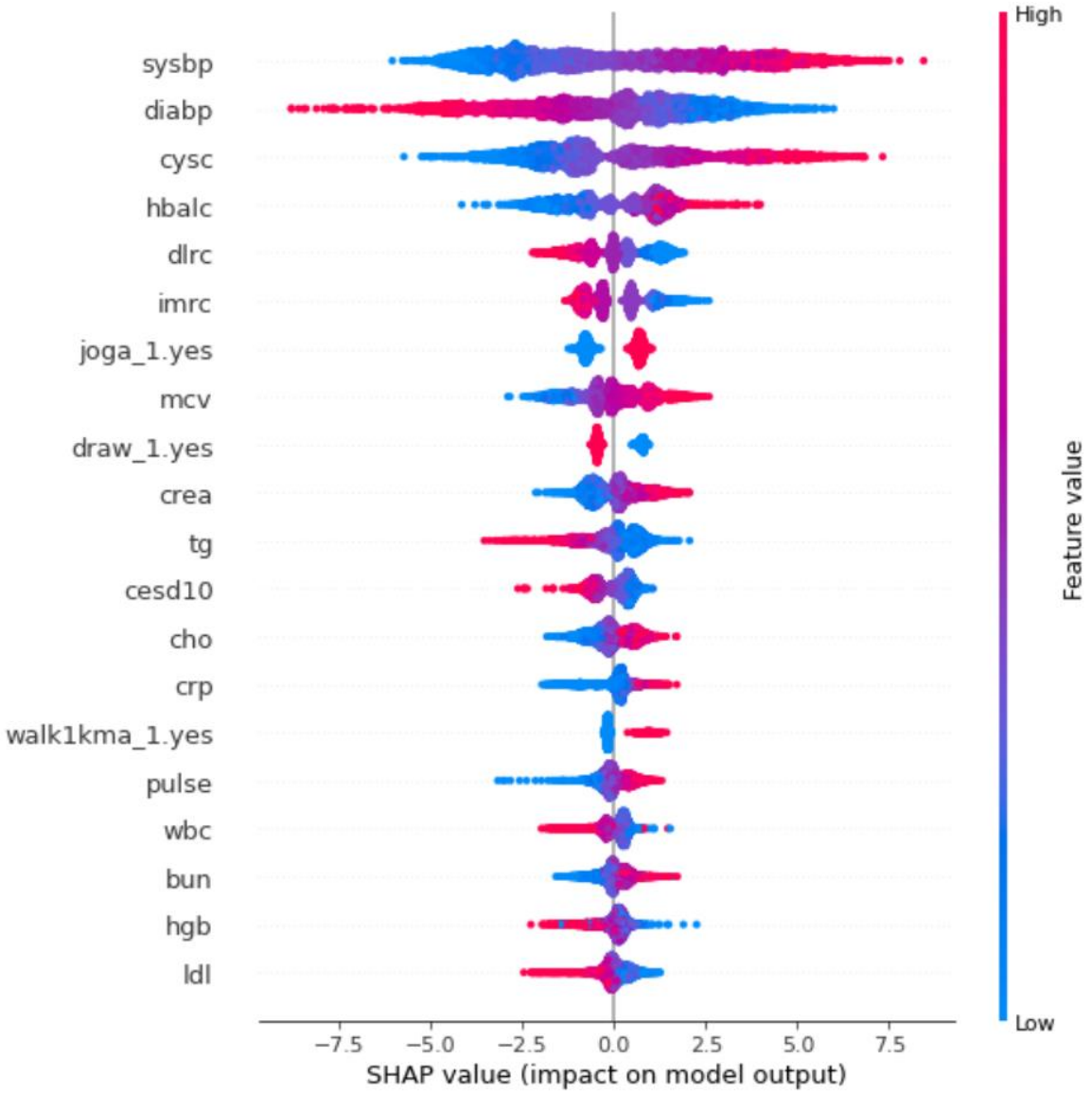
Normalization:min_max

5. Output

R^2: bio->0.3844 => all->0.44

	MAE	MSE	RMSE	R2	RMSLE	MAPE
0	5.2951	43.7383	6.6135	0.4501	0.1085	0.0896
1	5.4813	46.9082	6.8490	0.4523	0.1119	0.0922
2	5.5422	48.2022	6.9428	0.4465	0.1114	0.0913
3	5.5566	48.1986	6.9425	0.4195	0.1126	0.0930
4	5.6539	49.5082	7.0362	0.3834	0.1142	0.0946
5	5.3852	44.6713	6.6837	0.4644	0.1078	0.0893
6	5.3986	44.6716	6.6837	0.3960	0.1097	0.0916
7	5.4323	45.2677	6.7281	0.4371	0.1092	0.0909
8	5.2905	42.7327	6.5370	0.4695	0.1059	0.0878
9	5.1904	42.6476	6.5305	0.4814	0.1068	0.0871
Mean	5.4226	45.6546	6.7547	0.4400	0.1098	0.0907
SD	0.1337	2.2961	0.1695	0.0301	0.0025	0.0022

6. Feature importance



7. Model re-train with top feature-importance features

MAE	MSE	RMSE	R2	RMSLE	MAPE
5.5612	48.0171	6.9274	0.4348	0.1130	0.0935

Compare to model with all variables:

MAE	MSE	RMSE	R2	RMSLE	MAPE
5.4226	45.6546	6.7547	0.4400	0.1098	0.0907

Change of R^2 = 0.01, which indicates that features we choose can almost represent all the predict information of all the variables in the original model.

Features to focus:
[*'sysbp','diabp','cysc','hbalc','dlrc','imrc','joga','mcv','draw','crea','tg','cesd10','cho','crp','walk1kma','pulse','wbc','bun','hgb','ldl'*]