



# MR-MEETING UPDATES

---

Luis Castro-de-Araujo<sup>a</sup>

23 February 2023

Virginia Institute for Psychiatric and Behavioral Genetics & The University of Melbourne

---

<sup>a</sup>Post-doc T32. [luis.araujo@vcuhealth.org](mailto:luis.araujo@vcuhealth.org)

MRDoC Power Comparisons

MRDoC Power Comparisons - Data generating model is MRDOC2

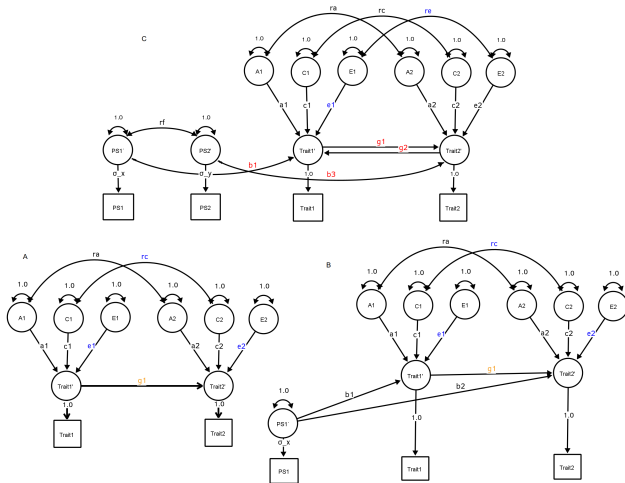
Longitudinal model

## MRDoC POWER COMPARISONS

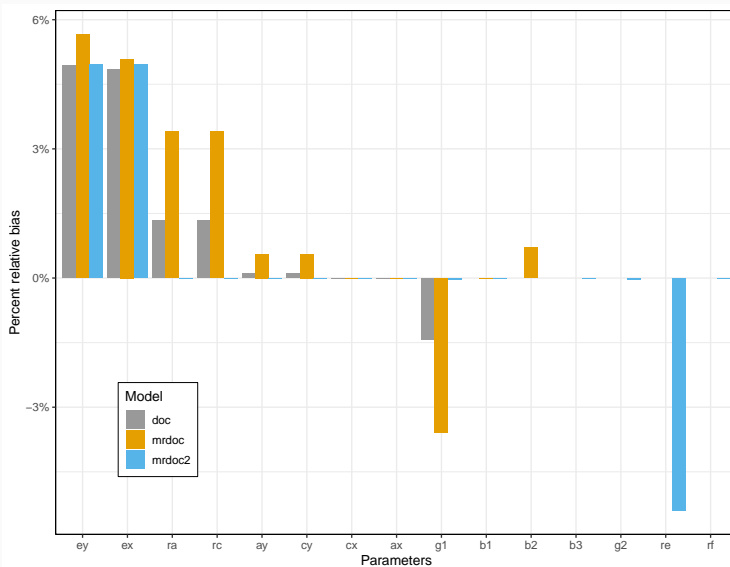
---



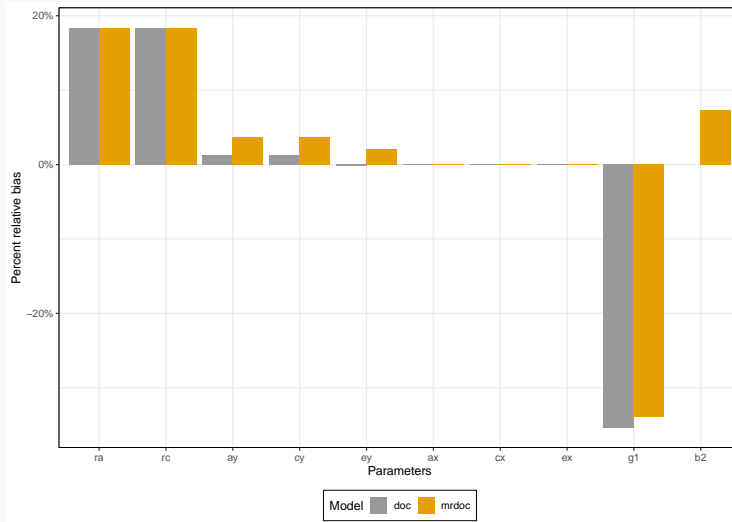
MR-DoC (A), DoC (B), and MR-DoC2 (C) model specifications for a single twin member. They include the effects of additive genetic (A), common environment (C) and specific environment (E) factors for both Trait 1 and Trait 2, and their effects may correlate (parameters  $r_a$ ,  $r_c$ , and  $r_e$ ). Path labels in red are important to the model's overall power, those susceptible to measurement error in blue, and in orange are those that are both susceptible to measurement error and are important to the model's overall power.



