A Regression Discontinuity Model to Evaluate the Effect of Retirement on Phenotypic Aging Results from a Large Cohort in China

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What is Already Known on This Topic:

- Global aging is accelerating, with 65+ population projected to increase from 703 million (9.1%) in 2019 to 1.6 billion (16%) by 2050.
- Retirement's health impact shows mixed evidence in current literature:
  - Some studies demonstrate improved mental health and life satisfaction post-retirement[1]
  - Others indicate increased health risks through reduced income and social connections[2]
- Current research heavily relies on subjective self-reported health measures and single biological indicators
- Existing studies often suffer from limited sample sizes and generalizability

What This Study Adds:

- Introduces phenotypic age as a comprehensive objective health outcome measurement, provides more objective health assessment compared to traditional self-reported measures
- Incorporates multiple physiological indicators (Albumin, Creatinine, etc.)
- Examines retirement's health impact across a broader population demographic

How This Study Might Affect Research, Practice or Policy:

- Offers a more reliable methodology for assessing retirement's health impact
- Enables evidence-based retirement policy recommendations through objective health metrics
- Supports the development of targeted health interventions for retirees.[3][4]

Objective and Method

- Causal relationship between retirement and biological aging, Gender-specific impacts on phenotypic age markers.
- Data Source: Large-scale health examination data from China.
- Methodology: Fuzzy regression discontinuity design
- The retirement age threshold is 60 or 55 for men and 55 or 50 for women. Analyze retirement's health impact through phenotypic age changes.

Key outcome Measurement-phenotypic age calculation

- Original Model[5]: Used 42 clinical biomarkers and chronological age Finally selected 9 clinical biomarkers plus chronological age.
- Current Study Modification: Used 8 biomarkers instead of 9 (No C-reactive protein). Validated modification through correlation analysis. Correlation coefficient between 9-biomarker and 8-biomarker phenotypic age: 0.99, p=0.000. This shows that the modified indicators are still very close to the original model.

$$\text{phenotypic age} = 141.50225 + \frac{\ln[-0.00553 \times \ln(1 - \text{mortality risk})]}{0.090165} \tag{1}$$

where

$$\text{mortality risk} = 1 - e^{-e^{xb}\exp(120\times\gamma)-1/\gamma} \tag{2}$$

$$\gamma = 0.0076927 \tag{3}$$

$$\begin{aligned} xb = &-19.907 - 0.0336 \times \text{albumin} + 0.0095 \times \text{creatinine} + 0.1953 \times \text{glucose} - \\ &0.012 \times \text{lymphocyte percentage} + 0.0268 \times \text{mean corpuscular volume} + \\ &0.3306 \times \text{red cell distribution width} + 0.00188 \times \text{alkaline phosphatase} + \\ &0.0554 \times \text{white blood cell count} + 0.0804 \times \text{chronological age} \end{aligned}$$

Excluding the term $0.0954 \times \ln(\text{C-reactive protein})$ in the original model.

