0.1 Question 1: Using Linear Algebra for Optimization

In recommender system module, low-rank matrix factorization was used to execute latent factor modeling of movie ratings data.

Specifically, we calculated matrices U and V to solve the following optimization problem (if all ratings were given):

$$\min_{U,V} f(U,V) = \min_{U,V} \|R - VU^T\|_F^2 = \min_{U,V} \left\{ \sum_{m=1}^{M} \sum_{i=1}^{I} D_{mi}(r_{mi} - v_m u_i^T)^2 \right\},$$

where

$$D_{mi} = \begin{cases} 1, \text{ if } r_{mi} \text{ is observed} \\ 0, \text{ if } r_{mi} \text{ is missing.} \end{cases}$$

The best U and V were calculated iteratively by improving on current estimates:

$$u_i^{\text{new}} = u_i + 2\alpha D_{mi}(r_{mi} - v_m u_i^T) \cdot v_m$$
$$v_m^{\text{new}} = v_m + 2\alpha D_{mi}(r_{mi} - v_m u_i^T) \cdot u_i,$$

where α is the step-size that is to be chosen by the user, $i = 1, 2, \ldots, I$, $m = 1, \ldots, M$. (We won't discuss the role of α in this class, but treat it as an arbitrary, but given, parameter)

We can make calculating the updates more efficient by calculating them with matrix operations. For example, instead of calculating each deviation $\gamma_{mi} = r_{mi} - v_m u_i^T$ separately for all $m = 1, 2, \ldots, M$ and $i = 1, 2, \ldots, I$, matrix Γ of all deviations can be computed together using matrix operation *(verify for yourself)*:

$$\Gamma = R - VU^T$$

Similarly, updating U and V can be combined into matrix calculations which makes the optimization procedure more efficient.

First, note that updates for u_i, $i = 1, 2, \ldots, I$ can be rewritten as

$$\begin{aligned} u_1^{\text{new}} &= u_1 + 2\alpha D_{m1}\gamma_{m1} \cdot v_m \\ u_2^{\text{new}} &= u_2 + 2\alpha D_{m2}\gamma_{m2} \cdot v_m \\ \vdots \qquad & \qquad \vdots \\ u_I^{\text{new}} &= u_I + 2\alpha D_{mI}\gamma_{mI} \cdot v_m. \end{aligned}$$

Stacking all I equations into a matrix form,

$$U^{\text{new}} = U + 2\alpha(D_{m-} \circ \Gamma_{m-})^T v_m,$$

where I_{m-} and Γ_{m-} are the m-th row of Γ and D (use the notation Γ_{-i} for the i-th column). Hadamard product (elementwise matrix product) is denoted with $\circ$. When evaluating U^{new}, the latest updated values of U, V, and Γ are used.

Note that there are M such update equations (one for each $m = 1, 2, \ldots, M$) that can also be combined into one matrix update equation involving matrices U, V, Γ and scalars. As stated earlier, since α is assumed to be an arbitrary step-size parameter, we can replace α/M with α.

0.1.1 Question 1a: Using Linear Algebra for Optimization

Complete the following update equations:

$$U^{\text{new}} = U + 2\alpha[\text{some function of } \Gamma][\text{some function of } V]$$
$$V^{\text{new}} = V + 2\alpha[\text{some function of } \Gamma][\text{some function of } U]$$

SOLUTION

$$U^{\text{new}} = U + 2\alpha((D_{m-} \circ \Gamma_{m-})^T V)$$
$$V^{\text{new}} = V + 2\alpha((D_{m-} \circ \Gamma_{m-})U)$$

0.1.2 Question 1d: Interpret Diagnostic Plots

Following figures tell us if the optimization algorithm is working properly.

In [193]:
```
import altair as alt
logscale = alt.Scale(type='log', base=10)
fig_rmse = \
    alt.Chart(output1['rmse'])\
    .mark_line()\
    .encode(
        x='iteration:Q',
        y=alt.Y('rmse:Q', scale=logscale)
    )
fig_max_residual_change = \
    alt.Chart(output1['rmse'])\
    .mark_line()\
    .encode(
        x='iteration:Q',
        y=alt.Y('max residual change:Q', scale=logscale)
    )
fig_updates = \
    alt.Chart(output1['update'])\
    .mark_line()\
    .encode(
        x='iteration:Q',
        y=alt.Y('max update:Q', scale=logscale)
    )
alt.vconcat(
    fig_rmse | fig_max_residual_change,
    fig_updates
)
```

Out[193]:
```
alt.VConcatChart(…)
```

By referring back to the function used to calculate the quantities in each figure, describe what each figure is showing and interpret the behavior of the optimization algorithm.

