

# CONSTRAINED HARMONIZATION ALGORITHM FOR POOLING MULTI-SITE DATASETS

POSTER



Vishnu Lokhande, Akshay Mishra, Kersten Diers, Emrah Düzel, Martin Reuter, Barbara B Bendlin and Vikas Singh

We discuss novel datasets pooling methods for the analysis of AD imaging datasets using harmonization constraint techniques.

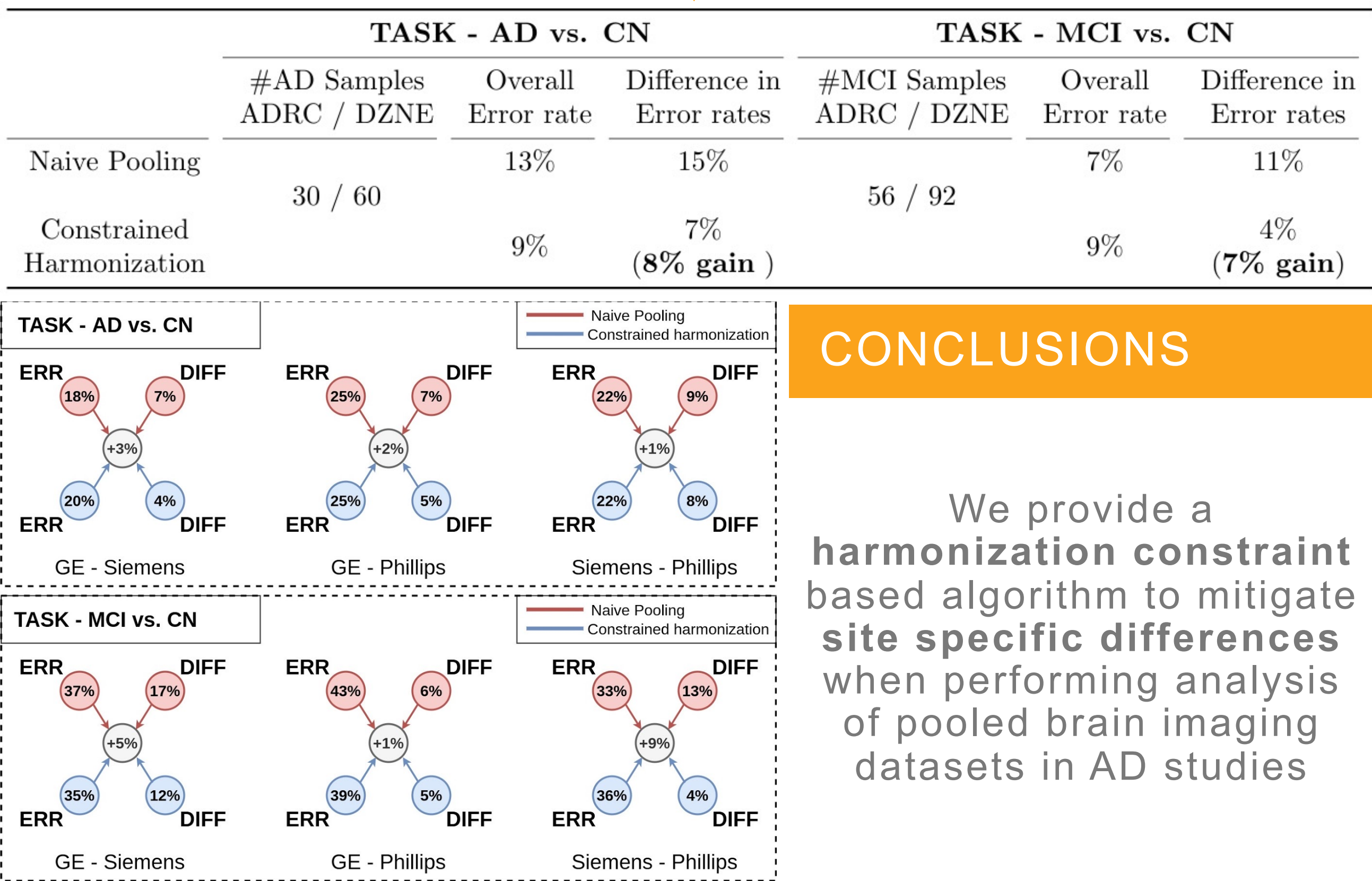
## INTRODUCTION

- **Pooling datasets** from multiple studies can significantly improve **statistical power**.
- Deep learning in scientific / biomedical problems suffer from small **sample sizes** at individual sites/institutions.
- Off-the-shelf models may utilize **site-specific artifacts** rather than disease-specific features in making predictions
- **Fairness constraints** can be adopted to harmonize the performance of models across scanners/sites.

## METHODS

- (a) Pooling across Sites
- Freesurfer summaries of **Wisconsin ADRC** and **German DZNE**
- (b) Pooling across Scanners
- MR images **ADNI** on scanners – **Phillips, GE** and **Siemens**.
- A **constraint** to equalize the performance of the **trained classifier** across the domains added to the **optimization objective**.
- Naïve pooling method and harmonization constraint approach are compared.

## RESULTS



## REFERENCES

Lokhande, V. S., Akash, A. K., Ravi, S. N., & Singh, V. (2020, August). Fairalm: Augmented lagrangian method for training fair models with little regret. In European Conference on Computer Vision (pp. 365-381). Springer, Cham.

Moyer, D., Ver Steeg, G., Tax, C. M., & Thompson, P. M. (2020). Scanner invariant representations for diffusion MRI harmonization. Magnetic resonance in medicine, 84(4), 2174-2189.

Research supported by NIH R01 AG062336

## CONTACT



Vishnu Lokhande,  
[lokhande@cs.wisc.edu](mailto:lokhande@cs.wisc.edu)

Vikas Singh,  
[vsingh@biostat.wisc.edu](mailto:vsingh@biostat.wisc.edu)

