A Nurse-Community Health Worker-Family Partnership Model: Addressing Uptake of COVID-19 Testing and Control Measures

Statistical Analysis Plan (SAP)

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Contributors:

Melody Goodman, PhD – Senior Biostatistician

Kristyn Pierce, MPH – Junior Research Scientist/Data Manager

STATISTICAL DESIGN AND POWER

Measures.

Definition of Primary Outcomes

Household COVID testing uptake at the 9-month follow up is one of the main primary outcomes of interest. The investigative team will document all medical services administered by nurses during home visits, as well as self-reported information regarding COVID-19 testing uptake by study participants in the treatment and control groups. Participants will be asked whether they have received COVID-19 testing in the past three months [Yes/No]. Additionally, variables collected via the COVID-19 Symptoms, Diagnoses, and Testing Scale are the primary outcomes. This questionnaire is adapted from the COVID-19 Cannabis Health Questionnaire (CCHQ) (Vidot et al, 2020) and will measure COVID-19 symptoms, diagnoses, and testing. At the 9-month follow up point, participants will be asked questions regarding whether they are currently sick with an illness that might be related to COVID-19, any symptoms the participant experienced in the past three months [Check All That Apply], and the result of the participant's last COVID-19 test [Positive/Negative].

Definition of Secondary Outcomes

For the randomized trial, data collected utilizing the following questionnaires are secondary outcomes: **COVID-19 control measure uptake**, which is adapted from the COVID-19 Knowledge, Attitudes, and Avoidant Behaviors section of the Understanding America Study (CESR, 2020). Respondents will be asked questions regarding their engagement in behaviors associated with COVID-19 exposure on a 5-point scale [Almost Never, Sometimes, a Moderate Amount of the Time, Most of the Time, Always]. Greater values indicate higher frequency of uptake of COVID-19 prevention behaviors (e.g. "Canceled or postponed social activities." "Avoided riding the bus or subway") This questionnaire also includes questions regarding their uptake of COVID-19 control measures such as PPE usage and hand washing or sanitation. This will be measured both in immediate follow up (6 months), asking the participant to recall the past six months and also in delayed follow-up (9 months), asking the participant to recall the past three months.

Household COVID-19 Testing Uptake will be assessed as above, however at the immediate follow up time point (6 months). At the 6-month follow up point, participants will be asked whether they have received COVID-19 testing in the past six months [Yes/No]. Further, the COVID-19 Symptoms, Diagnoses, and Testing Scale will be administered at six months. Questions will ask respondents whether they are currently sick with an illness that might be related to COVID-19, any symptoms the participant experienced in the past six months [Check All That Apply], and the result of the participant's last COVID-19 test [Positive/Negative].

Vaccine Uptake will be documented by the study team via seasonal influenza and COVID-19 vaccination referrals by study nurses. Investigators will obtain self-reported information and documentation of influenza vaccine uptake by participants in both treatment arms by asking participants if they have received the influenza vaccine at the 6-month and 9-month follow up assessments [Yes/No] and whether they received the COVID-19 vaccine [Yes/No], the type of vaccine, and the number of doses.

COVID-19 Improved Household & Family Mutual Aid will be assessed by the reported overall impact of COVID-19 on family dynamics and relationships, psychological distress, food and housing insecurity, substance use, and sexual behavior at the 6-month and 9-month follow up assessments, in order to assess families' abilities to adjust to the COVID-19 pandemic. Further, the COVID-19 Household Environment Scale (Behar-Zusman, 2020) will be used to assess family mutual aid. This outcome assesses household togetherness by asking participants to rate how much more or less conflict there was (as compared to before COVID-19) about 15 topics (e.g., "Home maintenance;" "Decisions about visitors to the home"), on a 5-point Likert scale with higher values indicating greater frequency of family conflict concerning the topic. This will be used in both the 6-month immediate follow up ("in the past 6 months…") and in the 9-month final follow-up ("in the past 3 months…") to capture information for the three-month period between the 6-month and 9-month follow-ups.

Predictor Variables

COVID-19 Exposures are the main predictor variable(s) in this analysis. Exposures are measured in all of the questionnaires by asking participants if anyone in their household has tested positive for COVID-19 [Yes/No] or if they have had close contact with someone who was diagnosed with COVID-19 [Yes/No].

Confounding Variables

Previous infection and vaccination could introduce confounding if there are differences between the two intervention groups (see **Figure 1** below). Participants are asked if they have been vaccinated [Yes/No] or if they have previously been diagnosed with COVID-19 [Yes/No] in the baseline and subsequent follow-up questionnaires.

