

# Longitudinal Neighborhood Residential Segregation & Epigenetic Aging Among Participants in a Nationally Representative Study of Adults in the United States

Chantel L. Martin<sup>1,2</sup>, Sylvie Tuder<sup>1,2</sup>, Alena S. D'Alessio<sup>1,2</sup>, Brandt E. Levitt<sup>2</sup>, Allison E. Aiello<sup>3</sup>, Kathleen Mullan Harris<sup>1,2</sup>, Lauren Gaydos<sup>1,2</sup>, Taylor W. Hargrove<sup>1,2</sup>  
<sup>1</sup>UNC Chapel Hill, Chapel Hill, NC, USA, <sup>2</sup>Carolina Population Center, UNC Chapel Hill Chapel Hill, NC, USA, <sup>3</sup>Columbia University, New York, NY, USA

Residing in neighborhoods with higher levels of racial residential segregation across the life course associated with accelerated epigenetic aging in Black and White adults; faster epigenetic aging linked with neighborhood social context may signal adverse health outcomes and inequalities in later life.

## BACKGROUND

Does exposure to residential segregation across multiple life stages impact epigenetic aging among Black and White adults?

Black adults in the U.S. are physiologically 6-10 years older in chronological age than their White counterparts and have higher rates of aging-related diseases, including Alzheimer's Disease and Alzheimer's Disease-Related Dementias, cardiovascular disease, and diabetes. Racial residential segregation is an established fundamental driver of health inequalities in the U.S. and studies suggest residing in segregated neighborhoods can accelerate epigenetic aging, a biological risk factor of aging-related diseases.

## METHODS

- Data from Black (n=609) and White (n=2,396) participants in the National Longitudinal Study of Adolescent to Adult Health (Add Health)
- Participants followed from adolescence (1994-1995) into adulthood (2016-2018)
- Neighborhood racial residential segregation during adolescence and adulthood measured at census-tract level using Getis-Ord ( $G_i^*$ ) statistic
- Higher  $G_i^*$  values represent higher levels of segregation (values dichotomized at  $\geq 1.96$  for high segregation)
- Epigenetic aging assessed in adulthood using 4 DNA methylation-based epigenetic clocks: PhenoAge, GrimAge, DunedinPACE, and Zhang2017
- Used race-stratified survey-weighted regression models adjusting for: age at blood draw in adulthood, sex, parental education, household income, time lived in residence in adolescence.

## RESULTS

Characteristics	Total Sample (N=3,490)	NH Black Participants (N=811)	NH White Participants (N=2,679)
Age, mean (SE) <sup>A</sup>	38.4 (0.1)	38.7 (0.1)	38.3 (0.1)
Female sex assigned at birth	52%	52%	52%
Parental educational attainment in adolescence			
Less than college education	73%	76%	72%
College education or more	27%	21%	28%
Annual household income (thousands), mean (SE) <sup>A</sup>	48.5 (1.0)	35.4 (2.1)	51.7 (1.2)
$G^*$ Statistic in adolescence, mean (SE) <sup>A</sup>	-0.13 (0.05)	1.83 (0.16)	-0.61 (0.03)
$G^*$ Statistic in adulthood, mean (SE) <sup>A</sup>	-0.07 (0.04)	1.47 (0.12)	-0.45 (0.04)
Years in residence in adolescence, mean (SE) <sup>A</sup>	7.9 (0.1)	6.7 (0.3)	8.2 (1.5)
Epigenetic age in adulthood, mean (SE) <sup>A</sup>			
PhenoAge	30.2 (0.1)	30.3 (0.0)	30.1 (0.0)
GrimAge	52.8 (0.0)	53.8 (0.0)	52.5 (0.0)
Zhang2017	-1.3 (0.0)	-1.3 (0.0)	-1.2 (0.0)
DunedinPACE	1.0 (0.0)	1.1 (0.0)	1.0 (0.0)
Standardized epigenetic clock residuals, mean (SE) <sup>A</sup>			
PhenoAge	0.04 (0.02)	-0.02 (0.06)	0.05 (0.02)
GrimAge	0.09 (0.03)	0.28 (0.06)	0.04 (0.03)
Epigenetic clock z-scores, mean (SE) <sup>A</sup>			
Zhang2017	0.08 (0.02)	-0.09 (0.05)	0.12 (0.03)
DunedinPACE	0.03 (0.02)	0.51 (0.05)	-0.09 (0.03)

<sup>A</sup>Weighted means (Standard Error)