Result and Robust check

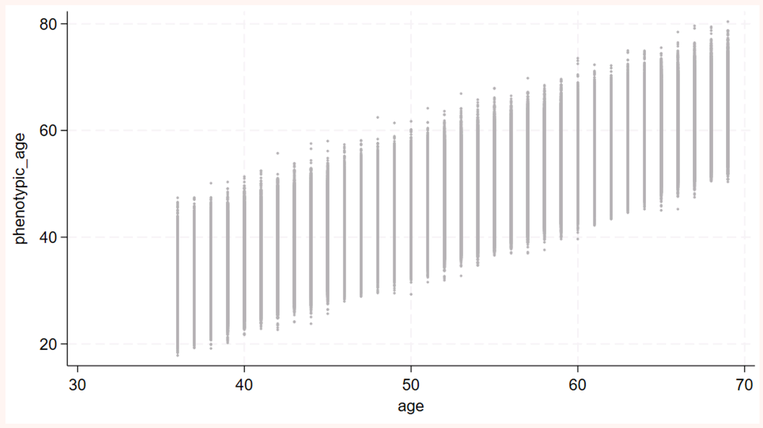

Figure 1. Scatter plot of age and phenotypic age

Table 1. Descriptive Statistics

Variable	Obs	Mean	Std.dev.	Min	Max
age	6,035,048	47.98254	9.248351	36	69
sex	5,601,918	0.5358154	0.4987157	0	1
married	5,601,918	1.585146	0.60505	1	3
Identity	5,601,918	2.567705	1.31355	1	8
Albumin	2,188,361	45.23484	2.064506	41.5	49
Creatinine	5,656,509	67.22327	12.78316	47	91
Glucose	5,751,402	5.654493	0.7603982	4.71	7.81
Lymphocyte percent	5,973,822	33.88426	6.721203	22.1	46.4
Mean (red) cell volume	5,973,833	90.46629	4.284422	82	98
Red cell distribution width	5,711,138	13.07913	0.8224637	11.7	14.9
Alkaline phosphatase_pve	2,144,517	70.11297	17.44607	43	106
White blood cell count	5,973,833	6.181174	1.404153	4	9.1
phenotypic_age	1,515,760	42.72514	9.880096	17.82907	80.41383

