1. Blau F, Koebe J, Meyerhofer P. Essential and frontline workers in the COVID-19 crisis. Econofact Report. April 30, 2020. Accessed May 16, 2020. https://econofact.org/essential-and-frontline-workers-in-the-covid-19-crisis

2. COVID-19 and workers at risk: examining the long-term care workforce. Kaiser Family Foundation Issue Brief. April 23, 2020.

3. American Community Survey Design and Methodology. Chapter 7: data collection and capture for housing units. January 2014. Accessed May 16, 2020. https://www2.census.gov/programs-surveys/acs/methodology/design_and_methodology/acs_design_methodology_ch07_2014.pdf

4. US Department of Homeland Security, Cybersecurity & Infrastructure Security Agency. Advisory memorandum on identification of essential critical infrastructure workers during COVID-19 response. April 17, 2020. https://www.cisa.gov/sites/default/files/publications/Version_3.0_CISA_Guidance_on_Essential_Critical_Infrastructure_Workers_1.pdf

5. LMI Institute. SOC codes for CISA critical infrastructure workers. Rev 1. Accessed April 28, 2020. https://www.lmiontheweb.org/more-than-half-of-u-s-workers-in-critical-occupations-in-the-fight-against-covid-19

6. American Community Survey response rates. Accessed May 16, 2020. https://www.census.gov/acs/www/methodology/sample-size-and-data-quality/response-rates/index.php

Associations Between Built Environment, Neighborhood Socioeconomic Status, and SARS-CoV-2 Infection Among Pregnant Women in New York City

The built environment is associated with infectious disease dynamics, particularly in diseases transmitted by contact, aerosols, or droplets.[1,2] A recent study of the ongoing severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) epidemic in New York revealed significant differences in hospitalization and death rates among the city's boroughs, with the highest rates in Queens and the Bronx.[3] To our knowledge, no studies have investigated associations between the built environment, markers of neighborhood socioeconomic status, and SARS-CoV-2 transmission. We leveraged a universal testing program for SARS-CoV-2 in pregnant women to examine associations between these factors and SARS-CoV-2 prevalence.

Methods | We conducted a cross-sectional study of New York City residents delivering at NewYork–Presbyterian/Columbia University Irving Medical Center or Allen Hospital after implementation of universal SARS-CoV-2 nasopharyngeal quantitative reverse transcriptase–polymerase chain reaction testing at the time of admission to the labor and delivery unit from March 22 through April 21, 2020. We linked patients to demographic and socioeconomic data from the US Census Bureau's American Community Survey,[4] a national survey with detailed demographic, socioeconomic, and housing data, and to real estate tax data from New York's Department of City Planning.[5] We abstracted building-level variables, including number of residential units per building and mean assessed value (per square foot), and neighborhood-level variables, including median household income, poverty rate, unemployment rate, population density, household membership (persons per household), and household crowding (percentage of households with >1 person per room). Neighborhood was defined using New York City neighborhood tabulation areas, which divide the city into 195 districts, with at least 15 000 residents each.[4]

We fit bivariable logistic regression models with cluster robust standard errors, modeling exposures as continuous independent variables. Because odds ratios (ORs) associated with a 1-unit change in independent variables can be difficult to interpret, we used these models both to estimate interdecile ORs—ie, the relative odds of SARS-CoV-2 infection for individuals at the 90th percentile of an independent variable relative to those at the 10th percentile—and to predict probabilities (and 95% CIs) of SARS-CoV-2 infection at the 10th and 90th percentiles of the independent variable distribution. Analysis was performed using Stata/MP version 16.0 (StataCorp). Two-sided $P < .05$ was considered significant. This study was exempted from informed consent and approved by the Columbia University institutional review board.

