# TERM CCA 2021 PROJECT

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# 01&02

#### **Problem Definition & Data**

#### Problem Definition: Curse of dimensionality

Sparse raw data

Computationally intractable

→ How to deal with high-dimensional data? Dimension Reduction

#### Breast cancer dataset

569 data (2 class: 212 malignant, 357 benign)

30 numerical features

provided with sklearn.datasets package

#### Method we used

#### Procedure

- 1. Apply the PCA function into breast cancer data for dimension reduction
- 2. Fit Ridge / Lasso / Logistic Regression to the data
- 3. Predict the result (malignant or benign) for classification
- 4. plot the data and linear regression
- 5. Compare real data and prediction result
- 6. Analize result (prediction accuracy, reason of misprediction)

# 04

#### Results: PCA

```
pcl_feature = list(zip(pca.components_[0], features))
pcl feature.sort()
pc1_feature
for i in range(29, 0, -1):
    print("{: .4f} {:s}".format(*pcl_feature[i]), end='\n')
0.8535 worst area
0.5145 mean area
0.0491 worst perimeter
0.0347 mean perimeter
0.0071 worst radius
0.0050 mean radius
0.0032 worst texture
0.0023 mean texture
0.0022 perimeter error
0.0003 radius error
0.0002 worst concavity
0.0001 worst compactness
0.0001 mean concavity
0.0001 worst concave points
0.0000 mean concave points
0.0000 mean compactness
0.0000 worst symmetry
0.0000 concavity error
0.0000 mean symmetry
0.0000 worst smoothness
```

```
pc2_feature = list(zip(pca.components_[1], features))
pc2 feature.sort()
pc2_feature
for i in range(29, 0, -1):
   print("{: .4f} {:s}".format(*pc2_feature[i]), end='\n')
 0.8533 mean area
 0.0095 area error
 0.0092 mean radius
 0.0008 perimeter error
 0.0004 texture error
 0.0001 mean concavity
 0.0000 mean concave points
 0.0000 concavity error
 0.0000 symmetry error
 0.0000 compactness error
 0.0000 concave points error
 0.0000 smoothness error
 0.0000 fractal dimension error
-0.0000 mean compactness
-0.0000 mean fractal dimension
-0.0000 mean smoothness
-0.0000 mean symmetry
-0.0000 worst concave points
-0.0000 radius error
-0.0001 worst fractal dimension
-0.0001 worst smoothness
```

```
print(pca.explained_variance_ratio_)
[0.9815 0.0167 0.0016 0.0001 0.0001 0. 0. 0. 0. 0. ]
```

n\_components = 2 → explaination\_ratio < 0.99, easy to visualization (2D)

