Assignment for *Bioinformatics aspects of aging and rejuvenation* lecture

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Assignment 1

Train epigenetic clock for microarray-based methylation dataset[3]

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```

Dataset

Source

- Genome-wide Methylation Profiles Reveal Quantitative Views of Human Aging Rates (Gene Expression Omnibus) [5] [6]
- approximately 450k CpGs from **human whole blood**
- Illumina Infinium 450k (microarray)

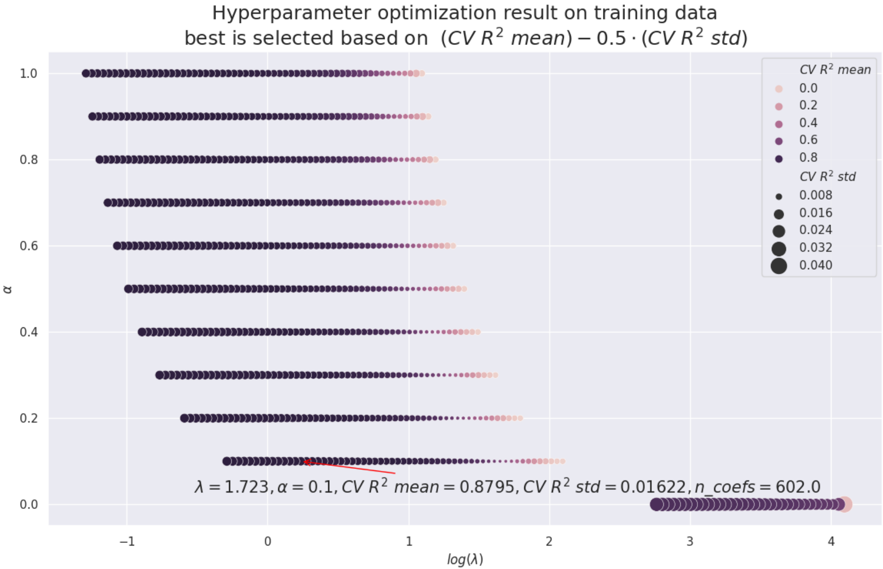
Details

- sample N=656
- features=473 034

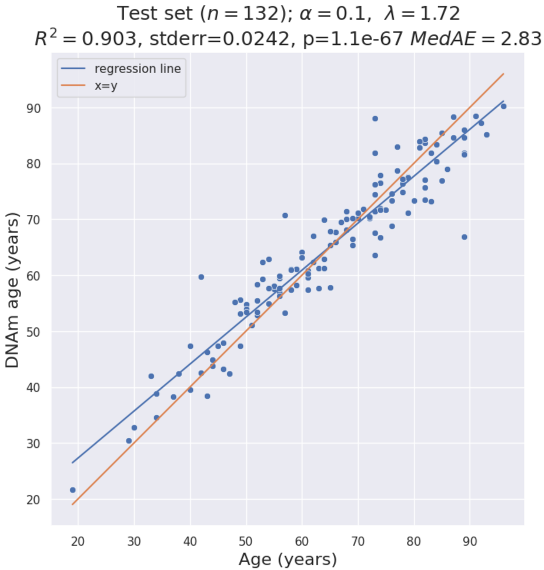
Model

- Elasticnet using Glmnet [1]
- 80-20 train-test split
- 10-fold CV

Hyperparameter Optimization (ElasticNet)

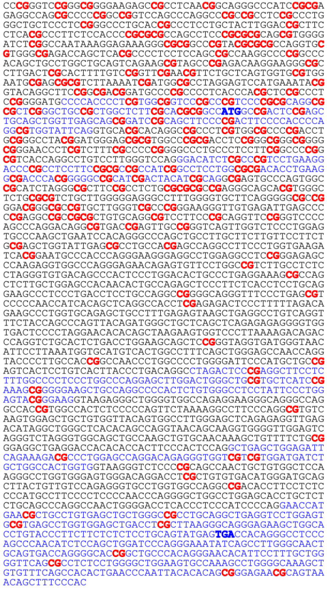


Results on Test Set



Assignment 2

Train epigenetic clock for RRBS-based methylation dataset (with missing data)[4]



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```

Dataset

Source

- Data from ”Depression and suicide risk prediction models using blood-derived multi-omics data” [2]
- Reduced Representation Bisulfite Sequencing (RRBS)