Results | We identified 434 New York City residents who were tested for SARS-CoV-2. Of the 396 patients (91%) linked to buildings and neighborhoods in the city, 71 (17.9%) were infected with SARS-CoV-2. Cohort characteristics are tabulated in the **Table**. The likelihood of SARS-CoV-2 varied substantially across measures of built environment and

Table. Cohort Characteristics

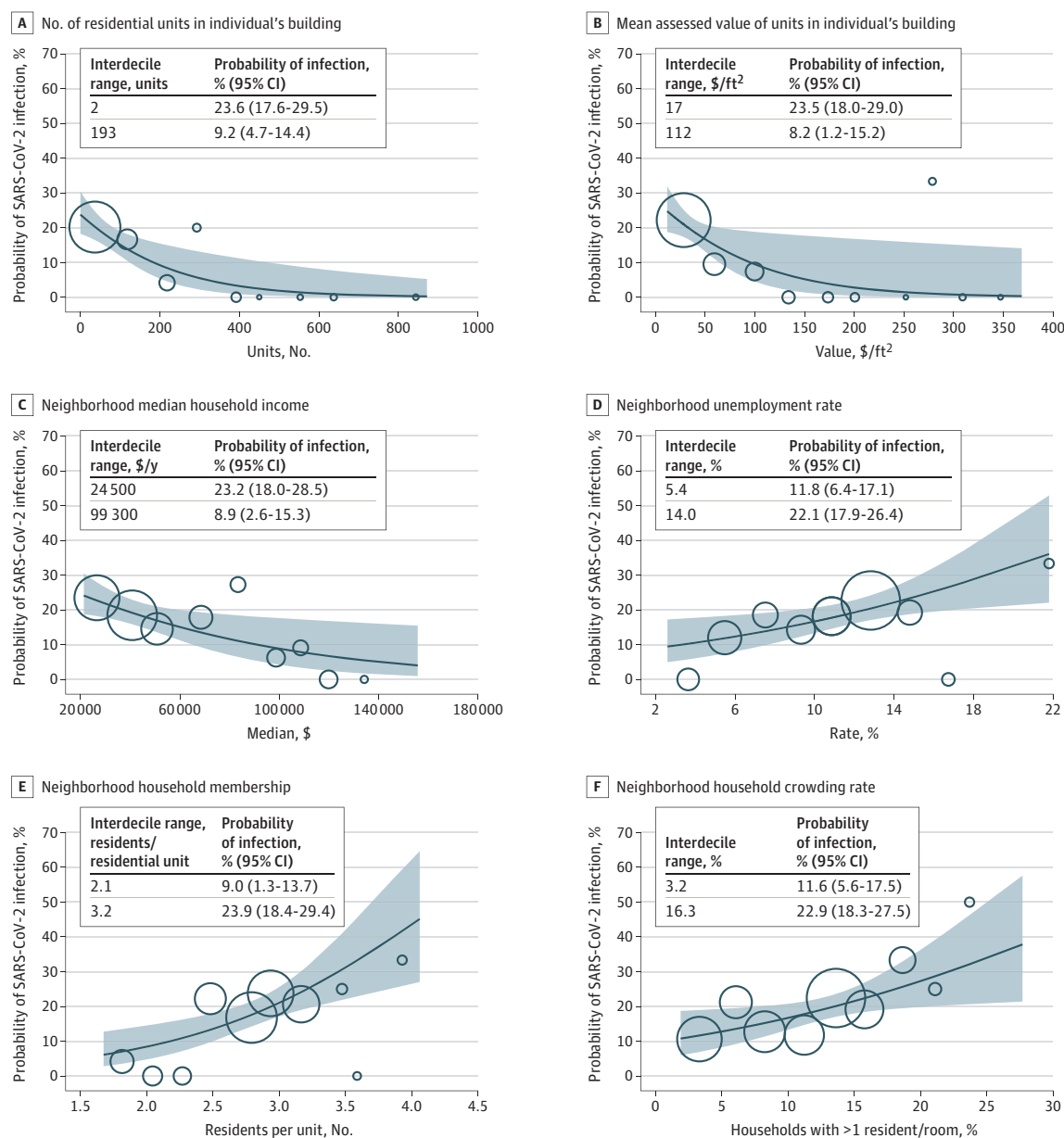|	SARS-CoV-2 status		
	Negative (n = 325)	Positive (n = 71)	P value
Maternal age, median (IQR), y	31.0 (27.0-35.0)	27.0 (24.0-32.0)	<.001[a]
Gestational age, median (IQR), wk	39.0 (38.1-39.7)	39.0 (37.4-39.7)	.63[a]
Gravidity (IQR)	2 (1-4)	2 (1-3)	.04[a]
Parity (IQR)	1 (0-1)	0 (0-1)	.37[a]
Hypertension, No. (%)[b]	26 (8.0)	7 (9.9)	.61[c]
Diabetes, No. (%)[b]	18 (5.5)	2 (2.8)	.34[c]