# 04

# Results: Logistic Regression

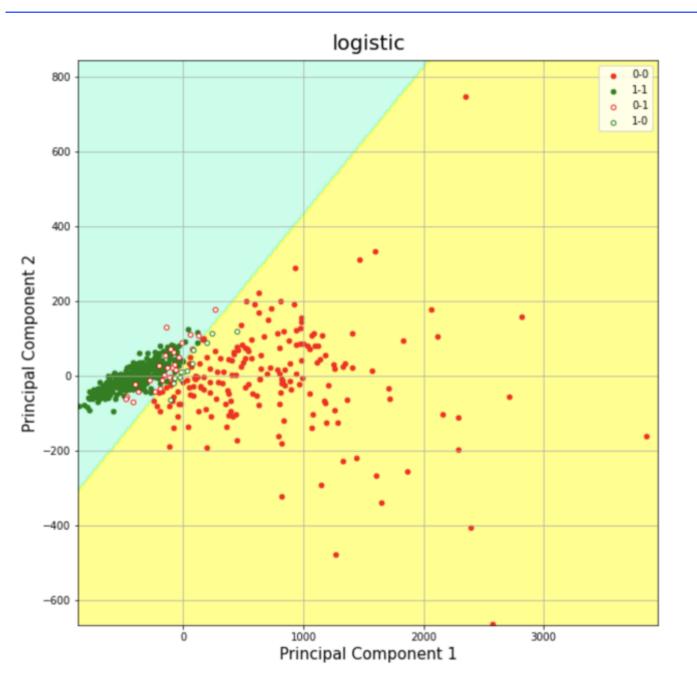
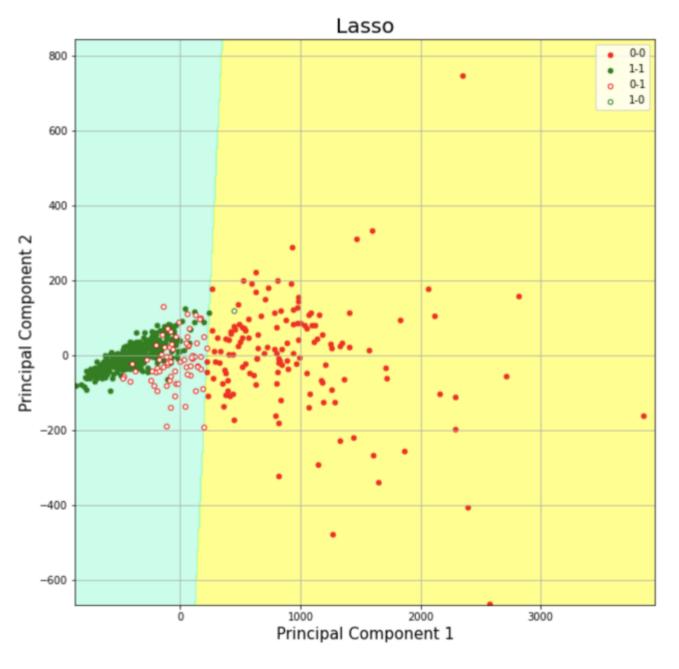


fig = plt.figure(figsize = (10,10)) ax = fig.add\_subplot(1,1,1) ax.grid() ax.set\_xlabel('Principal Component 1', fontsize = 15) ax.set\_ylabel('Principal Component 2', fontsize = 15) ax.set\_title('logistic', fontsize = 20, pad=10) colors = ['r', 'g'] targets = [0, 1]X\_set, y\_set = pc\_x, breast\_cancer.target X1, X2 = np.meshgrid(np.arange(start = X\_set[:, 0].min() - 1, stop = X\_set[:, 0].max() + 100, step = 10), np.arange(start = X\_set[:, 1].min() - 1, stop = X\_set[:, 1].max() + 100, step = 10)) plt.contourf(X1, X2, logisticRegr.predict(np.array([X1.ravel(), X2.ravel()]).T).reshape(X1.shape) -0.5, alpha = 0.5,cmap = ListedColormap(('yellow', 'yellow', 'aquamarine'))) scatters = list() for target, color in zip(targets, colors): indicesToKeep = df\_all['target'] == target correct = df\_all['target'] == df\_all['logistic\_predict'] scatters.append( ax.scatter(df\_all.loc[indicesToKeep & correct, 'PC1'] , df\_all.loc[indicesToKeep & correct, 'PC2'] , c = color , s = 20))for target, color in zip(targets,colors): indicesToKeep = df\_all['target'] == target wrong = df\_all['target'] != df\_all['logistic\_predict'] ax.scatter(df\_all.loc[indicesToKeep & wrong, 'PC1'] , df\_all.loc[indicesToKeep & wrong, 'PC2'] , edgecolor = color , s = 20))ax.legend(scatters, ['0-0', '1-1', '0-1', '1-0'])