SOLUTION

fig_rmse : The figure is showing the calculated rmse, how spread the residuals are, over iterations. It will give us an understanding of the model error, here we are seeing the decrease in RMSE as the amount of iterations increases which is what we are looking for. It's telling us the fit of the model to observed ratings is improving as more iterations occur, in other words, model accuracy and precision is getting better. The RMSE starts off high because we begin with random estimates.

fig_max_residual_change: For this figure we are seeing the model maximum residual change over iterations, the residuals are the difference between the observed and predicted ratings. In this case we are seeing a

decreasing pattern as more and more iterations occur, so the max residual change is getting smaller. This means the model is stabilizing as the change in residuals is becoming less over time, fewer changes are being made to the estimated values which tells us the model is becoming more consistent.

fig_updates: Maximum relative update of U and V over iterations, we do see a decreasing pattern as there are less max update peaks occuring after the first 500 iterations and it reaches a constant pattern where it can be infered that the model has stabilized and is consistent. That is a good sign since it tells us the model nearing optimization.

0.1.3 Question 1e: Analyze Large Dataset

Following code will analyze a larger dataset:

In [194]:
```
# run on larger dataset
Rbig = pd.read_pickle('data/ratings_stacked.pkl').unstack()[100:]

np.random.seed(134) # set seed for tests
output3 = compute_UV(Rbig, K=5, alpha=0.001, max_iteration=500)

Rhatbig = output3['V']@output3['U'].T
```

In [195]:
```
fit_vs_obs = pd.concat([
    Rhatbig.rename(columns={'rating':'fit'}),
    Rbig.rename(columns={'rating':'observed'}),
], axis=1).stack().dropna().reset_index()[['fit','observed']]

fit_vs_obs = fit_vs_obs.iloc[np.random.choice(len(fit_vs_obs), 5000)]

alt.Chart(fit_vs_obs).transform_density(
    density='fit',
    bandwidth=0.01,
    groupby=['observed'],
    extent= [0, 6]
).mark_bar().encode(
    alt.X('value:Q'),
    alt.Y('density:Q'),
    alt.Row('observed:N')
).properties(width=800, height=50)
```

```
/tmp/ipykernel_73/1847306426.py:4: FutureWarning: The previous implementation of stack is deprecated and
  ], axis=1).stack().dropna().reset_index()[['fit','observed']]
```

Out[195]: alt.Chart(…)

Question: Consider the above plot. - By reading the code, comment on what the plot is illustrating. - What happens when you add `counts=True` to `transform_density`? What can you conclude?

SOLUTION

In [196]:
```
alt.Chart(fit_vs_obs).transform_density(
    density='fit',
    bandwidth=0.01,
```

```
        groupby=['observed'],
        counts=True,
        extent= [0, 6]
    ).mark_bar().encode(
        alt.X('value:Q'),
        alt.Y('density:Q'),
        alt.Row('observed:N')
    ).properties(width=800, height=50)
```

```
Out[196]: alt.Chart(…)
```

The plot is illustrating the density distribution of fitted ratings vs observed ratings. Each graph represents a different observed rating 1-5 and the value of fitted rating is represented in the x-axis and the density for each value is on the y-axis. We can see that most observed ratings density graphs are normally distributed. When you add counts=True to transform_density, the graph will instead show the number of observations within each bin rather than the density for fitted ratings so rather than density distribution we will get a frequency distribution.

0.1.4 Question 1f: Make Recommendation

What movies would you recommend to `user id` 601? Do you see any similarities to movies the user rated high?

SOLUTION

```
In [197]: user_601 = Rhatbig.iloc[:,601]
          recommended_601 = user_601.sort_values(ascending=False)
          print(recommended_601.head(5))
```

```
movie id  movie title
174       Raiders of the Lost Ark (1981)                17.655701
172       Empire Strikes Back, The (1980)                9.984398
204       Back to the Future (1985)                      7.846455
1177      Dunston Checks In (1996)                       6.989592
1240      Ghost in the Shell (Kokaku kidotai) (1995)     6.892020
Name: (rating, 602), dtype: float64
```

For user 601 I would recommend "Raiders of the Lost Ark" (1981), "The Empire Strikes Back" (1980), "Back to the Future" (1985), "Dunston Checks In" (1996), and "Ghost in the Shell" (Kokaku kidotai) (1995) as the top five movies in that order. Yes, there are similarities to the movies the user rated high. They primarily liked movies with the genres action, adventure, and sci fi.