Abbreviations: IQR, interquartile range; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

[a] P value based on linear regression with cluster robust standard errors.

[b] Both pregestational and gestational conditions included.

[c] P value based on logistic regression with cluster robust standard errors.

Figure. Built Environment and Neighborhood Socioeconomic Factors Associated With SARS-CoV-2 Infection Among Pregnant Women

A No. of residential units in individual's building

Interdecile range, units	Probability of infection, % (95% CI)
2	23.6 (17.6-29.5)
193	9.2 (4.7-14.4)

B Mean assessed value of units in individual's building

Interdecile range, $/ft^2	Probability of infection, % (95% CI)
17	23.5 (18.0-29.0)
112	8.2 (1.2-15.2)

C Neighborhood median household income

Interdecile range, $/y	Probability of infection, % (95% CI)
24 500	23.2 (18.0-28.5)
99 300	8.9 (2.6-15.3)

D Neighborhood unemployment rate

Interdecile range, %	Probability of infection, % (95% CI)
5.4	11.8 (6.4-17.1)
14.0	22.1 (17.9-26.4)

E Neighborhood household membership

Interdecile range, residents/residential unit	Probability of infection, % (95% CI)
2.1	9.0 (1.3-13.7)
3.2	23.9 (18.4-29.4)

F Neighborhood household crowding rate

Interdecile range, %	Probability of infection, % (95% CI)
3.2	11.6 (5.6-17.5)
16.3	22.9 (18.3-27.5)

Values plotted against the probability of identifying severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection at universal testing. Solid lines indicate the predicted probability of infection from bivariable logistic regression models; shaded areas, 95% confidence bands. For each independent variable, circles are plotted at the mean values of the women residing in 10 equal-width bins. The circle size is proportionate to the number of women within each bin.

Since bins may contain no patients, there are fewer than 10 circles in some panels. Interdecile range indicates 10th and 90th percentiles. The probability (and 95% CI) of SARS-CoV-2 infection for women at the 10th and 90th percentile of each independent variable was predicted from the regressions shown in each panel.

neighborhood socioeconomic status (**Figure**). The lowest probability of infection was estimated for women living in buildings with very high assessed values (8.2% [95% CI, 1.2%-15.2%]) and the highest was for those residing in neighborhoods with high household membership (23.9% [95% CI, 18.4%-29.4%]). Odds of infection were lower among women living in buildings with more residential units (interdecile OR, 0.34 [95% CI, 0.16-0.72]) and higher assessed values (interdecile OR, 0.29 [95% CI, 0.10-0.89]) and in neighborhoods with higher median incomes (interdecile OR, 0.32 [95% CI, 0.12-0.83]). Odds of infection were higher among women residing in neighborhoods with high unemployment rates (interdecile OR, 2.13 [95 CI, 1.18-3.83]), large household membership (interdecile OR, 3.16 [95% CI, 1.58-6.37]), and greater household crowding (interdecile OR, 2.27 [95% CI, 1.12-4.61]). There was no statistically significant association between SARS-CoV-2 infection

and population density (interdecile OR, 0.70 [95% CI, 0.32-1.51]) or poverty rate (interdecile OR, 2.03 [95% CI, 0.97-4.25]). Neighborhood-level variables were moderately to highly correlated (r = 0.66-0.83).

