W. Alton Russell1, others

1School of Population and Global Health, McGill University, Montreal, Canada

**Corresponding author:**

**Key words:**

**Running title:**

# Abstract

**Background:** A

**Methods:** A

**Results:** A

**Conclusions:** A

# Introduction

Citation . See [Figure 1](#fig-sample), [Table S 1](#cor-sample), [Table 1](#thm-sample), and [Figure S 1](#lem-sample).

Need to figure out how to cite those figures and tables later.

**Citation Examples:**

This study was conducted by Dr. Marty et al., in which they found x is significantly associated with y [1]. This is a citation exists in the merged .bib file, see if it is presented correctly in the document.

Another study found that blablabla [2], we appreciate the work done by Dr. Charlton and her colleagues.

### Sampling Methods:

DBS and VBS

# Methods

## Dataset

The Canadian Longitudinal Study on Aging (CLSA) is a comprehensive national long-term study designed to track approximately 50,000 individuals aged 45 to 85 years at recruitment for a minimum of 20 years [citation for CLSA]. During the COVID-19 pandemic, several studies were conducted to collect and analyze blood samples from CLSA participants, aimed at comprehending and evaluating the pandemic’s population-level health impact.  
The dataset utilized in this study was sourced from the CLSA COVID-19 Antibody Study, with over 19,000 CLSA participants across ten provinces included [Insert citation here]. The dataset comprises demographic information, self-reported health status, vaccination and hospitalization history, and the results of SARS-CoV-2 immunoassay tests.

The CLSA COVID-19 Antibody Study has two complementary cohorts. The first one is called “comprehensive cohort”, in which 17,399 participants were invited and 9,753 of them agreed to participant and provided testable samples with complete results. Within this group, N=4,258 contributed venous blood samples, and N=5,495 provided dried blood samples. Participants in the comprehensive cohort were randomly selected from locations within 25-50 km of the data collection sites (DCS) and underwent in-person interviews, providing detailed information on demographics, physical and mental health status, as well as vaccination and hospitalization history. The second cohort, known as the “tracking cohort,” was interviewed by telephone. For our analysis, we will exclusively utilize data from the comprehensive cohort (N>9,753), as it provides more comprehensive demographic and health condition data.

[Can we cite the CLSA flow chart here? or is it OK to make our own version of it and put it here?]

## Bivariate Analysis and Multivariate Regression Modeling

Before conducting propensity score matching (PSM) to create matched pairs and analyze the matched data, we performed an initial unadjusted bivariate analysis to compare the DBS and VBS groups. Additionally, we developed multivariate logistic regression models, regressing VBS/DBS against demographic factors, physical and mental health conditions, travel distance, vaccination status, and time since the last COVID outbreak. The comprehensive results generated by those simple logistic regresion models and the full model are displayed in **Table X** and the odds ratio plot (**Fig. X**).

Upon completion of the full model, we constructed a best-fit model utilizing a backward stepwise model selection strategy. The model with lowest Akaike Information Criterion (AIC) value was selected as the best-fit model. Subsequently, we applied this best-fit model to calculate propensity scores for the selection of VBS over DBS. Participants from both groups will then be matched based on their propensity scores using subclass matching method.

## Analysis with Matched Data

To analyze the variation in quantitative Anti-S immunoassay results, we employed the empirical cumulative distribution function (eCDF) to visualize the distribution in the matched DBS and VBS cohorts (**Fig. Y**). We used Kolmogorov-Smirnov (KS) Test to assess whether the distributions are statistically-significantly different. Additionally, we utilized odds ratios to present differences in Anti-N and Anti-S assay positivity (**Table Y**).

# Results

A

# Discussion

A

# Declarations

**Funding:** A

**Conflicts:** A

**Ethics/Consent:** A

**Data and materials:** A

**Code availability:** A

**Authors’ contributions: A**

# References

1. Langham S, Wright A, Kenworthy J, Grieve R, Dunlop WCN. Cost-effectiveness of take-home naloxone for the prevention of overdose fatalities among heroin users in the United Kingdom. *Value in Health*. 2018;21(4):407-415. doi:[10.1016/j.jval.2017.07.014](https://doi.org/10.1016/j.jval.2017.07.014)

2. Charlton CL, Nguyen LT, Bailey A, et al. Pre-Vaccine Positivity of SARS-CoV-2 Antibodies in Alberta, Canada during the First Two Waves of the COVID-19 Pandemic. *Microbiology Spectrum*. 2021;9(1):10.1128/spectrum.00291-21. doi:[10.1128/spectrum.00291-21](https://doi.org/10.1128/spectrum.00291-21)

# Tables

**Table 1** Table caption here.

| **col1** | **col2** |
| --- | --- |
| **A** | |
| 1 | Yes |
| 2 | Yes |
| **B** | |
| 1 | No |
| 2 | No |

# Figures

|  |
| --- |
| **Figure** 1: Figure caption here. |

# Supplemental materials

# A. Supplement section

# Supplemental tables

**Table S 1** Table caption here.

| **col1** | **col2** |
| --- | --- |
| **A** | |
| 1 | Yes |
| 2 | Yes |
| **B** | |
| 1 | No |
| 2 | No |

# Supplemental figures

**Figure S 1** Figure caption here.