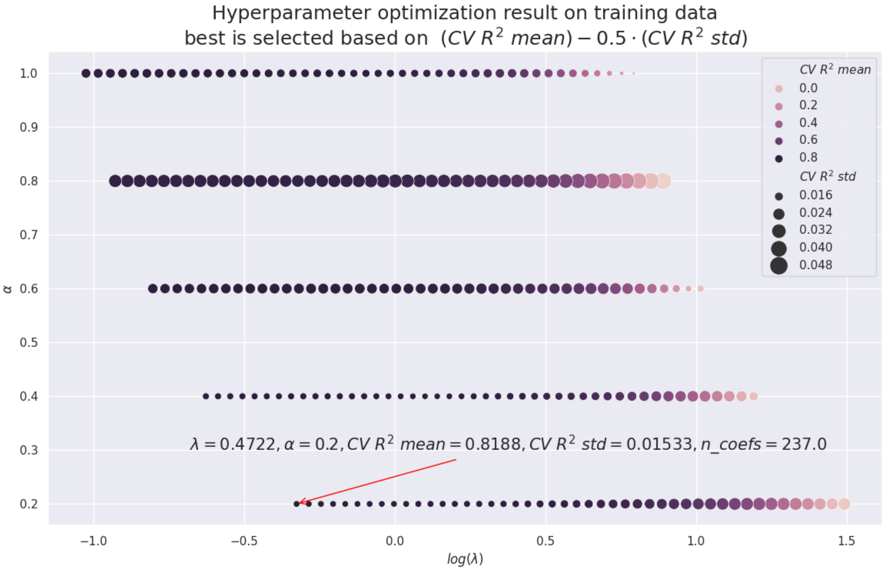
Details

- sample N=182 (Healthy/Control=87, Major Depressive Disorder (MDD)=39, Suicide Attempters (SA)=56)
- features=8 722 096

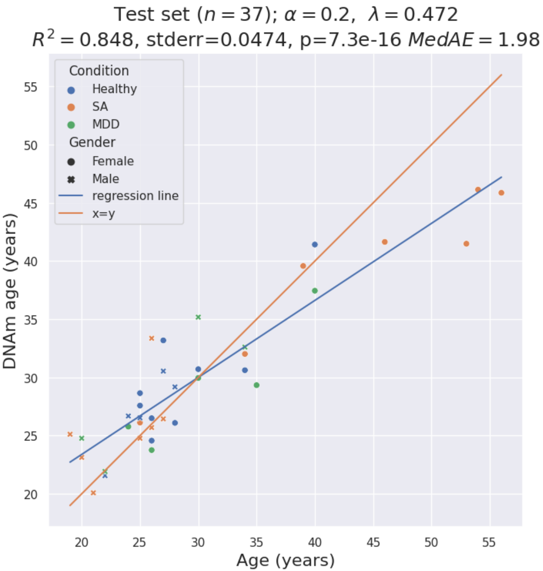
Model

- Elasticnet using Glmnet [1]
- 80-20 train-test split, 10-fold CV
- data for missing CpG sites was filled with **mean**

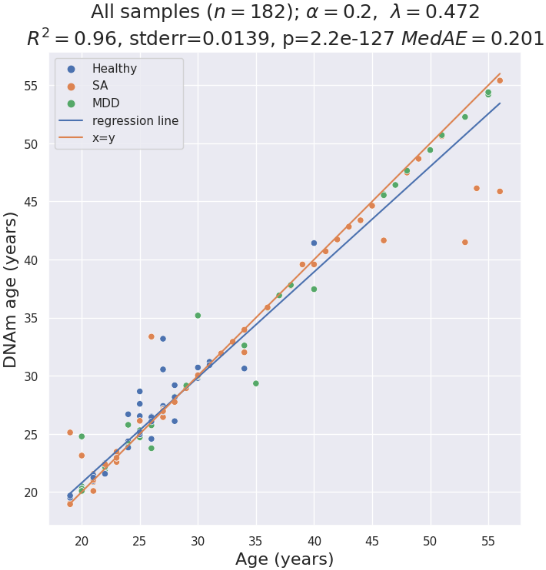
Hyperparameter Optimization (ElasticNet)