Moderating Variables

Gender, race/ethnicity, and age as measured using questions from the CCHQ in the baseline, 30-day, and 6-month questionnaires, as well as testing fatigue may modify the association between the intervention and the outcomes. Testing fatigue is measured with the statement, 'I am tired of being tested for COVID-19' and asking participants to respond from 'Strongly Disagree' to 'Strongly Agree.'

Mediating Variables

There are several mediating variables of interest including: knowledge and self-efficacy for COVID-19 prevention, testing salience, habitual processes, and medical mistrust. These measures are captured in the baseline, 6-month, and 9-month questionnaires. **Figure 2** features all mediating variables considered for these analyses.

Created Variables

We will create summary scores for all survey scales using validated scoring procedures. We will create difference variables (e.g., 6 month-baseline, 9 month – 6 month, 9 month-baseline) for time varying variables (e.g., vaccination status, COVID-19 exposure, employment status) measured at multiple time points.

Figure 1: Consort Flow Diagram

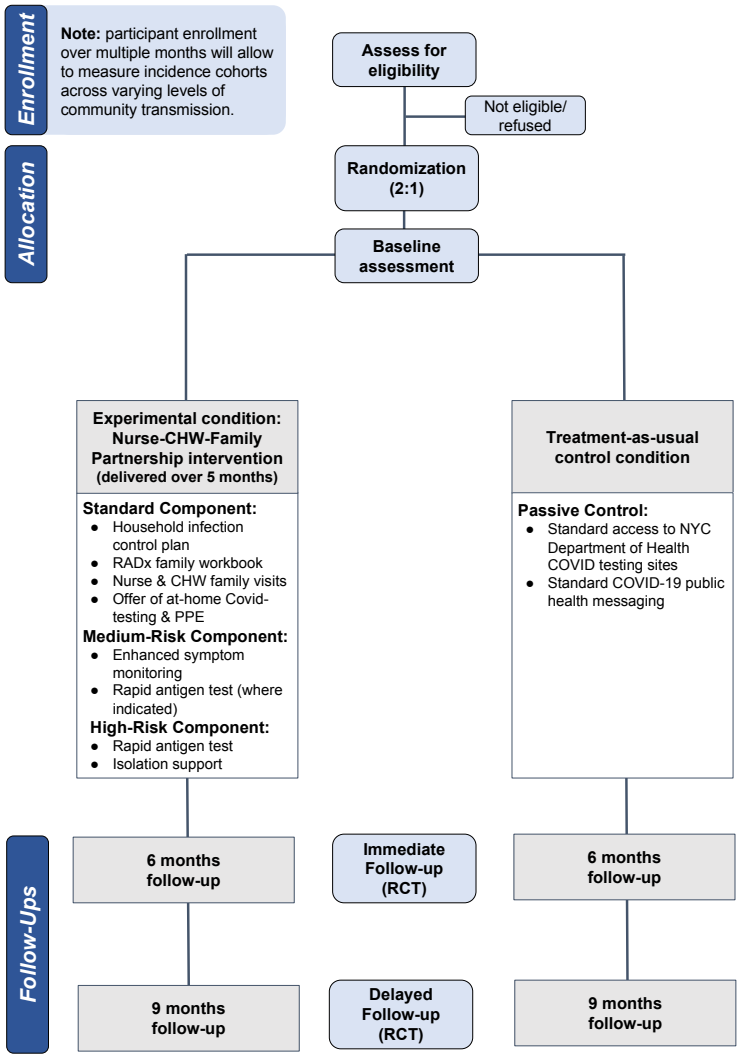
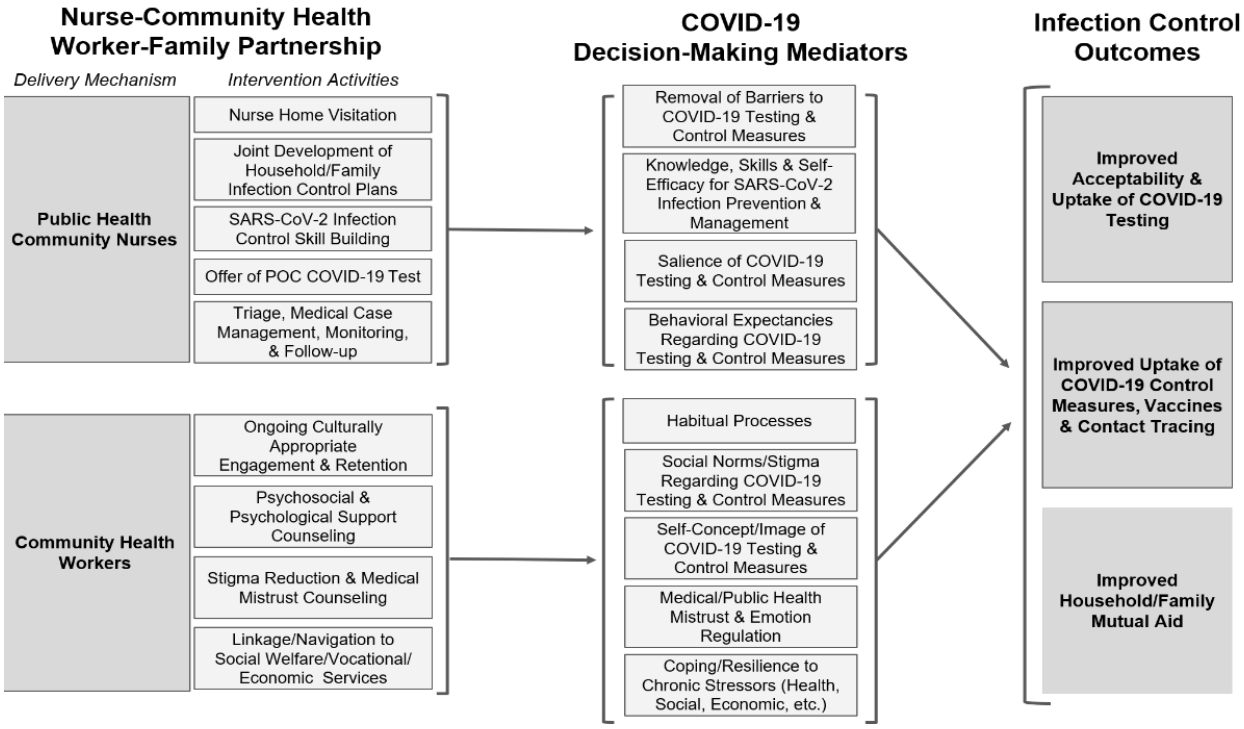


