```
clear; clc; close all
```

LOADING DATASET

```
filename='Explant_ResponseGroup_Allprot_DEGs.xlsx';
% note: duplicated gene removed from Allprot dat.
tbl_exp_dat=readtable(filename,...
    'Sheet', 'DEG expression');
tbl target class=readtable(filename,...
    'Sheet','Target labels');
tbl deg pval=readtable(filename,...
    'Sheet','DEG pvals');
% expression data (to be normalized)
exp_dat_raw=table2array(tbl_exp_dat(:,2:end));
% gene names (input variable)
gene name=tbl exp dat.GeneName;
% target lables (output labels)
response_dat = table2array(tbl_target_class);
% p-value (just for inform)
p_val=tbl_deg_pval.DEGs_Pval;
```

Expression data normalization

```
tmp_min = repmat(min(exp_dat_raw')',1,size(exp_dat_raw,2));
tmp_max = repmat(max(exp_dat_raw')',1,size(exp_dat_raw,2));
input_dat_norm = (exp_dat_raw - tmp_min)./(tmp_max - tmp_min);
```

RUN THE SIMULATION

Expression_ML/Response_ML Input-train Input-test Target-train Target-test

```
disp(masterIDX)
    [idx1,idx2]=ind2sub([nd1,nd2],masterIDX);
    % copy variables for par
    input_dat_norm_par = input_dat_norm;
    train_sample_idx_par = train_sample_idx;
    test_sample_idx_par = test_sample_idx;
    response_dat_par = response_dat;
    % organize input data to be used for learning (gradual increment)
    input_dat_organized = input_dat_norm_par(1:idx2,:);
   % pick up samples for training an test
    train idx=train sample idx par(idx1,:);
    test_idx=test_sample_idx_par(idx1,:);
    % Train & Test data
    predictor_train = input_dat_organized(:,train_idx); % training input
    predictor_test = input_dat_organized(:,test_idx); % test input
    class_label_train = response_dat_par(train_idx);
    class_label_true = response_dat_par(test_idx);
   % SVM options
    svmtemp=templateSVM('Standardize',1,...
        'KernelFunction', 'linear');
    Mdl = fitcecoc(predictor_train',class_label_train',...
        'Learners', svmtemp,...
        'ClassNames', {'NR', 'RD', 'PR'});
    % CVMdl = crossval(Mdl)
   % genError = kfoldLoss(CVMdl)
    % Model prediction
    predicted_class_label_par(:,masterIDX) = predict(Mdl,predictor_test');
    %[predict_class_par(:,masterIDX),~,~,cnum(:,:,masterIDX)]=predict(Mdl,input_test');
    true_class_label_par(:,masterIDX) = class_label_true';
end
   50
```

```
5698
       5697
       5696
       5695
       5694
       5693
       5692
       4980
       4979
       4978
       4977
       4976
       4975
       4974
       4973
       5217
       5216
       5215
       5214
       5213
       5212
       5211
       5210
       4516
       4515
       4514...
% reshaping the parfor-result
[nr1,~] = size(predicted_class_label_par);
predicted_class_label = reshape(predicted_class_label_par,[nr1,nd1,nd2]);
[nr2,~] = size(true_class_label_par);
```

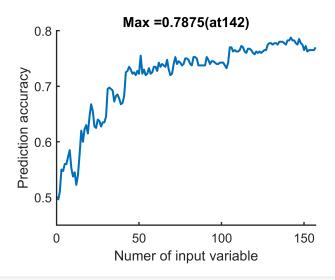
true_class_label = reshape(true_class_label_par,[nr2,nd1,nd2]);

% [nr3,nc3,~] = size(cnum);

```
% predict_prob = reshape(cnum,[nr3,nc3,nd1,nd2]);
```

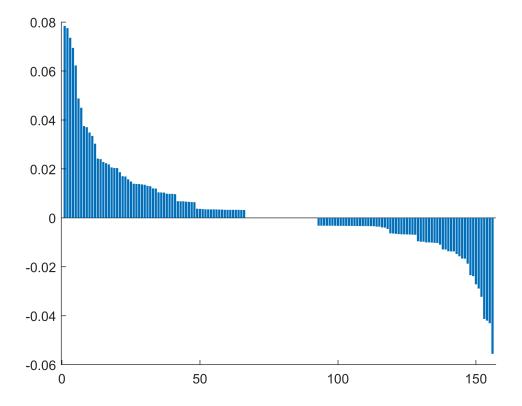
post-processing

Plot Prediction accuracy



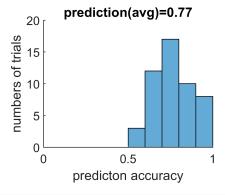
```
% plot
tmp_acc = predict_acc(2:end);
del_acc = (tmp_acc - predict_acc(1:end-1))./predict_acc(1:end-1);
del_acc_genes = gene_name(2:end);

[~,idx] = sort(del_acc,'descend');
figure,bar(del_acc(idx))
box off
```



```
tbl_del_acc = array2table(del_acc(idx)','RowNames',del_acc_genes(idx));
```

Plot Distribution of the prediction accuracy



confusion matrix

NR	149	24	5
PR ø	23	47	16
True Class Z	14	10	112

83.7%	16.3%
54.7%	45.3%
82.4%	17.6%

80.1%	58.0%	84.2%
19.9%	42.0%	15.8%
NR	PR Pr	RD edicted Class