Bioinformatics aspects of aging and rejuvenation

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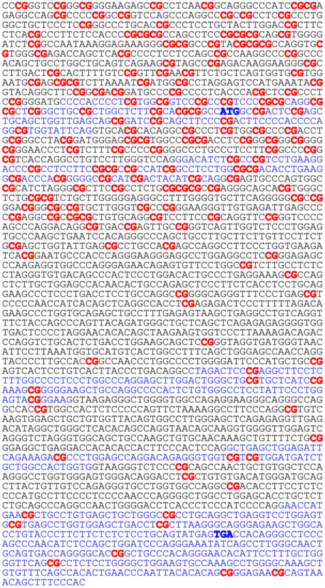
Assignment 1

Train epigenetic clock for microarray-based methylation dataset[2]



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Dataset

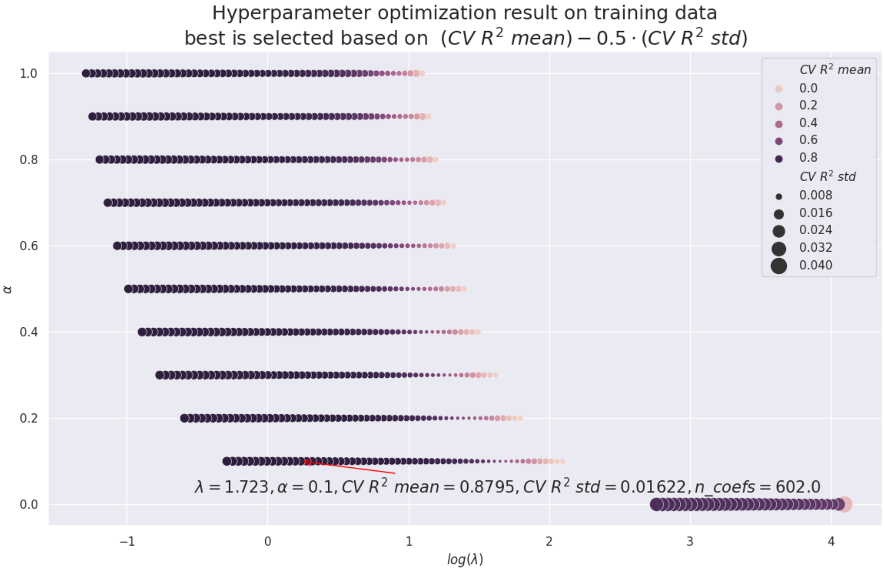
Source

- Genome-wide Methylation Profiles Reveal Quantitative Views of Human Aging Rates (Gene Expression Omnibus) [4]
- approximately 450k CpGs from **human whole blood**
- Illumina Infinium 450k (microarray)

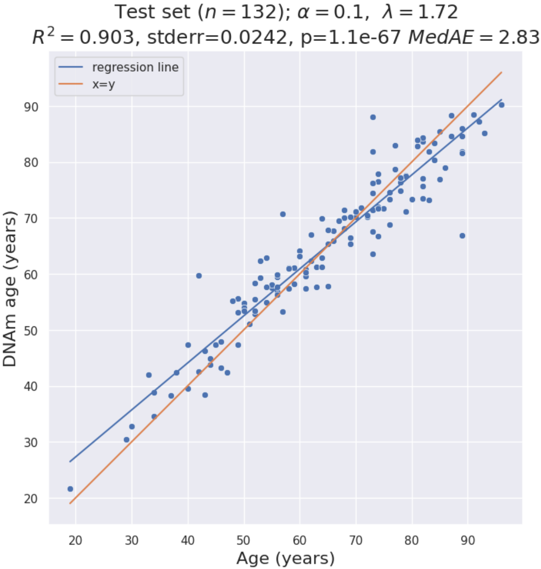
Details

- sample N=656
- features=473 034

Hyperparameter Optimization (ElasticNet)

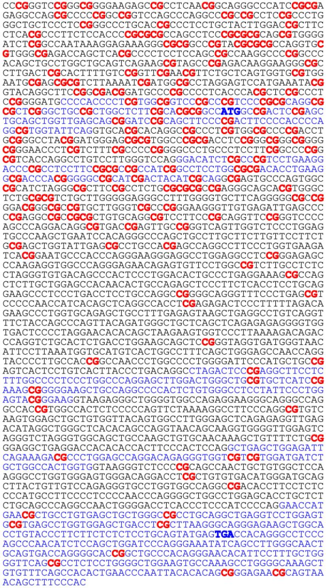


Results on Test Set



Assignment 2

Train epigenetic clock for RRBS-based methylation dataset (with missing data)[3]