Figure 2: NCFP Theoretical Model



Design.
The randomized control trial will include 150 households, and 400 individual household members who will be randomized into 2 arms with parallel assignment in a 2:1 ratio, intervention:control. Participants in the intervention arm will receive the Nurse-Community Health Worker-Family Partnership intervention. The control arm will receive standard access to NYC Department of Health COVID-19 testing sites and standard COVID-19 public health messaging for NYCHA residents.

Framework.
With regard to hypothesis testing, the trial will utilize a superiority hypothesis testing framework. The study team will compare differences between baseline data and data collected at the 9-month follow-up timepoint to assess whether or not the intervention group had a higher efficacy in regards to the outcomes of interest than that of the control group.

Randomization.
After the baseline assessment and confirmation of eligibility, treatment allocation will be determined using a household-level randomization scheme of 2:1. The study team will randomize households using the password-protected REDCap desktop app using a predetermined randomization algorithm entered into the EDC system.

Interim Analyses.
The data team will conduct interim analyses every 6 months during the duration of the trial. The analysis will review data on recruitment, participant characteristics, protocol compliance, and study outcome. This analysis will also assess the differential proportion of self-reported COVID-19 infection between the two treatment groups (a safety assessment of the trial primary outcome). There are no planned adjustments of the significance level due to interim analysis. In addition, cross-sectional analyses will be completed after data collection for each time point (baseline, 6-month, 9-months).

Final Analysis.
The final analysis will be conducted once outcome data for all enrolled participants is collected, outside of participants who withdrew early or were lost to follow-up. If the trial is not stopped early for any reason, the final analysis will be conducted using available data. Since the primary outcome is clearly defined, the level of

significance of this study will not be adjusted for multiplicity. All hypothesis tests will be 2 sided, with a 95% confidence interval.

Trial Population.

Inclusion Criteria

- Residence in one of the NYCHA complexes in Mott Haven, South Bronx
- English or Spanish-speaking
- Age 10 years or older
- Willing and able to provide informed consent or assent

Exclusion Criteria

- Non-resident of one of the NYCHA complexes in Mott Haven, South Bronx
- Does not speak English nor Spanish
- Younger than 10 years old, unless household index case tests antigen positive. In this instance, all members of family will be included.
- Unwilling or unable to provide informed consent or assent

Screening Data

Screening data will be summarized on a quarterly basis during the recruitment period, as well as in final reports, those invited to participate in the study will be classified as eligible or ineligible in order to describe the representativeness of the study population.

