

Modality Completion and Multi-View Disease Prediction via Enforcing Collective Modality-Specific Matrices using Deep Matrix Factorization

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1 Data Set

ADNI (Alzheimer’s Disease Neuroimaging Initiative) is a multisite study of the progression of Alzheimer’s Disease. The study examines patients through multiple modalities, such as T1-weighted MRI, diffusion-MRI, and genotypes. Each modality describes a patient in a particular perspective, while the dimensionality varies from one modality to another. Due to a variety of reasons, such as health conditions or dropping out from study, one or few modalities are missing for some patients.

2 Objectives

This project aims to achieve the following goals:

- Complete the missing modalities for the multi-modality problem setting, where the number of modalities can be larger than two;
- After completing the missing modalities, predict the disease label of a patient in a multi-view manner, so that the predictions incorporate information from multiple modalities.

3 Related Work

Wang et al. (2017) used collective deep matrix factorization on the ADNI data set and factorized each modality into a modality-specific and a modality-invariant matrix. The modality-specific matrix represents the features of a specific modality, while the modality-invariant matrix is the enforced shared representation of a patient across all modalities. Their work did not attempt to complete the missing modalities. Instead, for subjects whose modalities are incomplete, they defined an indicator which forces the missing modality to be a vector of 0, so that it will not contribute to the loss.

Suo et al. (2019) tackled the missing modality problem in the two modality setting by combining GAN and metric learning. Although they proposed an effective approach, the network can only handle data that has two modalities.

4 Critical Assumptions

This section discusses important assumptions of the proposed project. The similarities and differences of these assumptions from previous works will be discussed in section 5.

- **Assumption 1:** The information that a modality contains can be decomposed into nearly exclusively two components: (1) the features of a particular modality, and (2) the features of a particular patient that is being examined under that modality. Thus, it is reasonable to consider factorizing a modality matrix into a modality-specific matrix and a patient-specific matrix;
- **Assumption 2:** The features of a particular modality should hold regardless of the patient that is being examined, thus a shared modality-specific matrix can be extracted across all patients that have data on that particular modality;
- **Assumption 3:** Modalities express information about a patient from different perspectives, thus for different modalities, the patient-specific matrices of a particular patient can be different in value and dimensionality;
- **Assumption 4:** There is a non-linear relationship between the patient-specific matrices of the same patient, that means the patient-specific matrix/matrices of a patient extracted from one or several modalities have the predictive power of other patient-specific matrices of the same patient.
- **Assumption 5:** The patient-specific modalities of one patient extracted from respective modality matrices can be regarded as a multi-view representation of a patient. These patient-specific matrices can be used as multiple inputs in predicting the disease label of a patient.

5 Novelties and Contributions

Assumption 1 and **2** mentioned in section 4 hold the same as Wang et al. (2017). **Assumptions 3, 4** and **5** provide new insights to the multi-modality problem and enables the completion of missing modalities for the situations where the number of modalities is more than two.

Assumption 3 and **4** are the vital assumptions of this project for completing missing modalities. **Assumption 3** assumes that different modalities of a particular patient do not necessarily share the same set of patient-specific features. Wang et al. (2017) factorized a shared modality-variant matrix across all modalities of the same patient. In this way, although the communal information that all modalities carries about one patient is extracted, especially the AD-related features, the discrepancy between the original modality matrix and the matrix recovered by the modality-variant and the modality-invariant matrix can be very large.

This project does not discard any patient-specific information that a modality can contain. By doing so, we are able to reconstruct the missing modalities using the modality-specific matrix and the patient-specific matrix, where the patient-specific matrix of the missing modality is predicted by a non-linear combination of other patient-specific matrices of the same patient.

Assumption 4 assumes non-linear relationships between patient-specific matrices of a particular patient in order to obtain predictions of a missing patient-specific matrix using other existing patient-specific matrices. Different from Assumption 4, Wang et al. (2017) only assumed a non-linear relationship between modality-specific matrices. This project can at the same time make the same assumption, however, since we do not intend to discover the associations between modalities, this additional assumption is not used.

Assumption 5 uses comprehensive information of a patient in a reduced dimensionality to predict the disease label. By combining all patient-specific information and by eliminating the modality-specific features and only using patient-specific features, we are able to make better predictions on the disease label, and reduce model complexity and computational requirements of the neural network.

6 Technical Problems

1. How to obtain collaborative modality-specific matrices?
2. How to obtain patient-specific matrices?
3. How to predict a patient-specific matrix that is missing using other existing patient-specific matrices of the same patient?
4. How to predict the disease label of a patient using all or some of the patient-specific matrices?

7 Proposed Methods

7.1 Collective Deep Matrix Factorization

We obtain the shared modality-specific matrix and the patient-specific matrix using Collective Deep Matrix Factorization on the observed modalities. Mathematical formulations and network architecture is under construction.

7.2 Missing Modality Completion

After obtaining the modality-specific matrices and the patient-specific matrices, we complete the missing modalities by firstly predicting the missing patient-specific matrix by training a neural network which takes the non-missing factorized patient-specific matrices of the same patient as the input, than combine the predicted patient-specific matrix with the modality-specific matrix which is obtained factorizing through all the matrices of the same modality.

To achieve predicting one missing patient-specific matrix using other patient-specific matrices of the same patient, we need to answer a question that is - what combination of input features would perform well in predicting the missing matrix? To answer this question, we need to understand more intrinsic properties of the patient-specific matrices and experiment through different combinations.

7.3 Multi-View Disease Prediction

We train a deep neural network that takes multiple patient-specific matrices of the same patient as the input, and output the prediction of the disease label. Although the information that a patient-specific matrix contains can be redundant (as we discussed in Section 5 **Assumption 3**), the deep neural network would perform feature selection as it attempts to improve the prediction performance.

7.4 Technical Difficulties

- This project may involve rather complex data-preprocessing procedures, which can take a considerable time to accomplish;
- Deep neural networks are highly non-convex and finding the global optimal can be a challenging task. The initialization of the deep neural networks should be carefully chosen;
- More items will be added as the project goes on.

8 References

[Wang et al.] Qi Wang, Mengying Sun, Liang Zhan, Paul Thompson, Shuiwang Ji, and Jiayu Zhou. 2017. Multi-Modality Disease Modeling via Collective Deep Matrix Factorization. In Proceedings of the 23rd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD '17). ACM, New York, NY, USA, 1155-1164. DOI: <https://doi.org/10.1145/3097983.3098164>

[Suo et al.] Qiuling Suo, Weida Zhong, Fenglong Ma, Ye Yuan, Jing Gao¹ and Aidong Zhang. 2019. Metric Learning on Healthcare Data with Incomplete Modalities (IJCAI '19)