# PERCENT BIAS - UNRELIABILITY FACTOR

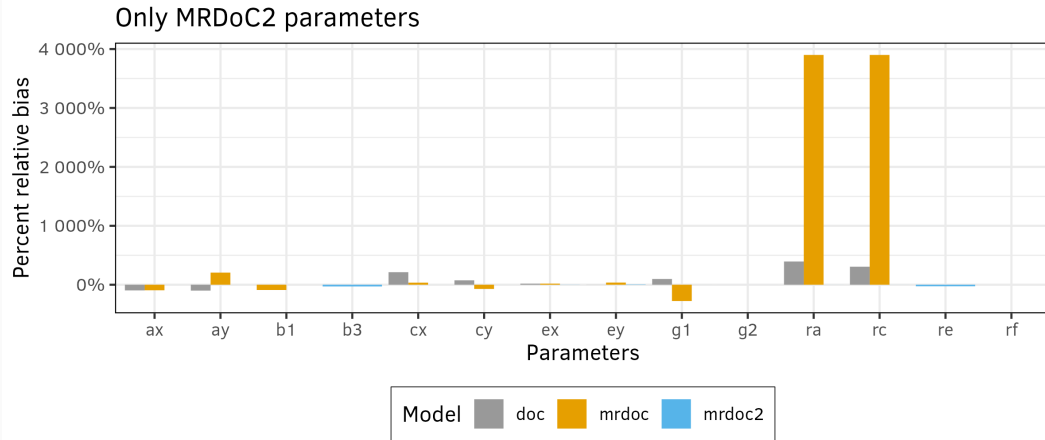


# PERCENT BIAS - RE UNMODELLED

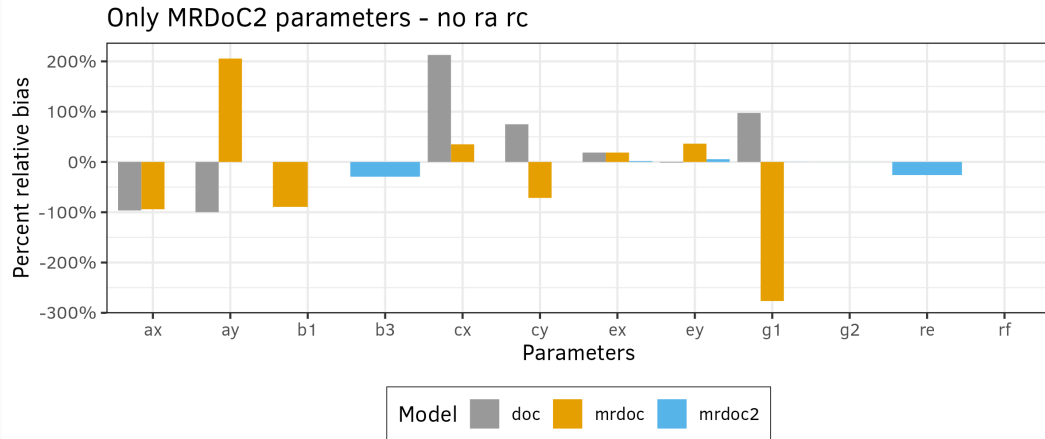


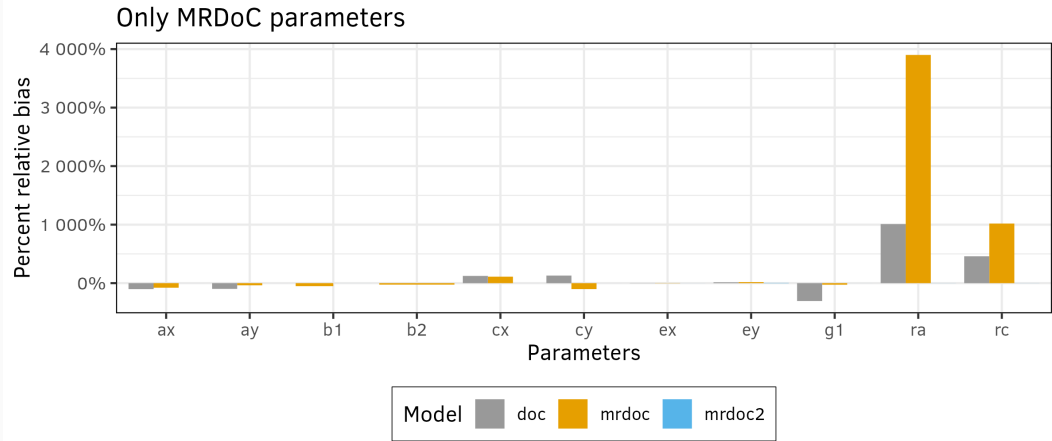
## **MRDoC POWER COMPARISONS - DATA GENERATING MODEL IS MRDOC2**

---

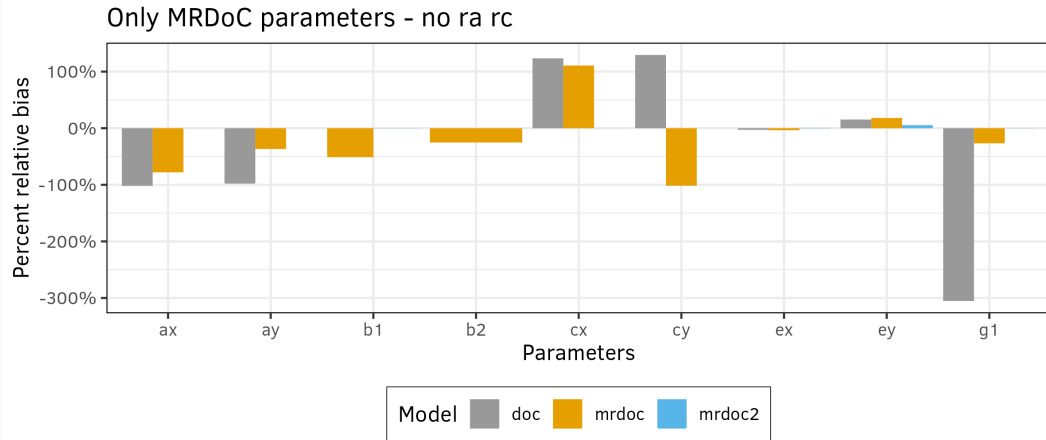


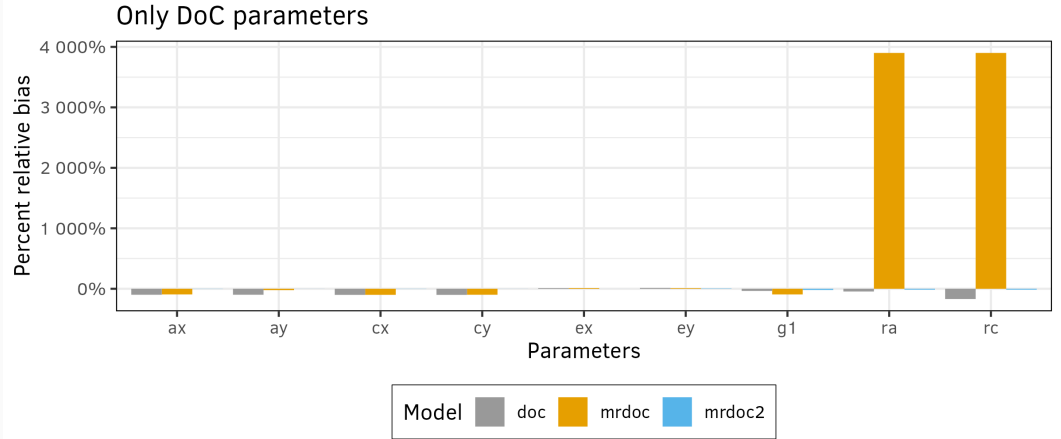




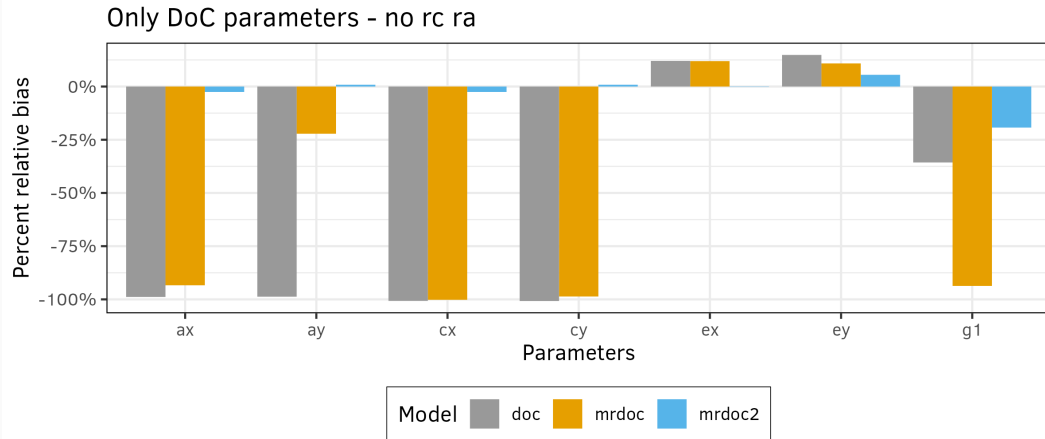