Withdrawal/Follow Up

The team expects a low level of attrition from withdrawal or loss to follow-up from the study due to the infrequency of study assessments, the community engaged research approaches used in the intervention, the average length of residency in NYCHA housing, and the duration of the follow up period. Withdrawal and lost to follow up data will be reported with the 6-month and 9-month follow up data. Demographic characteristics of participants who withdraw or are loss to follow-up will be examined and compared to those who complete the study.

Adherence to Study Protocol

For the purposes of this project, study adherence is defined as the participants completion of all study related activities (intervention visits, questionnaires). Field workers will routinely contact participants and alert the study team if a participant is unable to be reached. The data monitoring team will routinely produce reports to track participant status and compliance with protocol specified assessments and visits.

Protocol Deviations

All protocol deviations will be documented by the study team. A protocol deviation will be defined as any missed, or out-of-window study assessment, as well as randomization of a participant who is not eligible at baseline. All protocol deviations will be reported during routine data status reports, as well as to the IRB (as required).

Harms

There are no anticipated harms for this trial. All unexpected adverse events and serious adverse events will be captured in detail by the study team, as well as their severity, expectedness, and causality.

Statistical Methods.

SAS, M Plus, R, and/or Stata statistical software will be used for data analysis; statistical significance will be assessed as $p<0.05$. For the RCT we will conduct analysis in two stages, starting with cross-sectional analysis at each time point and subsequently conducting longitudinal analysis.

Baseline Participant Characteristics

We will analyze demographic variables such as age, biological sex, gender identity, sexual identity, race, ethnicity, language preference, body measurements, and several socioeconomic measures collected via

questions adapted from the General Social Survey (GSS) 2014. Initial descriptive analyses will include an examination of the sample characteristics at each level (participants, households) at each of the time points for the randomized controlled trial (baseline, 6 months, 9 months). Continuous variables will be summarized using the mean, standard deviation, median, range, and interquartile range, while nominal and ordinal variables will be summarized using frequencies and percentages.

Aim 1 is to describe self-reported baseline rates of SARS-CoV2 diagnostic testing (PCR and antibody), receipt of results, illness, hospitalization and severe disease.

Analysis for Aim 1

Analyses for Aim 1 will include a descriptive examination of household COVID testing uptake and previous COVID testing utilizing the COVID-19 Symptoms, Diagnoses, and Testing Scale for participants at baseline. This scale includes variables such as symptoms, whether participant has ever been tested for COVID, and COVID test results. These data are dichotomous and nominal in nature. To address Aim 1, the following analyses will be conducted. Data will be stratified with respect to important demographic factors (e.g., age, race, gender, ethnicity, essential worker). Nominal variables (i.e. COVID-19 symptoms, test frequency) will be summarized using frequencies and percentages. Bivariate analyses will be conducted to examine associations between testing practices and key predictors (intervention group), confounders (i.e. previous infection or vaccination), moderators (i.e. essential worker status, testing fatigue), and demographic characteristics (e.g., age, gender, race, ethnicity). A two-sample test for proportions will be used to compare the baseline testing practices of the two treatment groups. Chi-square tests will be used to assess group differences for nominal data. The Fisher's exact test will be considered for contingency tables with sparse cells. We will compare outcomes across 3 racial/ethnic groups (White, Black, Hispanic). These differences will be examined in bivariate analyses (unadjusted) and multivariable analysis (adjusted). We will develop multilevel multivariable regression models to examine the association between the key predictors, mediators, and moderators, such as vaccination, testing fatigue, or exposure, on baseline testing uptake.

Aim 2 is to explore acceptability, facilitators and barriers to testing, social distancing, wearing face masks, naming contacts, isolation or quarantine, and accessing COVID-19 related health services.

