Template for Short Paper Submissions for the MICCAI KiTS23 Challenge

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Abstract. Write a brief ~200 word abstract here describing the problem and your approach. Once results are announced, please mention your test set metrics and leaderboard place here.

Keywords: First keyword, second keyword, another keyword

1 Introduction

Provide a brief introduction to the segmentation problem that you are approaching. Make sure to mention any information that might help to explain why you chose your specific approach later on. Don't spend too much time explaining the clinical background -- you are not expected to be an expert in this area.

2 Methods

This is a good place to briefly introduce your approach and provide a teaser figure that illustrates how it works and any ways in which it might be unique.

2.1 Training and Validation Data

You are allowed to use any other *publicly available* dataset in conjunction with the official training set in order to prepare your submission for this challenge. Please describe the data you used here. If you only used the official training set, simply state "Our submission made use of the official KiTS23 training set alone."

2.2 Preprocessing

Full description of your pre-processing strategy. Make sure to answer the following questions:

1. How was the data spatially transformed and/or resampled?
2. How were the HU values normalized/transformed, if at all?
3. How was the data cleaned and/or filtered, if at all?

2.3 Proposed Method

This will be your longest section. Use this space to describe your approach in detail, adding ``subsubsections'' as desired. Make sure cover the following topics:

1. Network architecture, including hyperparameters such as strides, kernel sizes, etc.
2. Loss function, including any class-weighting or other hyperparameters
3. Optimization strategy, including any hyperparameters
4. Validation strategy, including selection criteria for final models

5. Ensembling strategy, if any
6. Any other post-processing performed on the predictions to enhance the output

3 Results

You will be given the opportunity to add your test set results to this section once they are announced, but before then, please use this section to describe how your approach appears to perform on the publicly available data alone. Be sure to include:

1. Metric values during validation -- this is a good place for a table that breaks these metrics down by class
2. Some examples of predictions next to human-labels -- especially valuable if they illustrate a common mode of disagreement

This is also a good place to include details about how training went, such as how long training and inference took on a given computing setup.

3 Discussion and Conclusion

This space should be used to once again summarize your approach and results. You are also encouraged to use this space to provide an analysis of why your approach did or didn't work well on this problem, and how it might be improved in the future.

In addition, we invite you to discuss here any comments you have on the challenge itself, including suggestions or criticisms about how the challenge was organized. Please be honest, we can take it :-)

Acknowledgements

References

1.	Smith, T.F., Waterman, M.S.: Identification of Common Molecular Subsequences. J. Mol. Biol. 147, 195--197 (1981)