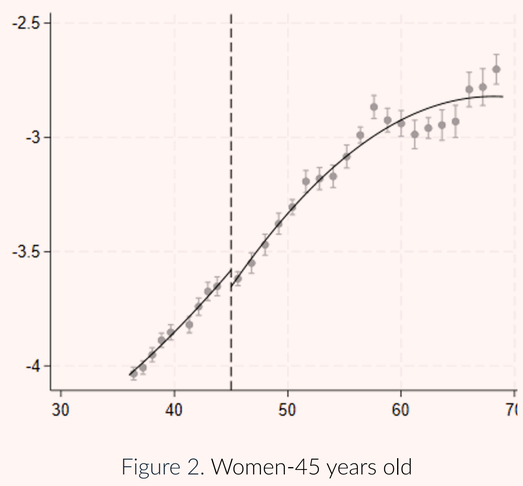

Figure 2. Women-45 years old

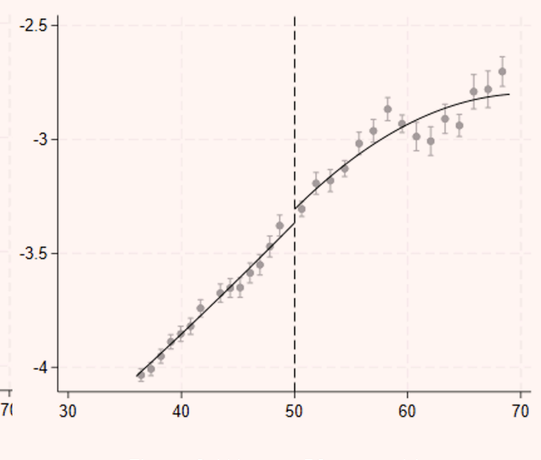

Figure 3. Women-50 years old

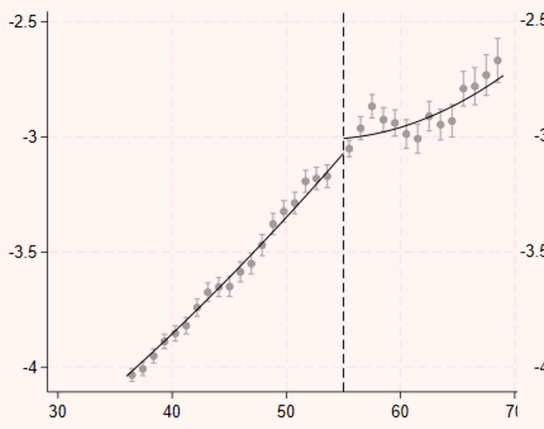

Figure 4. Women-55 years old

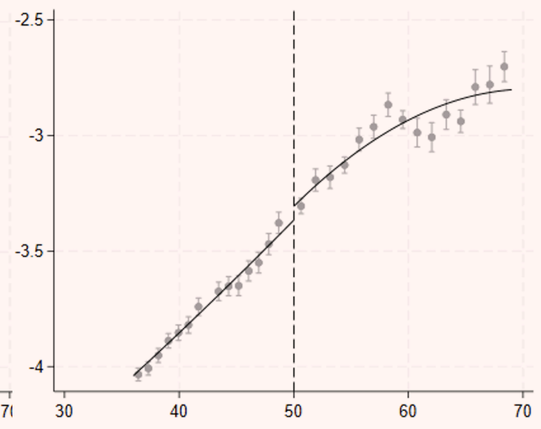

Figure 5. Men-50 years old

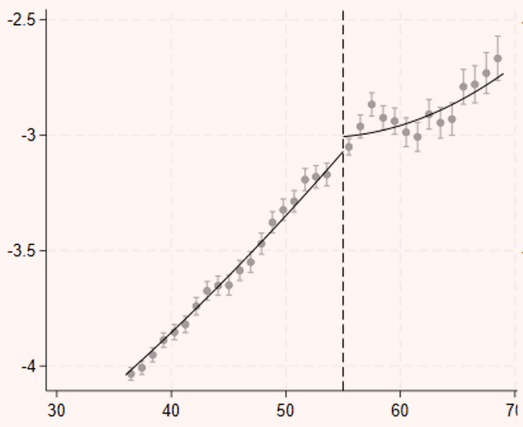

Figure 6. Men-55 years old

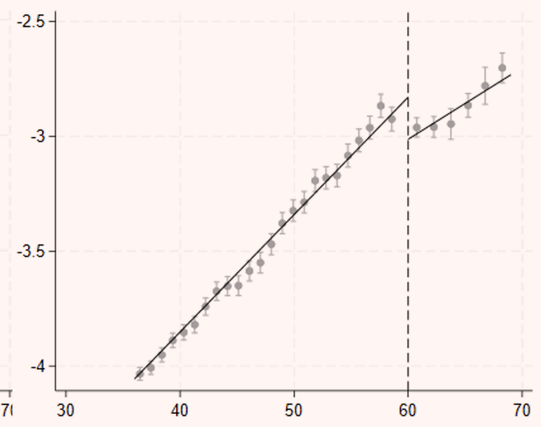

Figure 7. Men-60 years old

Pre-Retirement Trends:

1. All graphs show a consistent upward linear trend before retirement
2. The slope is relatively steep, indicating gradual biological aging
3. Data points show relatively small variance (tight error bars)

For Women:

1. All groups show no meaningful effect

For Men:

1. Only 60-year retirement shows a significant impact (P = 0.000).
2. Early Retirement for Special Positions (50/55) shows no meaningful effect.

Conclusion

1. Using phenotypic age as an objective biological aging marker, this study reveals gender-specific health effects of retirement through a robust regression discontinuity design.
2. For male retirees at standard retirement age (60), we find significant deceleration in biological aging (P = 0.000), showing retirement's positive health effects.
3. In contrast, female retirees show no significant changes in biological aging across all retirement ages, consistent with prior studies suggesting women's health trajectories are less sensitive to retirement transitions due to their diverse social roles and activities.
4. These findings suggest that retirement age policies might benefit from gender-specific considerations, particularly in providing targeted health support programs for men approaching standard retirement age.

References

[1] Thang T. Vo and Tran T. Phu-Duyen.
2. mental health around retirement: evidence of ashenfelter's dip.
Global Health Research and Policy, 2023.

[2] Asal Pilehvari, Wen You, and Xu Lin.
3. retirement's impact on health: what role does social network play?
European Journal of Ageing, 2023.

[3] Lijun Bian, Zhimin Ma, Xiangjin Fu, Chen Ji, Tianpei Wang, Caiwang Yan, Juncheng Dai, Hongxia Ma, Zhibin Hu, Hongbing Shen, et al.
Associations of combined phenotypic aging and genetic risk with incident cancer: A prospective cohort study.
Elife, 13:RP91101, 2024.

[4] Daniele Pala, Yuezhi Xie, Jia Xu, Yuqin Zhang, and Li Shen.
Causal effects of environmental exposures and biological traits on the difference between phenotypic and chronological ages.
In *2023 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pages 4382–4388. IEEE, 2023.

[5] Gan Yang, Xingqi Cao, Xueqin Li, Jingyun Zhang, Chao Ma, Ning Zhang, Qingyun Lu, Eileen M Crimmins, Thomas M Gill, Xi Chen, et al.
Association of unhealthy lifestyle and childhood adversity with acceleration of aging among uk biobank participants.
JAMA network open, 5(9):e2230690–e2230690, 2022.

[6] Hafiz T. A. Khan, Kennedy Kwasi Addo, and Helen Findlay.
1. public health challenges and responses to the growing ageing populations.
Public health challenges, 2024.

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