Analysis for Aim 2

Analyses for Aim 2 will include an analysis of variables collected utilizing tools adapted from the following validated scales: Avoidant Behaviors Scale (CESR, 2020), Contact Tracing Cooperation Scale, COVID-19 Household Environment Scale (Behar-Zusman, 2020), COVID-19 Family Impact Survey (The Center for Pediatric Traumatic Stress, 2020), COVID-19 Parent Relationships Scale (UCSD, 2020), and their relationships with key predictors (COVID-19 exposure), confounders (i.e. previous infection or vaccination) and moderators (i.e. age, gender, essential worker status). These scales capture variables such as reasons why participant was not tested, attitudes toward people who get tested, and workplace PPE accessibility. Variables included in the analysis for Aim 2 are nominal, ordinal, and discrete in nature. The initial analysis will summarize the variables of interest at the individual and household level for the baseline and follow-up timepoints. Nominal and ordinal variables will be summarized using frequencies and percentages. Bivariate analyses will be conducted to examine associations between the facilitators and barriers to COVID-19 precautions and key predictors (intervention group), confounders (e.g., previous infection, vaccination, moderators (e.g. gender, testing fatigue), and demographic characteristics (e.g., age, race, essential worker). To examine bivariate associations between continuous variables that are approximately normal or may become approximately normal after an appropriate transformation, the Student's t-test will be used. For other continuous variables where normality cannot be assumed, the Wilcoxon rank-sum test will be used instead. Chi-square tests will be used to assess group differences for nominal data. We will use Chi-square tests and the Cochran Mantel-Haenszel tests for comparison in ordinal characteristics (i.e. how often participant washes hands, uses PPE, agreeableness to isolate). The Fisher's exact test will be considered for contingency tables with sparse cells. We will compare outcomes across 3 racial/ethnic groups (White, Black, Hispanic). These differences will be examined in bivariate analyses (unadjusted) and multivariable analysis (adjusted). We will develop multilevel multivariable regression models to examine the association between predictors, mediators,

and moderators on COVID protection practices.

Aim 3 is to describe novel adaptations to COVID-19 public health mitigation strategies by the community, including safer ways to use public transportation, to quarantine or isolate within public housing and within households, safely obtain and use illicit drugs, and access HIV and other health care during the pandemic.

Analysis for Aim 3

The analysis for Aim 3 will encompass the variables collected regarding modes of transportation, access to healthcare, drug and alcohol cessation treatment, and street drugs. Descriptive analyses will include participant and household level use of public health mitigation strategies at each of the time points for the randomized controlled trial. Data will be stratified with respect to important demographic factors (e.g., age, race, gender, ethnicity). Continuous variables will be summarized using the mean, standard deviation, median, range, and interquartile range, while nominal and ordinal variables will be summarized using frequencies and percentages. Each scale will be scored according to established guidelines. Each of the items in each scaled will be examined individually in addition to the composite score variable. Chi-square tests will be used to assess group differences for nominal data (e.g. reasons for not obtaining medication for chronic conditions). We will use Chi-square tests and the Cochran Mantel-Haenszel tests for comparison in ordinal characteristics (e.g., agreeability to use public transportation). The Fisher's exact test will be considered for contingency tables with sparse cells. We will compare outcomes across 3 racial/ethnic groups (White, Black, Hispanic). These differences will be examined in bivariate analyses (unadjusted) and multivariable analysis (adjusted). We will develop multilevel multivariable regression models to examine the association between predictors (COVID-19 exposure), mediators (e.g., self-efficacy, medical mistrust), and moderators (e.g., household COVID cases, participant age), on COVID mitigation practices. We will use multivariable multilevel logistic (binary outcomes) and linear (continuous outcomes) regression models to conduct cross-sectional analysis at each time point. For outcomes were statistical distributional assumptions are violated we will use the *non-parametric multilevel mixture model (NPMM).* In this model, latent classes are extracted at multiple levels of a hierarchical data structure (e.g., individual, household) and, unlike the conventional multilevel models (MLM), there are no continuously distributed random effects.[1,2]

Aim 4 is to (With our community advisors) develop, implement and test the effectiveness of a Nurse-Community Health Worker-Family Partnership intervention to increase reach, acceptance and uptake of diagnostic testing, adherence to COVID-19 prevention strategies, and development of a household mutual aid strategy to respond to COVID-19 related events within the home and community.

Analysis for Aim 4

The analysis for Aim 4 will encompass all variables of interest in Aims 1, 2, and 3 collected at baseline, six months, and nine months. Descriptive analyses will include participant and household level testing uptake, adherence to public health mitigation strategies, and household cohesion at each of the time points for the randomized controlled trial. Data will be stratified with respect to important demographic factors (e.g., age, race, gender, ethnicity). Continuous variables will be summarized using the mean, standard deviation, median, range, and interquartile range, while nominal and ordinal variables will be summarized using frequencies and percentages. Bivariate analyses will be conducted to examine associations between the outcomes of interest (testing uptake, COVID mitigation practices, and household mutual aid) and key predictors (intervention group), confounders (previous infection or vaccination), moderators (e.g., gender, age, testing fatigue), and demographic characteristics. To examine bivariate associations between continuous variables that are approximately normal or may become approximately normal after an appropriate transformation, the Student's t-test will be used. For other continuous variables where normality cannot be assumed, the Wilcoxon rank-sum test will be used instead. Chi-square tests will be used to assess group differences for nominal data. We will use Chi-square tests and the Cochran Mantel-Haenszel tests for comparison in ordinal characteristics. The Fisher's exact test will be considered for contingency tables with sparse cells. We will compare outcomes