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Dataset

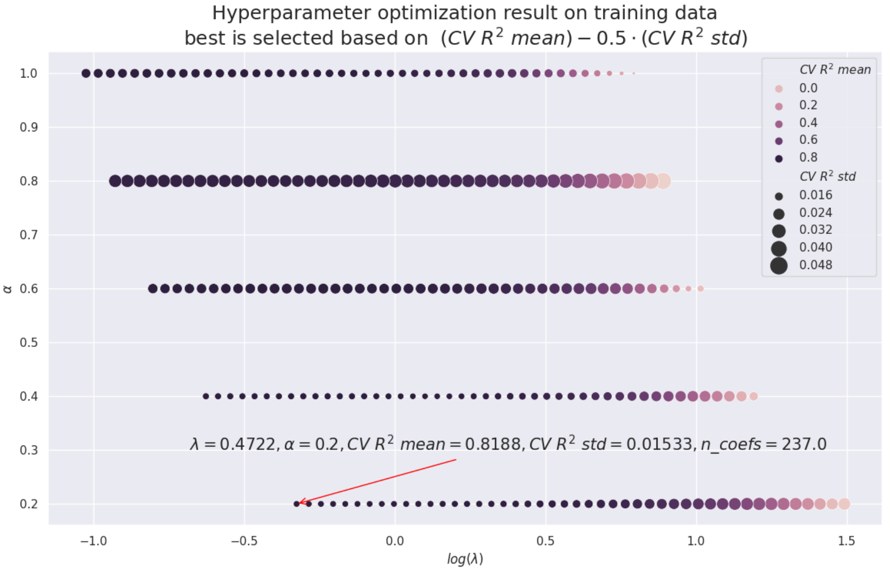
Source

- Data from ”Depression and suicide risk prediction models using blood-derived multi-omics data” [1]
- **Human blood**
- Reduced Representation Bisulfite Sequencing (RRBS)

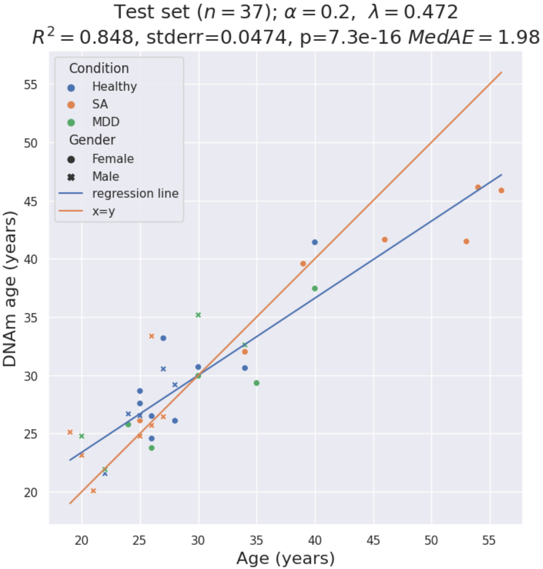
Details

- sample N=182
- conditions:
  - Healthy/Control=87
  - Major Depressive Disorder (MDD)=39
  - Suicide Attempters (SA)=56
- features=8 722 096
- data for missing CpG sites was filled with **mean**

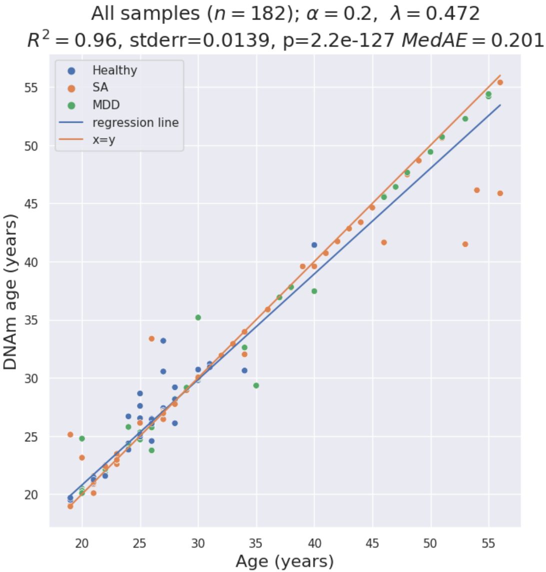
Hyperparameter Optimization (ElasticNet)