- →Affected by PC1 and PC2 both
- → Highest prediction accuracy

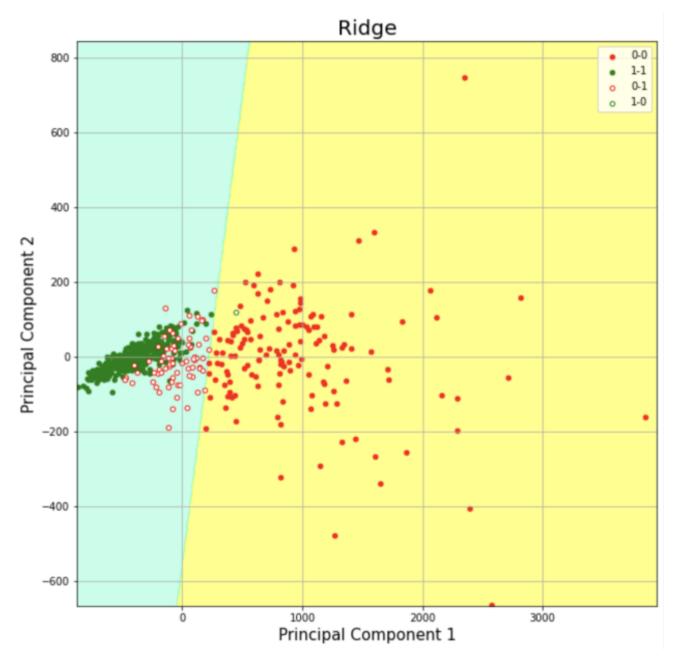
### Results: Lasso Regression



```
fig = plt.figure(figsize = (10,10))
ax = fig.add_subplot(1,1,1)
ax.set_xlabel('Principal Component 1', fontsize = 15)
ax.set_ylabel('Principal Component 2', fontsize = 15)
ax.set_title('Lasso', fontsize = 20)
colors = ['r', 'g']
targets = [0, 1]
X_set, y_set = pc_x, breast_cancer.target
X1, X2 = np.meshgrid(np.arange(start = X_set[:, 0].min() - 1,
                     stop = X_set[:, 0].max() + 100, step = 10),
                     np.arange(start = X_set[:, 1].min() - 1,
                     stop = X_set[:, 1].max() + 100, step = 10))
predict = lasso.predict(np.array([X1.ravel(), X2.ravel()]).T).reshape(X1.shape)
predict[predict < 0.5] = 0
predict[predict >= 0.5] = 1
plt.contourf(X1, X2, predict, alpha = 0.5,
             cmap = ListedColormap(('yellow', 'aquamarine')))
scatters = list()
  or target, color in zip(targets,colors):
    indicesToKeep = df_all['target'] == target
    correct = df_all['target'] == df_all['lasso_predict']
        ax.scatter(df_all.loc[indicesToKeep & correct, 'PC1']
               , df_all.loc[indicesToKeep & correct, 'PC2']
              , c = color
  or target, color in zip(targets,colors):
    indicesToKeep = df_all['target'] == target
    wrong = df_all['target'] != df_all['lasso_predict']
        ax.scatter(df_all.loc[indicesToKeep & wrong, 'PC1']
               , df_all.loc[indicesToKeep & wrong, 'PC2']
              , edgecolor = color
ax.legend(scatters, ['0-0', '1-1', '0-1', '1-0'])
```

- →Affected by PC1
- →low prediction accuracy than logistic regression

# Results: Ridge Regression



```
fig = plt.figure(figsize = (10,10))
ax = fig.add_subplot(1,1,1)
ax.set_xlabel('Principal Component 1', fontsize = 15)
ax.set_ylabel('Principal Component 2', fontsize = 15)
ax.set_title('Ridge', fontsize = 20)
colors = ['r', 'g']
 targets = [0, 1]
X_set, y_set = pc_x, breast_cancer.target
X1, X2 = np.meshgrid(np.arange(start = X_set[:, 0].min() - 1,
                     stop = X_set[:, 0].max() + 100, step = 10),
                     np.arange(start = X_set[:, 1].min() - 1,
                     stop = X_set[:, 1].max() + 100, step = 10))
predict = ridge.predict(np.array([X1.ravel(), X2.ravel()]).T).reshape(X1.shape)
predict[predict < 0.5] = 0
predict(predict >= 0.5) = 1
plt.contourf(X1, X2, predict, alpha = 0.5,
             cmap = ListedColormap(('yellow', 'aquamarine')))
scatters = list()
  or target, color in zip(targets,colors):
    indicesToKeep = df_all['target'] == target
    correct = df_all['target'] == df_all['ridge_predict']
        ax.scatter(df_all.loc[indicesToKeep & correct, 'PC1']
               , df_all.loc[indicesToKeep & correct, 'PC2']
              , c = color
              , s = 20))
   target, color in zip(targets, colors):
    indicesToKeep = df_all['target'] == target
    wrong = df_all['target'] != df_all['ridge_predict']
    scatters.append(
        ax.scatter(df_all.loc(indicesToKeep & wrong, 'PC1')
               , df_all.loc[indicesToKeep & wrong, 'PC2']
               , edgecolor = color
               , s = 20))
ax.legend(scatters, ['0-0', '1-1', '0-1', '1-0'])
```

