

Manuscript Title

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Abstract

In the subchallenge 2, the training set were collected very differently in comparison with the test set. Especially, training set is *in vivo* transcription data set described in [1] while test set is *in vitro* transcription data set. To adjust know batch effects, ComBat algorithm[2] in sva package[doi:10.1093/bioinformatics/bts034] was applied on the high-throughput transcription data and principal component analysis plots on the raw data and adjusted data were made for checking the performance of adjustment (Fig. 1).

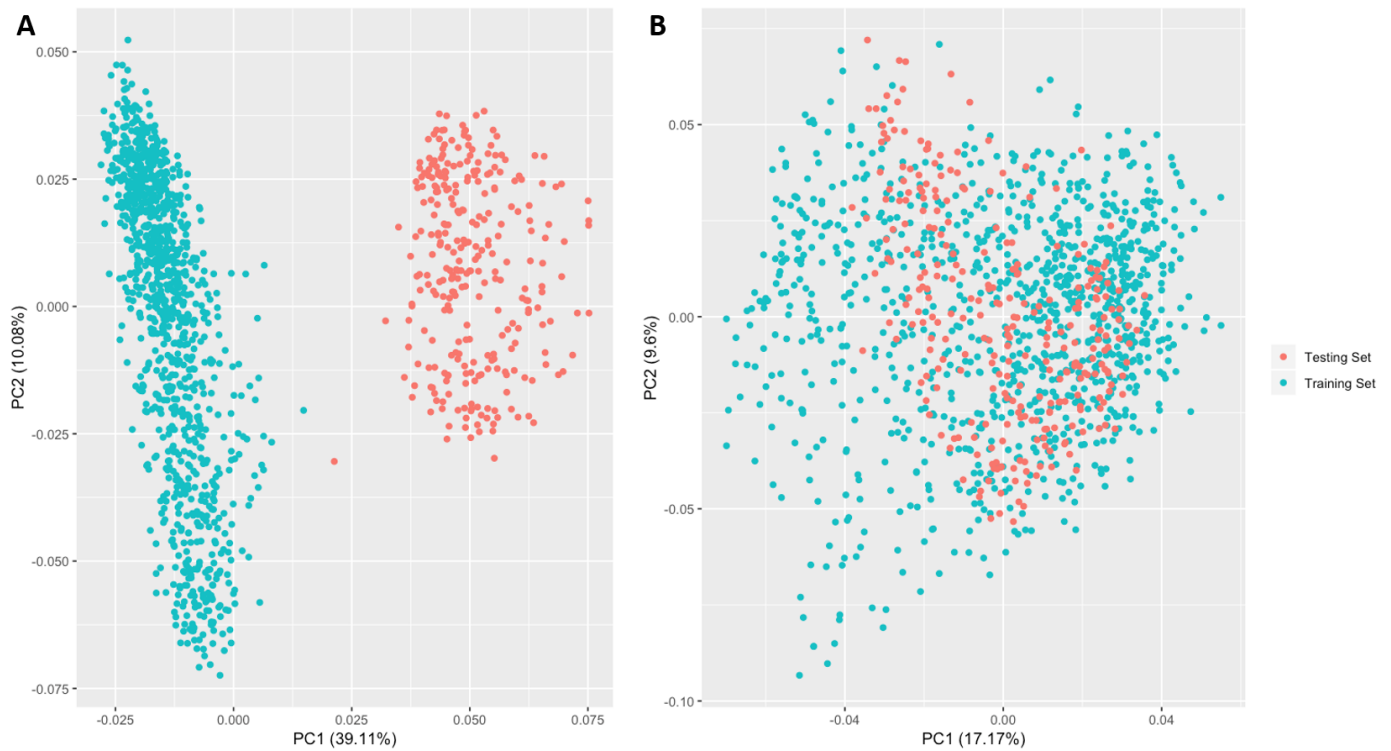


Figure 1: Principal component analysis plots before (A) and after (B) adjusting batch effects

References

1. Population transcriptomics of human malaria parasites reveals the mechanism of artemisinin resistance

S. Mok, E. A. Ashley, P. E. Ferreira, L. Zhu, Z. Lin, T. Yeo, K. Chotivanich, M. Imwong, S. Pukrittayakamee, M. Dhorda, ... Z. Bozdech

Science (2014-12-11) <https://doi.org/f3ph2f>

DOI: [10.1126/science.1260403](https://doi.org/10.1126/science.1260403) · PMID: [25502316](https://pubmed.ncbi.nlm.nih.gov/25502316/) · PMCID: [PMC5642863](https://pubmed.ncbi.nlm.nih.gov/PMC5642863/)

2. Adjusting batch effects in microarray expression data using empirical Bayes methods

W. Evan Johnson, Cheng Li, Ariel Rabinovic

Biostatistics (2006-04-21) <https://doi.org/dsf386>

DOI: [10.1093/biostatistics/kxj037](https://doi.org/10.1093/biostatistics/kxj037) · PMID: [16632515](https://pubmed.ncbi.nlm.nih.gov/16632515/)