DATA.ML.360, Assignment 2b

Optimizing Group Recommendations: Our Proposal

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Kendall Tau Distance and Disagreement

- Kendall tau distance is a metric that counts the pairwise disagreements of two rankings.
 - It is the number of pairs that are in different order in the two rankings.
 - $\tau_{A,B}$ is the Kendall tau distance between rankings A and B.
- Disagreement captures the differences in the item ratings between group members.
- We have defined disagreement to be large when users have very large Kendall tau distance difference, and small when they are very close to each other.
- Now disagreement d for movie ranking R and users' personal movie suggestion rankings M_u of user u in the group g is defined as follows:

$$d_R = \max_{u \in g} (\tau_{R,M_u}) - \min_{u \in g} (\tau_{R,M_u})$$

Kemeny-Young Method

- Finds optimal order of recommendations. Logic is as follows:
- 1. Generate a permutation of the order of the items (movies) in the group recommendations.
- 2. Calculate the Kendall tau distance between the permutation and the group members' rankings.
- 3. Sum the Kendall tau distances (calculated at step 2) for all group members.
- 4. Repeat steps 1-3 for all permutations.
- Choose the permutation that minimizes the sum of Kendall tau distances.This is now the optimal aggregation order.

Our Proposal I

- Modify Kemeny-Young to minimize our disagreement metric.
- Now our aggregation method:
 - 1. Find the movies that are in all users' recommendations and find the common ones.
 - 2. From all the movie permutations, find the one which minimizes disagreement defined above.
 - 3. This is now the group movie recommendations, where the disagreement between users is the smallest.

Our Proposal II

- Our method takes disagreement into account, unlike the previous methods.
 - Average: some like, others may not.
 - Least Misery: nobody hates or loves.
- Thus, the resulting group recommendations are both:
 - 1. movies recommended to the users (they are predicted to like them), and
 - 2. movies for which their opinions align best with each other.
- Please see our <u>repository</u> and <u>README.md</u> for futher details.