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Report 67
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Summary

During the past week I implemented the proposed method in [1] called MDNNMD. I prepared the experiments that I will compare later with my proposed method. I improved my previous work about these method using the reviews I got. For example one of the reviews made me realize that the oversampling task was not applied for all the methods except for mine. And in order to have consistency I added this for all methods. Morover, adding MDNNMD to my experiments gives a more valid comparison since I will be comparing 5 methods with different integration stages: (1) Early stage by concatenation and using LR, SVM, RF; (2) Late stage by using MDNNMD; (3) Middle stage by applying the proposed method. Then the necessity of middle stage integration can be demonstrated since it can lead to extracting between modalities relations. Table 1 indicates the research progress timeline that I plan to follow durin this semester. Of course there might be some tasks that are unkown at this time and I will update this table in future.

Classification Task		
Oct. 22	✓	Implement other methods for comparison.
Oct. 29	•	Implement proposed method and compare with other methods.
Nov. 5	•	Evaluate previous work using a new dataset and write the first draft of paper.
Biomarker Extraction Task		
Nov. 12	•	Implement weight extraction from a trained netwrok and rank features(genes).
Nov. 19	•	Evaluation of top features.
⋮		
Dec. 31	•	Finish Paper

Table 1: Research Progress Timeline

Data

Since I was implementing MDNNMD, I tried my best to do a similar job to theirs. Therefor for these experiments I used their exact preprocessed dataset which is a reduced version of METABRIC breast cancer categorized into short-term and long-term survival.

		Long term (0)	**Short term (1)**
Whole		1489	491
MDNNMD	Train after oversampling	1072	1072
	Validation	268	89
	Test	149	49
SVM,LR,RF	Train after oversampling	1340	1340
	Test	149	49

Table 2: Dataset distribution in details

Results and Conclusions

After implementing all the methods, the results seem to be contradicting with what is achieved in [1]. Below I mention a list of differences between my implementation and what was mentioned in [1]:

- Oversampling on training set. (not mentioned)
- Concatenation of modalities for LR, SVM, RF. (not mentioned)
- No validation set for LR, SVM, RF. (not mentioned)
- Percentage of dropout layer (not mentioned, I used 0.8)
- Network optimizer (only mentioned the initial rate = 0.001, I used Adadelta which uses an adaptive learning rate initiazed by 0.001)
- For ROC curve I used long term patients as positive class. (not mentioned)
- They did not mention specifically how they integrate the final result among modalities. What I did was to sum the prediction probability of the three networks using the weights they mentioned and then set the max probability as the predicted class.
- I mostly used Keras built in libraries to apply regularizer, dropout, loss function, etc. while [1] mostly implemented these themselves.

Since MDNNMD is a pretty straight forward method and there is not much complexity that could cause to misleading results, specially while using built-in packages, I think we can count on these result and still use them for comparison.

Model	**%Acc.**	**%Pre.**	**%Spe.**	**%F1-Score**
RF	74.24	78.91	**72.40**	76.51
LR	**80.56**	**81.61**	72.16	**81.08**
SVM	75.15	56.54	24.78	64.53
MDNNMD	76.72	75.55	55.47	76.13

Table 3: Comparision of Accuracy, Precision, Specificity, and F1-score for different model.

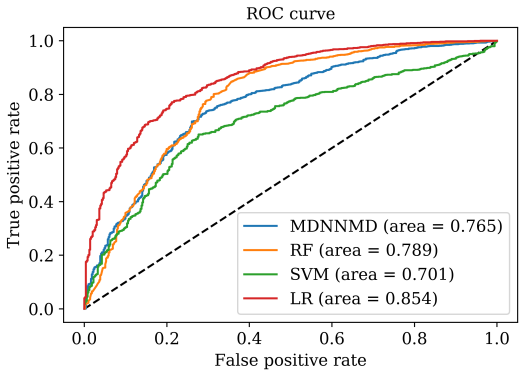
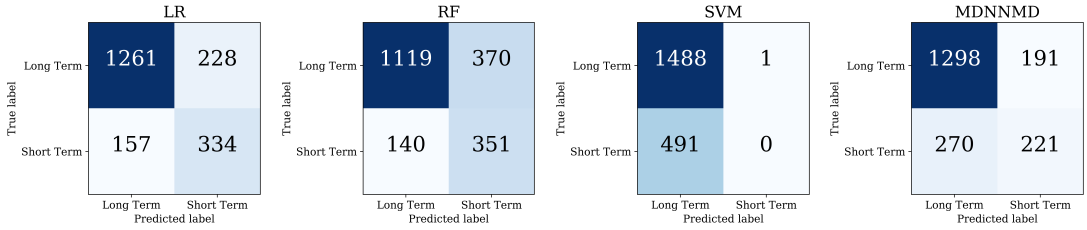


Figure 1: ROC curve of MDNNMD [1], LR, RF, SVM.



(a) (b) (c) (d)

Figure 2: Confusion matrices for MDNNMD [1], LR, RF, SVM.

References

[1] Dongdong Sun, Minghui Wang, and Ao Li. A multimodal deep neural network for human breast cancer prognosis prediction by integrating multi-dimensional data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2018.