0.1.5 Question 2a: Derive New Gradients and Update Rules

Based on the new objective function $g(U, V)$, derive its gradients and update rules for U^{new} and V^{new}.

$$U^{\text{new}} = U - \alpha(-2(R - VU^T)^T V + 2\lambda(U))$$
$$V^{\text{new}} = V - \alpha(-2(R - VU^T)U + 2\lambda(V))$$

0.1.6 Question 2d: Investigating the Effects of Regularization

Adding the regularization terms to the objective function will affect the estimates of U and V. Here, we consider comparing the user matrix U.

Using the dataset *Rsmall*, obtain two estimated user matrices, say $\hat{U}$ for a non-regularized model and $\hat{U}_{\text{reg}}$ for a regularized model. Select $K = 20$ and $\lambda = 5$. Come up with an effective visualization for comparing $\hat{U}$ and $\hat{U}_{\text{reg}}$, and describe any differences you notice. Additionally, analyze whether the observed differences in patterns align with the concept of regularization.

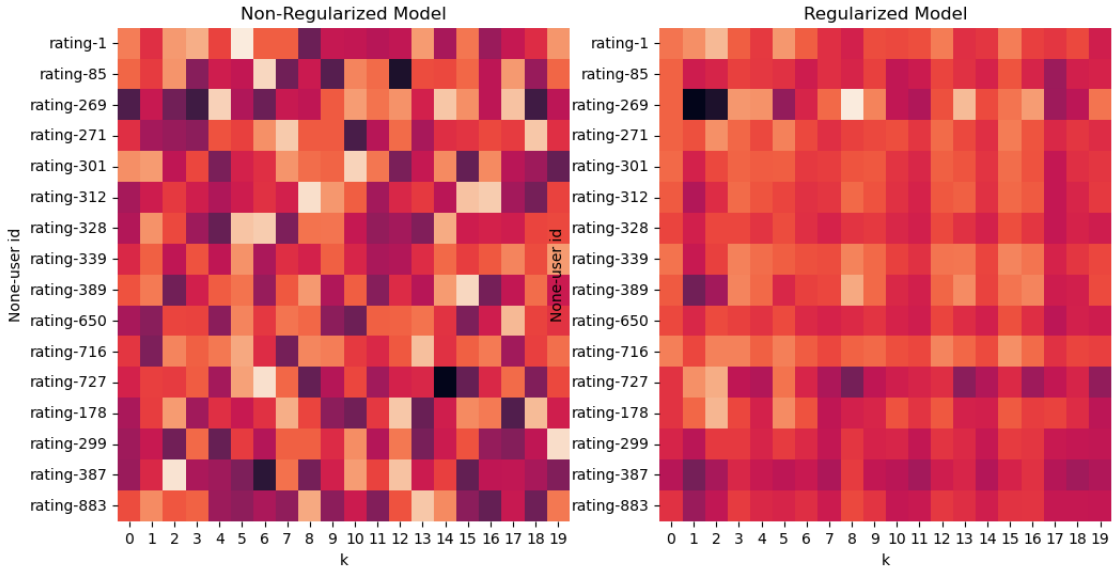
Provide reasoning supported by evidence, such as code implementation and results.

SOLUTION

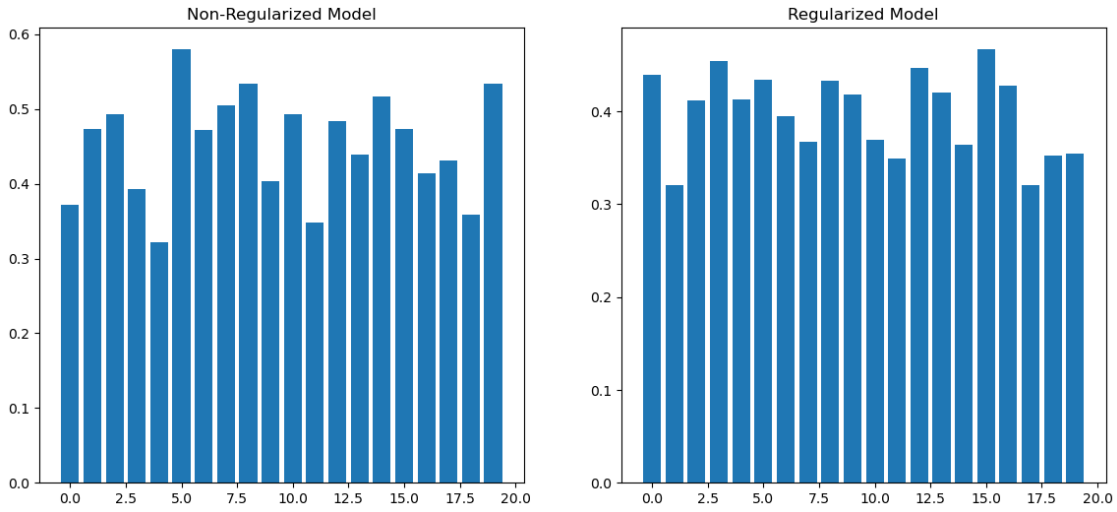
```
In [202]: np.random.seed(134) # set seed for tests
          output_noreg = compute_UV(Rsmall, K=20, alpha=0.001)
          output_reg = compute_UV_reg(Rsmall, K=20, lam=5.0, alpha=0.001)
```

```
In [263]: output_noreg['U'].shape
          output_noreg['U'].index
          output_noreg['U'].columns
          U_noreg = output_noreg['U']

          output_reg['U'].shape
          output_reg['U'].index
          output_reg['U'].columns
          U_reg = output_reg['U']
```