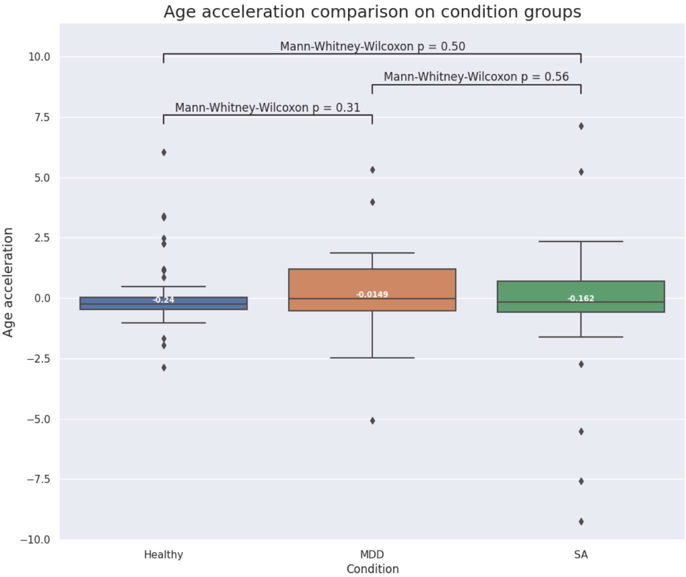
Results on Test Set



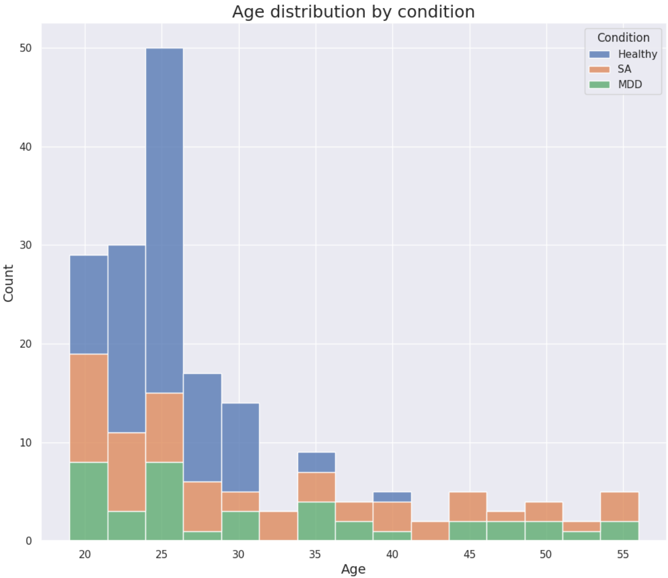
Results for All Instances



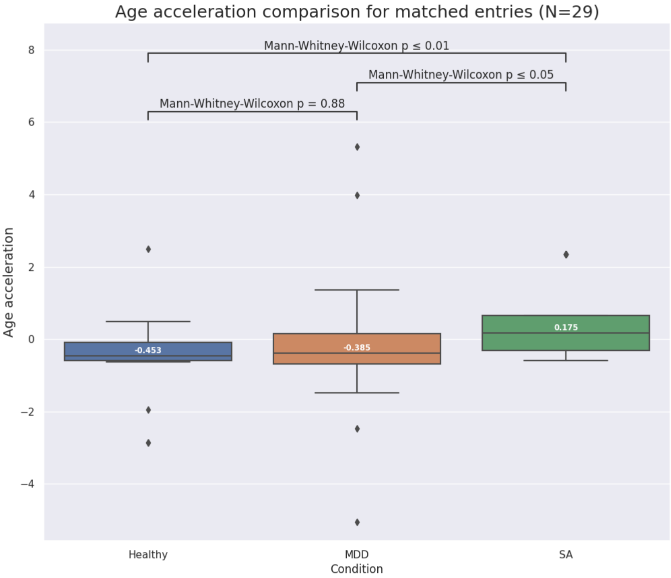
Age acceleration comparison by condition



Age distribution by condition



Age acceleration comparison by condition (controlled)



References

[1] Youngjune Bhak et al. “Depression and suicide risk prediction models using blood-derived multi-omics data”. en. In: *Transl. Psychiatry* 9.1 (Oct. 2019), p. 262.

[2] *Epigenetic clock assignment 1*. https://github.com/szazo/epigenetic-clock/blob/main/assignment1_microarray.ipynb. 2024.

[3] *Epigenetic clock assignment 2*. https://github.com/szazo/epigenetic-clock/blob/main/assignment2_rrbs.ipynb. 2024.

[4] *Genome-wide Methylation Profiles Reveal Quantitative Views of Human Aging Rates*. https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE40279. [Accessed 13-05-2024]. 2012.