- →Affected by PC1
- →low prediction accuracy than logistic regression

# 05

#### Discussion of our work

worst area	PC2	▼ target	t ▼ la	asso 4	lasso_predict	<b>₽</b> T	ridge 🔻	ridge_predict	•	logistic	•	logistic_predict	t w
1153	-189.30336	02	0	0.50054133	1	1	0.47508471	2	0	8.49E-	05		0
1095	-86.458856	92	0	0.51205585	7	1	0.50020668	3	1	0.0021657	35		0
1070	21.39450	51	0	0.5019998	6	1	0.50432647	5	1	0.0375943	41		0
1050	-34.006161	72	0	0.52666606	7	1	0.52179421	3	1	0.0136703	15		0
1044	-94.534269	17	0	0.5460626	9	1	0.53329393	5	1	0.0037414	88		0
1035	-2.382145	55	0	0.52915339	6	1	0.52846125	5	1	0.03535	56		0
1032	115.49671	86	1	0.50258228	5	1	0.51731719	3	1	0.3762063	14		0
1031	51.808810	71	0	0.51872118	5	1	0.52512873	2	1	0.1215527	88		0
1030	-27.225632	88	0	0.53831732	8	1	0.53438906	3	1	0.0215711	98		0
1025	-30.329214	61	0	0.54156881	6	1	0.53724526	5	1	0.0212557	79		0
1009	91.280028	99	1	0.52291293	1	1	0.53454197	9	1	0.3232146	98		0
993.6	-134.72292	78	0	0.58596008	8	1	0.56806327	5	1	0.0029289	39		0
989.5	-2.7917026	52	0	0.55751456	4	1	0.55688938	1	1	0.0650120	13		0
988.6	33.387818	01	0	0.54952435	9	1	0.55363476	9	1	0.1415352	65		0
985.5	-51.89299	13	0	0.57129073	2	1	0.56425111	1	1	0.0225270	41		0
981.2	101.31837	23	0	0.53744414	1	1	0.550458549	9	1	0.4714443	13		0
980.9	-8.3311884	17	0	0.56344364	6	1	0.56211345	9	1	0.0635695	87		0
975.2	99.406023	48	0	0.54116090	9	1	0.55393905	5	1	0.4789565	74		0
973.1	0.3984372	76	0	0.56704157	6	1	0.56687758	9	1	0.0867048	71		0
971.4	-25.703969	24	0	0.57196894	9	1	0.56838480	7	1	0.0475754	05		0
967	-3.7820118	25	0	0.5712843	5	1	0.57058733	5	1	0.0848678	91		0
959.5	-47.739819	16	0	0.5856202	6	1	0.57918927	5	1	0.0348735	43		0
947.9	90.220898	71	1	0.5610396	6	1	0.57269167	7	1	0.5267427	35		1
943.2	-28.505480	22	0	0.59159392	5	1	0.58772414	1	1	0.0674535	56		0
939.7	108.32250	25	0	0.56126724	3	1	0.57530662	7	1	0.6538947	32		1
932.7	34.172076	75	1	0.5838588	7	1	0.58821909	7	1	0.2708447	49		0
931.4	29.536771	29	0	0.58501666	4	1	0.5887707	1	1	0.2501389	65		0
928.8	26.350978	91	0	0.58686451	9	1	0.59020648	2	1	0.2409311	73		0
928.2	117.35519	79	1	0.56685769	4	1	0.5821117	3	1	0.7361758	01		1
925.1	-10.887432	63	0	0.59870878	9	1	0.59719199	3	1	0.1242304	94		0
922.8	70.449621	84	1	0.58103668	1	1	0.59016746	5	1	0.4986762	42		0
915.3	72.129871	39	0	0.58445127	1	1	0.5938181	3	1	0.5304265	58		1
915	35.890683	94	0	0.5936459	1	1	0.59827444	5	1	0.3283763	45		0
909.4	51.32434	78	0	0.59348543	5	1	0.60014795	3	1	0.4322819	53		0
907.2	-107.25005	58	0	0.63284308	8	1	0.61876805	7	1	0.0187627	93		0
906.6	14.626596	81	1	0.60447032	5	1	0.60634170	5	1	0.2531193	07		0
906.5	-74.837839	11	0	0.62529571	1	1	0.61546150	5	1	0.0394518	36		0
897	-73.700780	28	0	0.63064787	7	1	0.62098639	9	1	0.0458066	88		0
896.9	-16.485872	81	0	0.61752123	7	1	0.61534661	1	1	0.1567802	36		0
888.7	-187.43775	97	0	0.66288742	2	1	0.63836910	3	1	0.0037328	96		0
888.3	-137.21980	12	0	0.65143810	4	1	0.63349136	1	1	0.0121679	01		0
880.8	12.403344	31	1	0.62061857	1	1	0.6222657	2	1	0.3153889	57		0
876.5	112.36906	21	0	0.59920753	4	1	0.61394219	2	1	0.8355928	35		1
873.2	-7.0716007	58	1	0.62952409	5	1	0.62864177	5	1	0.2434427	43		0
869.3	-41.22170	01	0	0.64064926	1	1	0.63531226	3	1	0.1339548	62		0
867.1	40.780322	45	1	0.62228252	7	1	0.62767780	5	1	0.5211141	69		1