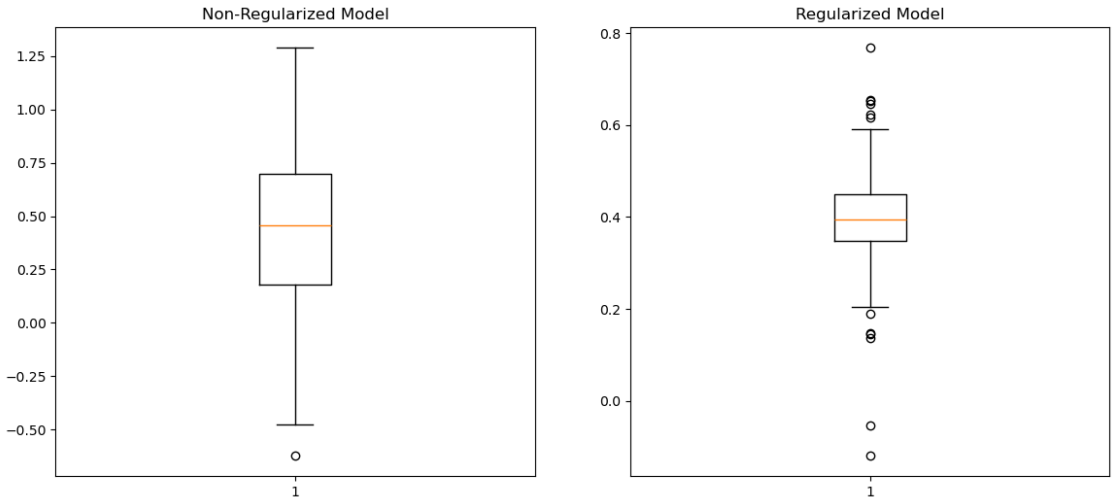
```
In [204]: import matplotlib.pyplot as plt
          import seaborn as sns

          plt.figure(figsize=(12, 6))
          plt.subplot(1, 2, 1)
          sns.heatmap(U_noreg, cbar=False)
          plt.title('Non-Regularized Model')

          plt.subplot(1, 2, 2)
          sns.heatmap(U_reg, cbar=False)
          plt.title('Regularized Model')
          plt.show()
```



In [205]:
```
plt.figure(figsize=(14, 6))
plt.subplot(1, 2, 1)
plt.bar(range(U_noreg.shape[1]), height = U_noreg.mean(axis=0))
plt.title('Non-Regularized Model')

plt.subplot(1, 2, 2)
plt.bar(range(U_reg.shape[1]), height = U_reg.mean(axis=0))
plt.title('Regularized Model')
plt.show()
```



```
In [206]: plt.figure(figsize=(14, 6))
          plt.subplot(1, 2, 1)
          plt.boxplot(U_noreg.values.flatten())
          plt.title('Non-Regularized Model')

          plt.subplot(1, 2, 2)
          plt.boxplot(U_reg.values.flatten())
          plt.title('Regularized Model')
          plt.show()
```



Regularization vs Non-regularization Looking at the heatmap right away we notice that for the regularized model it is more smooth overall and the color intensity is more balanced, there is less of a presence of extremely dark or light values which makes sense as regularization's goal is stabilize the model and stay away from extreme values, less variability. Next we have the bar plot, in the regularized model the bar heights have a smaller range difference in comparison to the unregularized model. The smaller differences in bar heights is showing how regularization is scaling the model to be more consistent and thus improving generalization while the nonregularized model is more variable. Our third visualization is the box plot, similarily to the other visualizations we can see a smaller spread of data of the regularization model. The box which represents the IQR of value distribution is considerably smaller than the non-regularized model one so the 25th to 75th data percentile is much more dense as they are closer to one another. Furthermore, looking at the whiskers, the regularized model has a smaller reach meaning we have a larger minimum and smaller maximum. This all tells us the regularized model is reducing data spread which decreases variance and removes complexity to help with overfitting.