across 3 racial/ethnic groups (White, Black, Hispanic). These differences will be examined in bivariate analyses (unadjusted) and multivariable analysis (adjusted). We will develop multilevel multivariable regression models to examine the association between predictors, mediators, and moderators on the primary outcome (testing uptake) and secondary outcomes (COVID mitigation practices, and family mutual aid). We will use multivariable multilevel logistic (binary outcomes) and linear (continuous outcomes) regression models to conduct cross-sectional analysis at each time point. For outcomes were statistical distributional assumptions are violated we will use the *non-parametric multilevel mixture model (NPMM).* In this model, latent classes are extracted at multiple levels of a hierarchical data structure (e.g., individual, household) and, unlike the conventional multilevel models (MLM), there are no continuously distributed random effects.[1,2]

Longitudinal Analysis

We will use a random-intercepts logistic (with a binary response) or linear (continuous outcome) multilevel regression model, for each timepoint *t,* individual *i,* that is a member of household *j*. A random-intercepts model will give the conditional assessment of the extent to which household-level exposures vary on the outcomes after taking into account individual-level exposures, assuming the household-level variation is normally and independently distributed with a constant variance. The variance partitioning coefficient (VPC), or the amount of variability in the outcome attributed to predictors at each level, will be calculated. This will tell us to which extent household level and individual-level variables contribute to the outcome allowing for an examination of the impacts of COVID-19 at multiple levels. Structural equation models (SEM) will be used to examine mediating and moderating variables in the regression analyses. In addition, we will conduct sensitivity analyses (e.g., intent to treat vs receive intervention, components of intervention received, per protocol) and subgroup analyses (e.g., race/ethnicity, gender, age, education, essential worker) based on findings from aims 1-3.

For binary outcomes, we will use a random-intercepts logistic multilevel regression model, for each timepoint *t,* individual *i,* that is a member of household *j*. The basic equation will follow the form:

$$y_{tij} = \ln\left(\frac{\pi_{tij}}{1-\pi_{tij}}\right) = B_0 x_{0ij} + \beta_1 x_{tij} + \beta_2 x_{ij} + \beta_3 x_j + \varepsilon^{(2)}_{i(j)} + \varepsilon^{(3)}_j$$

For continuous outcomes, we will use a random-intercepts multilevel regression model, for each timepoint *t,* individual *i,* that is a member of household *j*. The basic equation will follow the form:

$$y_{tij} = B_0 x_{0ij} + \beta_1 x_{tij} + \beta_2 x_{ij} + \beta_3 x_j + \varepsilon^{(2)}_{i(j)} + \varepsilon^{(3)}_j$$

A random-intercepts model will give the conditional assessment of the extent to which household-level exposures vary on the outcomes after taking into account individual-level exposures, assuming the household-level variation is normally and independently distributed with a constant variance. Where y_{tij} represents the outcome for the *i*th individual that resides in household *j* and time *t,* x_{tij} denotes the vector of time-varying covariates (e.g., exposure to COVID-19, household member exposed, household member infected), x_{ik}denotes the vector of individual-level variables (e.g., age, gender, race, ethnicity, comorbidities), and x_k is a vector of household–level variables (e.g., household plan developed). The vector of regression coefficients for the time-varying variables is denoted as β_1; similarly, β_2 denotes the vector of regression coefficients for the individual-level variables, and β_3 denotes the vector of regression coefficients for the household-level variables. The random effect for individual *i* that is a member of household *j* is denoted by $\varepsilon^{(2)}_{i(j)}$, and $\varepsilon^{(3)}_j$ denotes the random effect for the third (household–level) cluster. We assume the random effects are independent and normally distributed [5-7]. The variance partitioning coefficient (VPC), or the amount of variability in the outcome attributed to predictors at each level, will be calculated. This will tell us to which extent household level and individual-level variables contribute to the outcome allowing for an examination of the impacts of COVID-19 at multiple levels. In order to examine these impacts, a test for the difference in two proportions using a mixed-effects regression model based on a clustered 3-Level Hierarchical Design with level-3 (household) randomization will be utilized.