Wrong prediction analysis

: value of worst area, mean area

Case of malignant

: value of worst/mean area is large

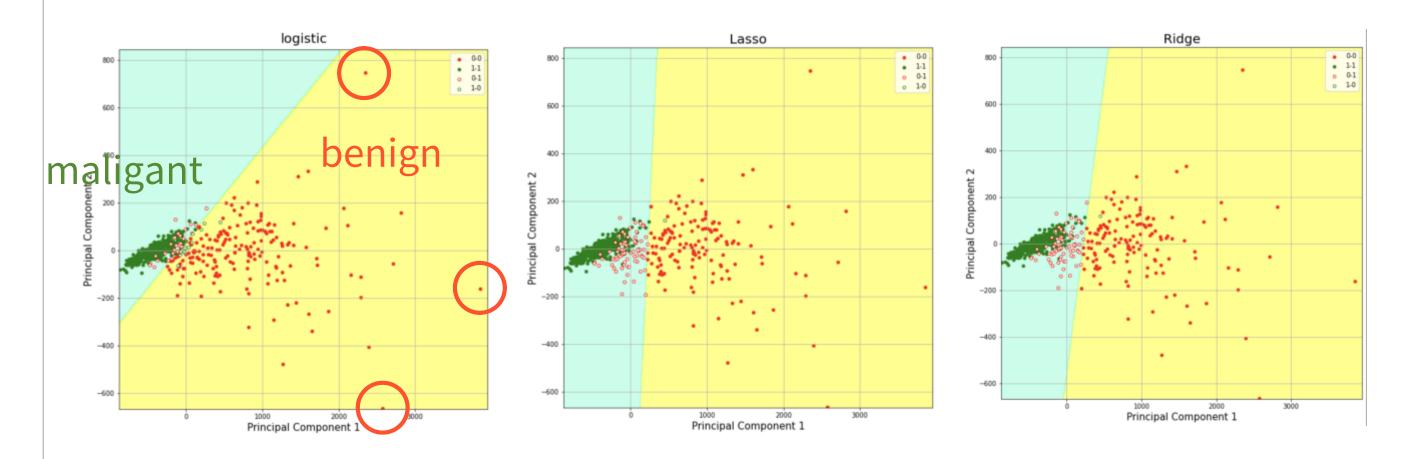
Case of benign

: value of worst/mean area is small

→ If the value is on the border,

the prediction is wrong.

#### Discussion of our work



Why is the predictive power of lasso/ridge regression less than that of logistic?

Logistic regression use sigmoid function: the value is 0 or 1

Lasso/Ridge regression: the value is real number

→ vulnerable to the outlier

# THANKYOU