0.1.7 Question 2e: Practical Aspects

In the previous question, a specific values for K and λ were provided. Now, try applying various K's and λ's. Specifically, try the following:

- While keeping K constant, experiment with different values of λ. What do you notice? Why do you think this happens?
- While keeping λ constant, experiment with different values of K. What do you notice? Why do you think this happens?

If your optimization algorithm is correctly implemented, you will notice that the choice of K and λ has a significant impact on the final estimates. Hence, selecting appropriate values for K and λ is crucial when applying the recommendation algorithm in practice. As a practitioner, how would you approach choosing K and λ?

Provide reasoning supported **by evidence**, such as code implementation and results.

SOLUTION

```
In [207]: def update_k(Rdf, K_values, lambda_value=5.0, alpha=0.001, max_iteration=5000):
              results = {}

              for K in K_values:
                  output = compute_UV_reg(Rdf, K=K, lam=lambda_value, alpha=alpha, max_iteration=max_it
                  results[K] = output['rmse']

              return results

          K_values = [5, 10, 15, 20, 25, 30]

          def update_lambda(Rdf, lambda_values, K_value = 20, alpha=0.001, max_iteration=5000):
              results = {}

              for lam in lambda_values:
                  output = compute_UV_reg(Rdf, lam=lam, K=K_value, alpha=alpha, max_iteration=max_itera
                  results[lam] = output['rmse']

              return results
          lambda_values = [0.1 ,1.0, 5.0, 10.0, 15.0]  # Experiment with different values of lambda

          # Perform experiments
          k_rmse = update_k(Rsmall, K_values)
          lambda_rmse = update_lambda(Rsmall, lambda_values)
```

```
In [208]: print(k_rmse[30])
          print(k_rmse[25])
```

```
print(k_rmse[20])
print(k_rmse[10])
print(k_rmse[5])
```

```
     iteration      rmse  max residual change
0            0  2.805573             1.783747
1            1  2.062546             1.094210
2            2  1.594024             0.750113
3            3  1.290219             0.544046
4            4  1.093264             0.410382
..         …       …                   …
705        705  0.910393             0.000076
706        706  0.910400             0.000076
707        707  0.910407             0.000076
708        708  0.910414             0.000076
709        709  0.910421             0.000075

[710 rows x 3 columns]
     iteration      rmse  max residual change
0            0  2.007447             1.336697
1            1  1.617004             0.905890
2            2  1.363514             0.648870
3            3  1.198268             0.483379
4            4  1.091111             0.370785
..         …       …                   …
743        743  0.911193             0.000049
744        744  0.911197             0.000049
745        745  0.911202             0.000049
746        746  0.911206             0.000049
747        747  0.911210             0.000049

[748 rows x 3 columns]
      iteration      rmse  max residual change
0             0  1.487517             0.729601
1             1  1.263428             0.546170
2             2  1.117676             0.421966
3             3  1.024174             0.333962
4             4  0.965329             0.269388
…           …       …                   …
1905       1905  0.913060             0.000008
1906       1906  0.913061             0.000008
1907       1907  0.913061             0.000008
1908       1908  0.913062             0.000008
1909       1909  0.913062             0.000008

[1910 rows x 3 columns]
     iteration      rmse  max residual change
0            0  1.690750             0.216510
1            1  1.602276             0.205747
2            2  1.521809             0.200737
3            3  1.449246             0.193702
4            4  1.384331             0.185084
..         …       …                   …
```

```
698        698  0.917337             0.000352
699        699  0.917311             0.000351
700        700  0.917286             0.000349
701        701  0.917260             0.000348
702        702  0.917235             0.000346

[703 rows x 3 columns]
     iteration      rmse  max residual change
0            0  2.518965             0.211864
1            1  2.390739             0.215905
2            2  2.264229             0.217565
3            3  2.141061             0.216667
4            4  2.022757             0.214066
..         …       …                  …
702        702  0.923687             0.000522
703        703  0.923639             0.000520
704        704  0.923592             0.000518
705        705  0.923544             0.000517
706        706  0.923497             0.000515

[707 rows x 3 columns]
```