## RESULTS CONTINUED

Figure 1. Proportion of Black and White Participants Residing in Neighborhoods with High ( $G_i^*$  statistic  $\geq 1.96$ ) vs. Low ( $G_i^*$ Statistic  $< 1.96$ ) Residential Segregation during Adolescence and Adulthood

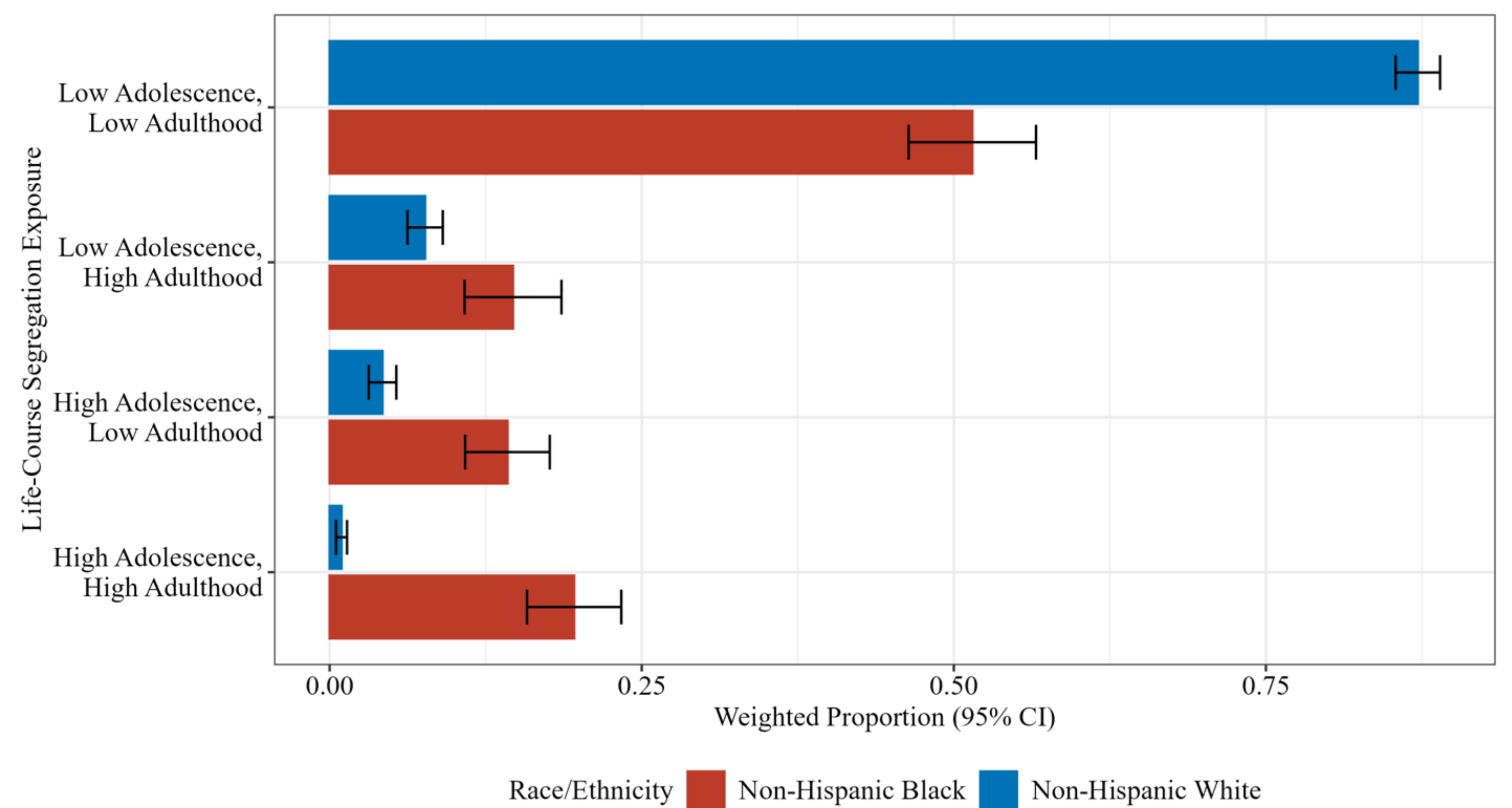
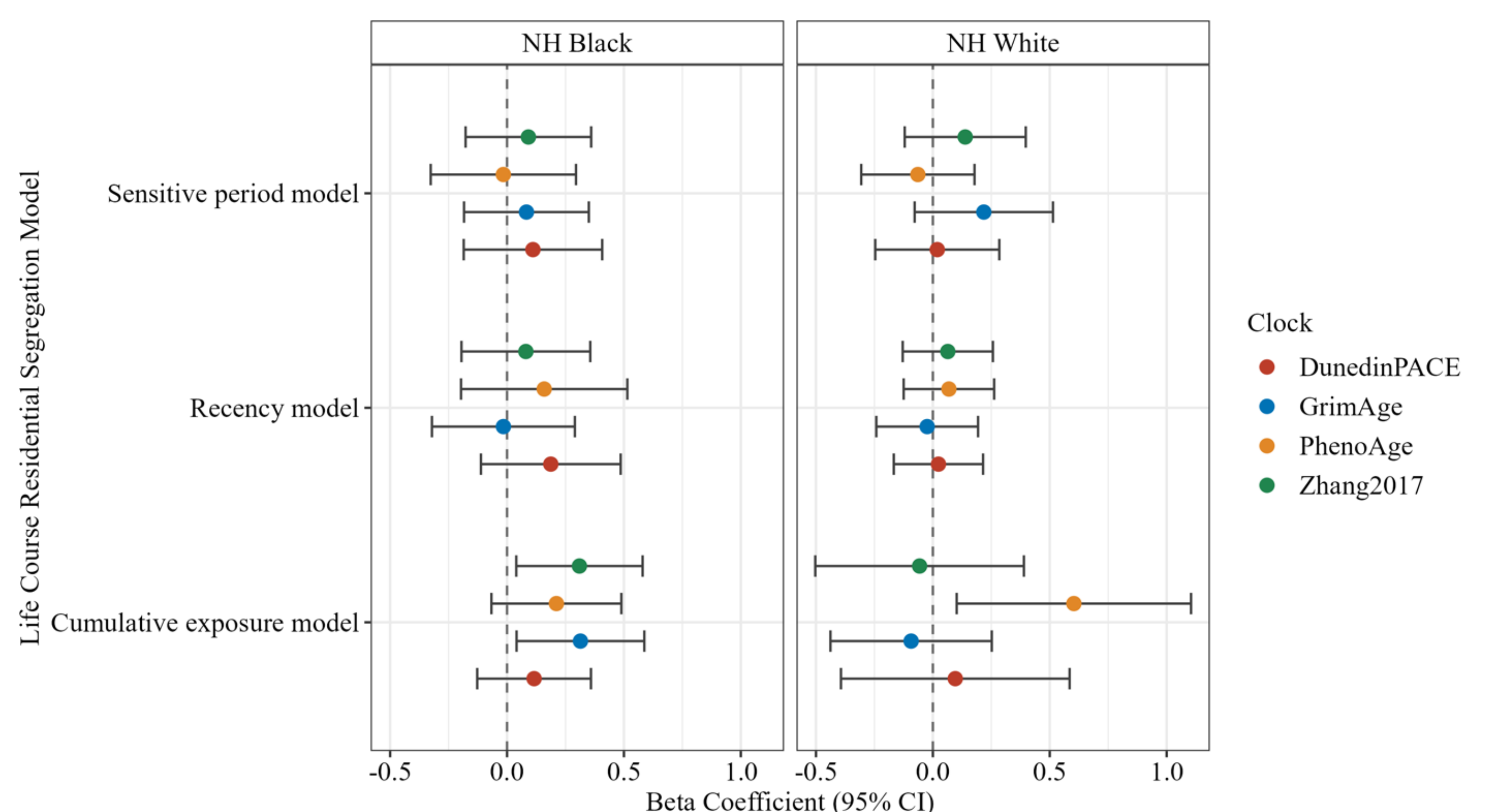


Figure 2. Life course neighborhood models<sup>A</sup> of residential segregation and epigenetic aging



<sup>A</sup>Sensitive period model: high adolescence/low adulthood; Recency model: low adolescence/high adulthood; Cumulative exposure model: high adolescence/high adulthood; No exposure (reference): low adolescence/low adulthood

## CONCLUSIONS

- Black individuals more likely exposed to residential segregation across early and midlife stages
- Exposure to racial residential segregation in both adolescence and adulthood associated with accelerated epigenetic aging for Black (Zhang2017 & GrimAge) and White (PhenoAge) participants
- Accelerated epigenetic aging may be an important signal of adverse health outcomes and inequalities later in life

## ADDITIONAL KEY INFORMATION

Author email: [chantelmartin@unc.edu](mailto:chantelmartin@unc.edu)

Acknowledgements: This research was supported by the National Institute on Aging (R01AG077947) and National Institute of Minority Health and Health Disparities (R01MD013349) of the National Institutes of Health. The content is solely the responsibility of the authors and do not necessarily represent the official views of NIH.