Mediation, moderation, and mediated moderation, moderated mediation analyses

In mediated moderation a moderating effect is mediated, whereas in moderated mediation one or more paths in a mediation model are moderated. The intervention components are assumed to influence the mediators/moderators in addition to the outcome. These differential effects on the mediators are assumed to persist over time and influence the outcomes with the possibility of lagged effects of the mediators on the 9-month outcomes. Moderating effects will be examined using multiple group comparison strategies in SEM. This strategy fits the same model across groups and compares fit under conditions where across group equality constraints of coefficients are induced versus conditions where the solution is unconstrained. If the equality constraints adversely affect model fit, then this suggests non-equivalence of coefficients across groups. A useful feature of this analytic scheme is that it permits testing for metric equivalence across groups. This is important for making valid across group comparisons. In instances, where we seek to evaluate non-linear relational forms, we will adopt a limited information estimation approach within our SEM framework. We will create quadratic and polynomial terms and/or re-categorize variables in ways that will allow us to detect non-linear relational forms.

Handling Missing Data.

In some analyses, there is likely to be missing data due to a respondent not answering a question. In general, this occurs infrequently, but occasions may arise where missing data must be formally dealt with. Data can be missing at random (MAR), missing completely at random (MCAR) or missing in a systematic way that precludes application of simple methods of missingness, such as the Expectation-Maximization methods. To gain perspective on the nature of the missingness for a given variable, we will create a dummy variable coded for each respondent as 1 = has a missing value on the variable in question and 0 = does not have a missing value, and then test for associations between these missing data indicators and other variables in the models. We will also apply Little's multivariate test for MCAR. Ideally, missingness will not be related to other variables. Missing data also can result from study attrition. We will differentiate these two sources of missingness and explore the dynamics of each. We will approach missing data using either full information maximum likelihood methods, multiple imputation methods or systematically model missing data bias, depending on the nature of the data and the models being evaluated.

Dealing with violations of statistical assumptions.

Many traditional tests rely on maximum likelihood or least squares analytic schemes that make population level assumptions. When either theory or data suggest that the assumptions are questionable, robust estimation methods as implemented in M Plus will be used. In addition, if statistical assumptions are violated nonparametric statistical methods (as proposed above) will be used.

Outliers. We will be sensitive to outliers in all analyses. We will apply standard methods for outlier detection (e.g., analysis of leverage statistics, residuals, and dfBetas) and use graphical approaches.

Specification error. We will be sensitive to issues of specification error, being careful to explore a wide range of model diagnostics to protect against gross model misspecification.

Measurement error. Where possible, we will adopt analytic strategies that explicitly model measurement error, such as using SEM with multiple indicators. For single indicator SEM, measurement error can be modeled by fixing error variances of measures at *a priori* specified values that map onto their reliability as suggested by previous research [8,9]. If it is a multi-item measure, we can create multiple indicators using split-half methods. When we cannot formally model measurement error, we will take care to recognize biasing effects of measurement error when interpreting the results of statistical analyses.

Aim 5 is to use FDA-authorized tests, characterize the community and household epidemiology of SARSCoV2/COVID-19 including prevalence of current infection, incidence of new infection,

symptomatic illness, accessing care, hospitalization and mortality.

Analysis for Aim 5

To address Aim 5, we will estimate current infection using SARS-CoV2 RNA testing of baseline specimens from the intervention group. Incidence of new infection per 100 person-months will be estimated from the results of repeat voluntary in-home RNA and antigen testing (intervention group) and approximated from self-reported results of repeat voluntary tests in the controls. Occurrence of symptomatic illness, accessing COVID-19 care, hospitalization and mortality will be measured in both groups by self-report from family members. Qualitative methods will use a grounded theory approach in which ethnographers identify key themes for further inquiry and analyses and contribute to quantitative data triangulation.

Aim 6 is to (with our community and scientific advisory boards,) develop pilot projects that will address knowledge and implementation gaps that are uncovered as new diagnostic testing is developed and as the investigative team and community partners work together to address Aims 1-5.

Analysis for Aim 6

The analysis plans for Aim 6 will be developed for projects as appropriate.

Power and Sample Size.