While keeping lambda constant and experimenting with different K values, I noticed that both lowering and increasing the K value from 20 increased the rmse. K affects complexity of the model, so lower K would make the model more prone to overfitting and also increasing K to a too high of a value would also cause overfitting as the model can fit noise in the data instead of patterns.

```
In [209]: print(lambda_rmse[15])
          print(lambda_rmse[10])
          print(lambda_rmse[5])
          print(lambda_rmse[1])
          print(lambda_rmse[0.1])
```

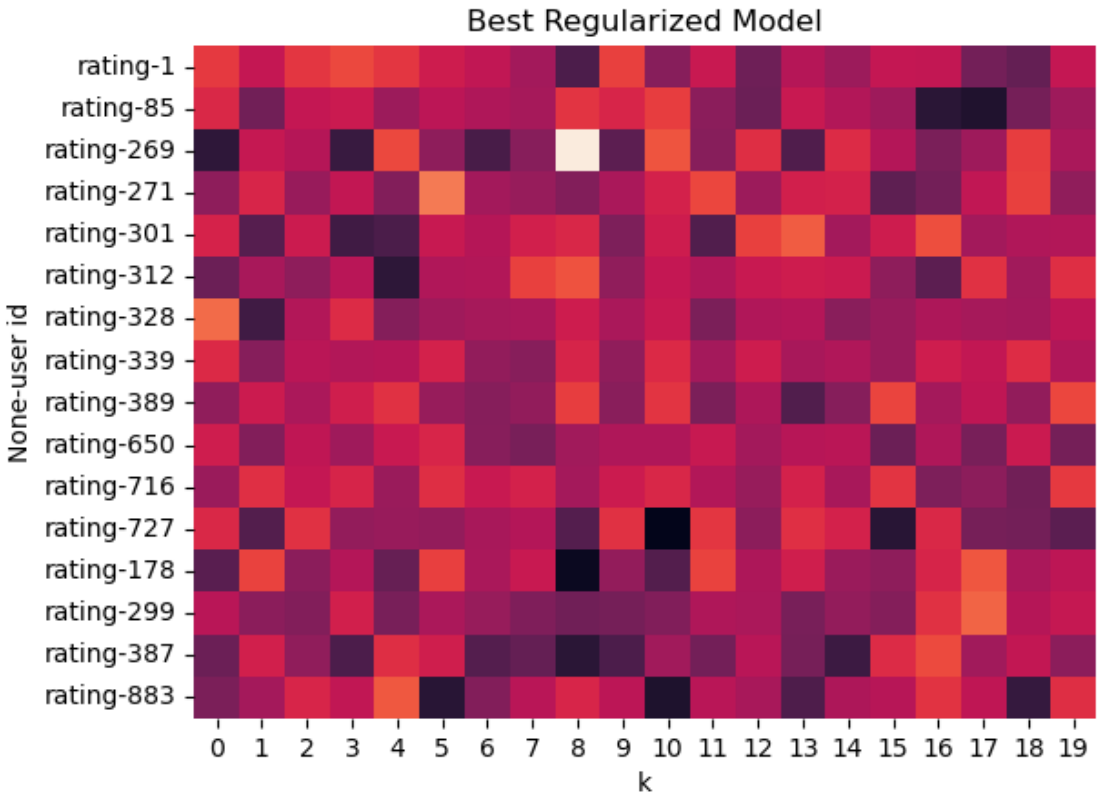
```
     iteration      rmse  max residual change
0            0  1.272112             1.043471
1            1  1.059526             0.765135
2            2  0.974675             0.585174
3            3  0.965286             0.461561
4            4  0.994038             0.372734
..         …       …                  …
177        177  1.682723             0.000037
178        178  1.682727             0.000035
179        179  1.682730             0.000034
180        180  1.682733             0.000032
181        181  1.682736             0.000031

[182 rows x 3 columns]
     iteration      rmse  max residual change
0            0  1.361629             0.736390
```

```
1            1  1.196961             0.559986
2            2  1.104400             0.439155
3            3  1.057574             0.352638
4            4  1.038590             0.288518
..         …       …                   …
284        284  1.297237             0.000072
285        285  1.297245             0.000072
286        286  1.297252             0.000071
287        287  1.297259             0.000070
288        288  1.297266             0.000069

[289 rows x 3 columns]
     iteration      rmse  max residual change
0            0  1.524476             0.667362
1            1  1.320792             0.500429
2            2  1.186472             0.390957
3            3  1.097975             0.312630
4            4  1.039745             0.255511
..         …       …                   …
677        677  0.912252             0.000151
678        678  0.912249             0.000150
679        679  0.912246             0.000150
680        680  0.912243             0.000149
681        681  0.912240             0.000148

[682 rows x 3 columns]
      iteration      rmse  max residual change
0             0  1.257137             0.572727
1             1  1.169391             0.470470
2             2  1.103093             0.392964
3             3  1.051938             0.332766
4             4  1.011633             0.285050
…          …       …                   …
4290       4290  0.255974             0.000005
4291       4291  0.255974             0.000005
4292       4292  0.255975             0.000005
4293       4293  0.255975             0.000005
4294       4294  0.255975             0.000005

[4295 rows x 3 columns]
      iteration      rmse  max residual change
0             0  1.593081             0.700148
1             1  1.397250             0.522127
2             2  1.257768             0.401400
3             3  1.156429             0.315882
4             4  1.081380             0.253208
…          …       …                   …
4995       4995  0.027323             0.000002
4996       4996  0.027323             0.000002
4997       4997  0.027323             0.000002
4998       4998  0.027323             0.000002
4999       4999  0.027323             0.000002

[5000 rows x 3 columns]
```