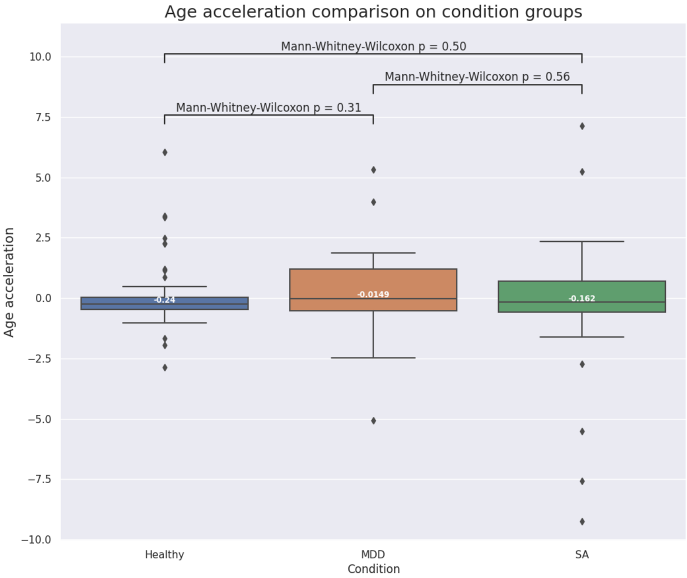
Results on Test Set



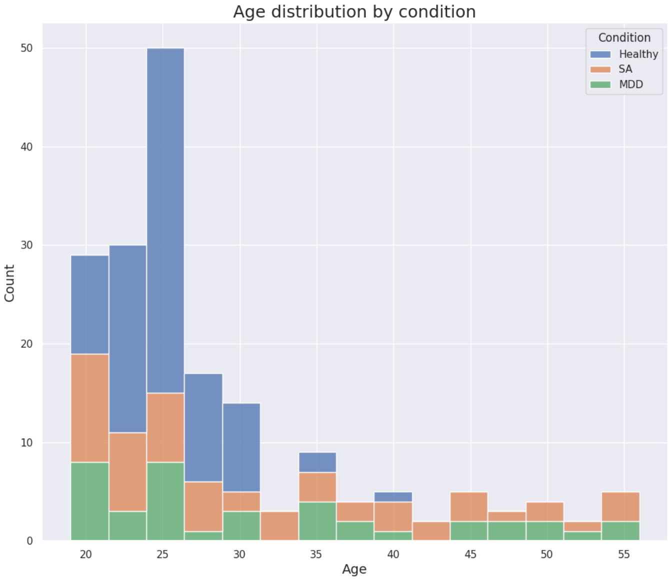
Results for All Instances



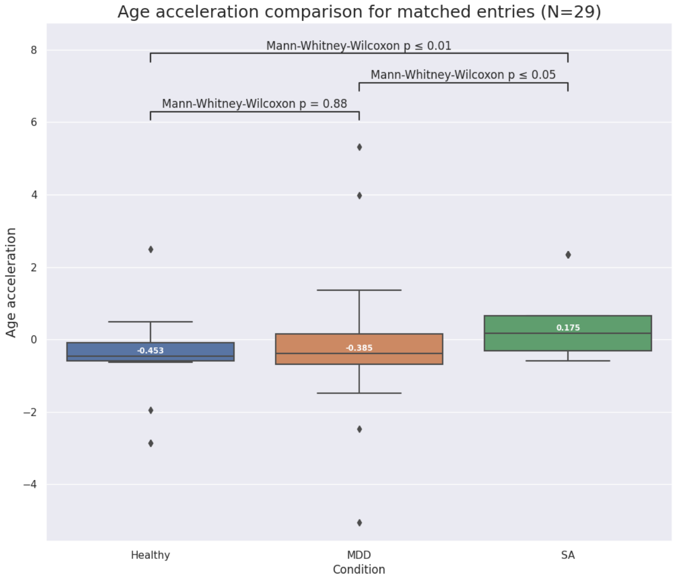
Age acceleration comparison by condition



Age distribution by condition



Age acceleration comparison by condition (controlled)



References I

[1] *An Introduction to ‘glmnet‘ — glmnet.stanford.edu*. https://glmnet.stanford.edu/articles/glmnet.html. [Accessed 16-05-2024].

[2] 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.

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

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

References II

[5] *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.

[6] Gregory Hannum et al. “Genome-wide Methylation Profiles Reveal Quantitative Views of Human Aging Rates”. In: *Molecular Cell* 49.2 (Jan. 2013), pp. 359–367. ISSN: 1097-2765. DOI: 10.1016/j.molcel.2012.10.016. URL: http://dx.doi.org/10.1016/j.molcel.2012.10.016.