Discussion | In this study, SARS-CoV-2 transmission among pregnant women in New York City was associated with neighborhood- and building-level markers of large household membership, household crowding, and low socioeconomic status. These data may aid policy makers in the design of interventions to reduce the spread of SARS-CoV-2. A key strength of this study was the use of a universally tested population, which allowed for ascertainment of asymptomatic cases among a defined at-risk population. Limitations of the study include that the findings may not apply to other populations given the unique demographic, physiologic, and social features of pregnant women. Additionally, the small sample size and high degree of correlation between neighborhood-level variables precluded multivariable analysis. Nonetheless, this study provides empirical support for the hypothesis that variation in the urban environment may be an important social determinant of SARS-CoV-2 transmission.

Ukachi N. Emeruwa, MD, MPH
Samsiya Ona, MD
Jeffrey L. Shaman, PhD
Amy Turitz, MD
Jason D. Wright, MD
Cynthia Gyamfi-Bannerman, MD, MSc
Alexander Melamed, MD, MPH

Author Affiliations: Department of Obstetrics and Gynecology, Columbia University College of Physicians and Surgeons, New York, New York (Emeruwa, Ona, Turitz, Wright, Gyamfi-Bannerman, Melamed); Department of Environmental Health Sciences, Columbia University Mailman School of Public Health, New York, New York (Shaman).

Corresponding Author: Alexander Melamed, MD, MPH, Division of Gynecologic Oncology, Vagelos College of Physicians and Surgeons, Columbia University, 161 Ft Washington Ave, New York, NY 10032 (am5195@cumc.columbia.edu).

1. Pinter-Wollman N, Jelić A, Wells NM. The impact of the built environment on health behaviours and disease transmission in social systems. *Philos Trans R Soc Lond B Biol Sci*. 2018;373(1753):20170245. doi:10.1098/rstb.2017.0245

2. Virtanen M, Terho K, Oksanen T, et al. Patients with infectious diseases, overcrowding, and health in hospital staff. *Arch Intern Med*. 2011;171(14):1296-1298. doi:10.1001/archinternmed.2011.313

3. Wadhera RK, Wadhera P, Gaba P, Figueroa JF, Joynt Maddox KE, Yeh RW, Shen C. Variation in COVID-19 hospitalizations and deaths across New York City boroughs. *JAMA*. 2020;323(21):2192-2195. doi:10.1001/jama.2020.7197

4. American Community Survey by neighborhood tabulation area. New York City Department of City Planning. Accessed May 6, 2020. https://www1.nyc.gov/site/planning/data-maps/open-data/dwn-acs-nta.page

5. PLUTO database. New York City Department of City Planning. Accessed May 6, 2020. https://www1.nyc.gov/site/planning/data-maps/open-data.page

SARS-CoV-2 Positivity Rate for Latinos in the Baltimore–Washington, DC Region

The black community has been disproportionally affected by the coronavirus disease 2019 (COVID-19) pandemic in the US.[1] Emerging data highlight sharp increases in cases within the Latino community.[1,2] We analyzed temporal trends in positivity rates for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in the Baltimore–Washington, DC region by race/ethnicity.

Methods | Samples were collected between March 11, 2020, and May 25, 2020, from 5 hospitals, including emergency departments, and 30 outpatient clinics that are part of the Johns Hopkins Health System (JHHS). SARS-CoV-2 testing inclusion criteria broadened over time (ie, initially high-risk individuals only and then all symptomatic patients) as local capacity increased but was standardized across JHHS sites. Samples collected via nasopharyngeal swabs were analyzed using SARS-CoV-2 reverse transcriptase–polymerase chain reaction. Data on patient demographics, comorbidities, SARS-CoV-2 status, and hospitalization were extracted from the integrated electronic health record system.

Patients self-identified race/ethnicity from fixed categories. Racial/ethnic groups were considered mutually exclusive; ie, Latinos were excluded from other groups (white, black, other) regardless of reported race. Those who self-reported American Indian, Alaska Native, Asian American, Native Hawaiian, Pacific Islander, or multiracial were grouped as "other."

Temporal trends in daily positivity rates (7-day moving average; number positive/number tested over the date and preceding 6 days) and testing volumes stratified by race/ethnicity were evaluated. Total rates of SARS-CoV-2 positivity, hospitalization, and categorical patient characteristics were