While keeping K constant and experimenting with different lambda values, I found that lambda=1 produced the best rmse. Increasing and decreasing lambda from the initial value of 5 with K=20 caused the rmse to both increase and decrease, this is because increasing lambda to a high value can decrease variance and lower overfitting, but it will greatly increase bias in the model as well as lower model flexibility. Too low of a lambda is not something you want because you are still trying to lower variance.

Since we knew K=20 was the best K value for us through looking at rmse, we experiment with different values of lambda with this constant K that would then also have the lowest rmse among all the lambda values tested.

```
In [309]: best_output_reg = compute_UV_reg(Rsmall, K=20, lam=1.0, alpha=0.001)
          best_U_reg = best_output_reg['U']

          sns.heatmap(best_U_reg, cbar=False)
          plt.title('Best Regularized Model')
          plt.show()
```



0.1.8 Question 3a: Concatenate matrix factors and cluster

Entries in either matrix factors are just points in k-dimensional latent variable space. We will use both U and V for segmentation by combining them into one large clustering problem.

Once clusters are identified, you will qualitatively inspect the users and movies in the cluster and decide on a "representative" movie from each cluster.

Consider concatenating U and V into one large matrix. Since these matrices have arbitrary scaling, it would be a good idea to standardize the columns before concatenating them. Standardize U and V separately, then concatenate with numpy's `concatenate` method. Call this concatenated matrix, `UVstd`.

Apply hierarchical and K-means clustering methods on `UVstd`. For each clustering method, identify 5 clusters. Compare the clustering results by applying three different cluster validation metrics to evaluate the clustering performance.

Which cluster performance metrics can you use? Do we have true labels? Does one performance metric seem to clearly be better than another? Why would you choose one metric over another? What interpretation, if any, does each metric have in the context of our problem? Explain.

Note: In this part, - Creating a new data `Rmedium` by `ratings_stacked.pkl` and `Rsmall`, 1. Loading `rantings_stacked.pkl` and adding the `user id` having less than 134 NA's in it to `user id` in `Rsmall`, 2. Adding movies with `movie id` $134 - 234$ to `movie id` in `Rsmall`, 3. Name the new dataset as `Rmedium` and use `Rmedium` to do clustering. - Using the 'best' model you select in Question 2e to compute `UVstd`.

SOLUTION

In [310]:
```
np.random.seed(134) # set seed for tests
ratings_stacked = pd.read_pickle('data/ratings_stacked.pkl').unstack()

na_ratings = ratings_stacked.isnull().sum(axis=0)
selected_users = na_ratings[na_ratings < 134].index
filter = ratings_stacked.loc[selected_users]

movie_ids = range(134, 235)
movie_ids_stacked = ratings_stacked.loc[movie_ids]

Rsmall_ids = pd.concat([Rsmall, movie_ids_stacked])
Rmedium = pd.concat([filter, Rsmall_ids], axis=1)
```

In [301]:
```
best_output_reg = compute_UV_reg(Rmedium, K=20, lam=1.0, alpha=0.001)
best_U_reg = best_output_reg['U']
best_V_reg = best_output_reg['V']

from sklearn.preprocessing import StandardScaler
```

```
U_std = StandardScaler().fit_transform(best_U_reg)
V_std = StandardScaler().fit_transform(best_V_reg)

UVstd = np.concatenate((U_std, V_std), axis=0)
```

```
In [302]: from sklearn.cluster import AgglomerativeClustering

          hierarchical_cluster = AgglomerativeClustering(n_clusters=5)
          hierarchical_labels = hierarchical_cluster.fit_predict(UVstd)
```

```
In [303]: from sklearn.cluster import KMeans

          kmeans_labels = KMeans(n_clusters=5, random_state=0).fit_predict(UVstd)
```