Consensus has yet to be determined on the precise power calculations for multilevel models[1-3]. Subramanian and other respected scholars in multilevel modeling argue that if the purpose of the multilevel model is to estimate the variation of level-1 variables, the size of the level-1 variable is really the driving factor [2,3]. Power for the proposed study was calculated using Power Analysis and Sample Size software (PASS 2020) based on household level randomization, individual level outcomes using conservative estimates and adjusting for 15% attrition and allowing for subgroup analyses [4]. A test for the difference in two proportions using a mixed model based on a clustered 3-Level Hierarchical Design with level-3 (household) 2:1 intervention: control randomization. The total sample size of 300, obtained from 100 level-3 units (households) in the intervention group and 50 level-3 units in the control group with an average of 2 level-2 units (individuals) per level-3 unit (household) and an average of 3 level-1 units (timepoints) per level-2 unit (individual), achieves >80% power to detect a difference between the group proportions of at least 0.15. The proportion in group 2 is 0.10. The correlation of level-1 units within a level-2 unit is <0.7. The correlation of level-2 units within a level-3 unit is <0.3. A test based on a mixed-effects logistic regression is anticipated at a significance level of 0.05.

References:

1. Maas CJM, Hox JJ. Sufficient sample sizes for multilevel modelling. Methodology 2005; 1(3): 86-92.
2. Snijders AT. Power and sample size in multilevel modeling. 2005;3:1570-1573.
3. NCSS LLC. PASS 2020 Power Analysis and Sample Size Software; 2020. ncss.com/software/pass.
4. Maas CJM, Hox JJ. Sufficient sample sizes for multilevel modeling. Methodology. 2005;1(3):86-92.
5. Rozi S, Mahmud S, Lancaster G, Hadden W, Pappas G. Multilevel Modeling of Binary Outcomes with Three-Level Complex Health Survey Data. Open J Epidemiol. 2017;07(01):27-43.
6. Robinson TJ. Multilevel Analysis: Techniques and Applications. J Am Stat Assoc. 2003;98(462):496-496.
7. Hox JJ. Multilevel Analysis: Techniques and Applications. Psychology Press; 2002.
8. Joreskog, K. G., & Sorbom D. (1988). PRELIS: A Program for Multivariate Data Screening and Data Summarization. A Preprocessor for LISREL. Chicago: SSI, Inc.
9. Joreskog, K. G. (1978). Structural analysis of covariance and correlation matrices. Psychometrika, 43, 443-477.

Reference added my MG on 2/18/2021

1 Asparouhov T, Muthén B. Advances in latent variable mixture models. In: Hancock GR, Samuelsen KM, editors. *Adv. Latent Var. Mix. Model.* Charlotte, NC: Information Age Publishing; 2008. p. 27–51.

2 Rights JD, Sterba SK. The relationship between multilevel models and non-parametric multilevel mixture models: Discrete approximation of intraclass correlation, random coefficient distributions, and residual heteroscedasticity. *Br J Math Stat Psychol* 2016;**69**:316–43. https://doi.org/10.1111/bmsp.12073.

3 Titterington DM, Makov UE, Smith AFM. Statistical analysis of finite mixture distributions 1985:x, 243 p.

References added by KP

1. NORC at the University of Chicago. (2014). The General Social Survey Questionnaire (GSS). Household Enumeration Form (HEF) Roster, items 5A–5D, 6, and 7. http://gss.norc.org/

2. Vidot DC, Messiah SE, Gattamorta K. COVID-19 Cannabis Health Questionnaire (CCHQ). El Centro Measures Library. https://elcentro.sonhs.miami.edu/research/measures-library/cchq/index.html.

3. Center for Economic and Social Research. (2020). Understanding America Study Coronavirus Tracking Survey - Long Form - Wave 2: April 1-14, 2020. Section: COVID-19 Knowledge, Attitudes, and Avoidant Behaviors. https://www.phenxtoolkit.org/toolkit_content/PDF/CESR_UAS_Knowledge.pdf

4. Behar-Zusman, V., Chavez, J. V., & Gattamorta, K. (2020). Developing a Measure of the Impact of COVID-19 Social Distancing on Household Conflict and Cohesion. Family Process, DOI: 10.1111/famp.12579.

5. Center for Pediatric Traumatic Stress. (2020). COVID-19 Exposure and Family Impact Survey (CEFIS). https://www.phenxtoolkit.org/toolkit_content/PDF/CPTS_CEFIS_Impact_v2.pdf

6. Center for Human Development, University of California, San Diego. (2015). Adolescent Brain Cognitive Development (ABCD) Study. https://www.phenxtoolkit.org/toolkit_content/PDF/UCSD_ABCD_Parent_Relationships.pdf