True labels are not known so clustering methods I will be using are Silhouette Score, Calinski-Harabasz Index, and Davies-Bouldin Index.

```
In [304]: from sklearn.metrics import silhouette_score, calinski_harabasz_score, davies_bouldin_score

          silhouette_hierarchical = silhouette_score(UVstd, hierarchical_labels)
          silhouette_kmeans = silhouette_score(UVstd, kmeans_labels)
          print(silhouette_hierarchical)
          print(silhouette_kmeans)

          calinski_harabasz_hierarchical = calinski_harabasz_score(UVstd, hierarchical_labels)
          calinski_harabasz_kmeans = calinski_harabasz_score(UVstd, kmeans_labels)
          print(calinski_harabasz_hierarchical)
          print(calinski_harabasz_kmeans)

          davies_bouldin_hierarchical = davies_bouldin_score(UVstd, hierarchical_labels)
          davies_bouldin_kmeans = davies_bouldin_score(UVstd, kmeans_labels)
          print(davies_bouldin_hierarchical)
          print(davies_bouldin_kmeans)
```

```
0.5248348219818862
0.5327258037593081
318.24610038671807
349.754271163516
3.5114883142141027
3.045376985566975
```

The Silhouette Coefficient is used to find the separation distance between clusters, so a measure of how close each point in one cluster is to another cluster with a range of [-1,1]. Negative values imply the value is assigned to the wrong cluster, near 1 tells us the clusters are far from neighboring clusters, and near 0

means clusters are close to one another. In this case, the kmeans has a higher silhouette coefficient than the hierarchical method so kmean clusters are farther from one another.

Calinski-Harabasz Index measures how similar a point is to its own cluster compared to other clusters. It calculates the distance from a data point to its own cluster centroid and then the distance from that cluster centroid to the global centroid. A higher value would mean that the clusters are well separated, more dense,and better defined, again in this case the kmeans has the higher number.

Davies-Bouldin Index calculates the similarity between a cluster and it's most similar cluster in the model, clusters with the closest distance. Here a lower score index is desirable as the Davies-Bouldin Index is the average similarity of clusters so a smaller number would mean lower average, clusters are well-separated from one another and compact. Looking at kmeans and hierarchical, kmeans has the lower score so again kmeans has the better clustering performance.

For our problem we are qualitatively inspecting users and movies in the cluster and deciding on a representative movie for each cluster so each cluster is a variation of user preference. This means that each cluster is distinctly different so we would therefore choose the metrics that detail cluster separation and distance. Through the cluster validation methods, kmeans proved to be better in the context we are looking for. Out of the three metrics we chose, they were very similar to one another in telling cluster separation however I would choose Calinski-Harabasz Index as it both looks for an objects relation within it's own cluster and then the relation to outside clusters, between and within cluster dispersion.

0.1.9 Question 3b: Visualizing Clusters in Latent Space

Select the clustering method based on the evaluation results in q3a and visualize the clusters using UMAP. Are the clusters and UMAP projection consistent?

SOLUTION

In [305]:
```
# install umap
# !pip install umap-learn
```

In [306]:
```
#!pip install cython
#!pip install numpy scipy
#!pip install scikit-learn
#!pip install hdbscan
```

In [307]:
```
import umap
import hdbscan
import sklearn.cluster as cluster
```

In [ ]:
```
umap_reducer = umap.UMAP(n_components=2)
umap_projection = umap_reducer.fit_transform(UVstd)

plt.figure(figsize=(8, 6))
for i in range(5):
    plt.scatter(umap_projection[kmeans_labels == i, 0], umap_projection[kmeans_labels == i, 1],

plt.title('K-means Clustering (2D UMAP)')
plt.legend()
plt.show()
```

Yes the clusters and Umap projection is consistent as in terms of cluster metric performance. We didn't get the best scores in our performance metrics such as for the Silhouette Coefficient. A near one number is ideal while we achieved a score of around 0.5 for both clustering methods and for Davies Bouldin Index a near zero score would indicate a great clustering model but we recieved values above 3. In the UMAP we can see an area where most of the clusters are very close to one another, even overlapping, while the orange cluster is the outlier being much farther away from the rest.