# ALL MRDoC PARS - NOT PLOTTING RA AND RC

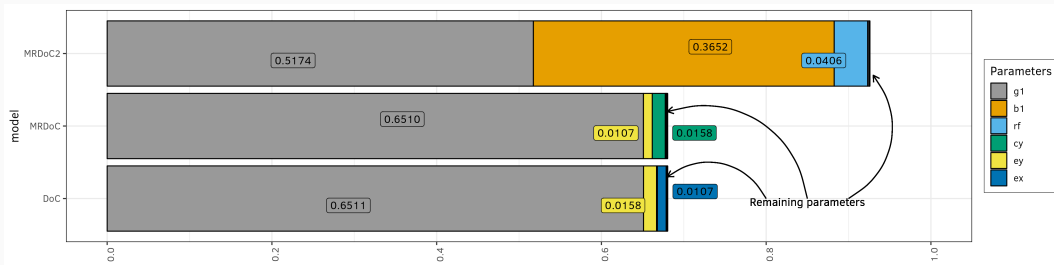




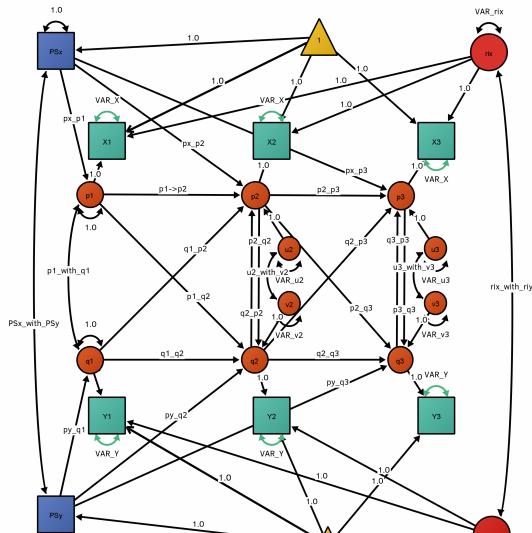
# ALL DoC PARS - NOT PLOTTING RA AND RC



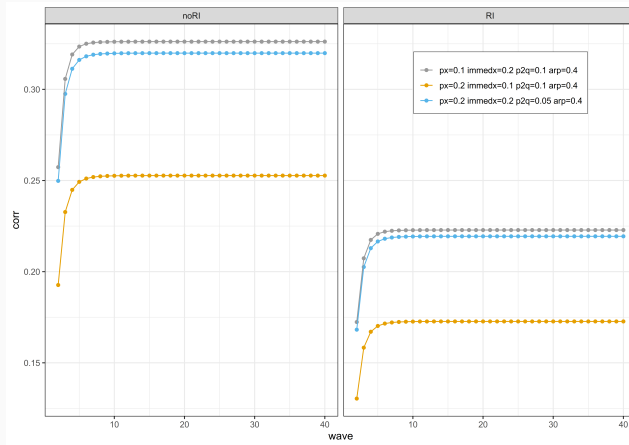
# VARIANCE EXPLAINED IN STATISTICAL POWER BY MODEL PARAMETERS.



**Figure 1:** Linear regression of NCP on the parameter values used for 19683 and 4097 exact data simulation power analyses in the ACE model for DoC, MR-DoC and MR-DoC2, respectively. The hypotheses are  $g1=0$  for all. These are stacked bar plots with semipartial correlation squared for each of the parameters. The total  $R^2$  for both DoC and MR-DoC models (including all parameters in the regression) was 0.945, and 0.93 for MR-DoC2. One can interpret these as  $g1$  having the largest effect on DoC and MR-DoC overall power, and  $g1$ ,  $b1$  and  $rf$  having the largest effects on the MR-DoC2 overall power.



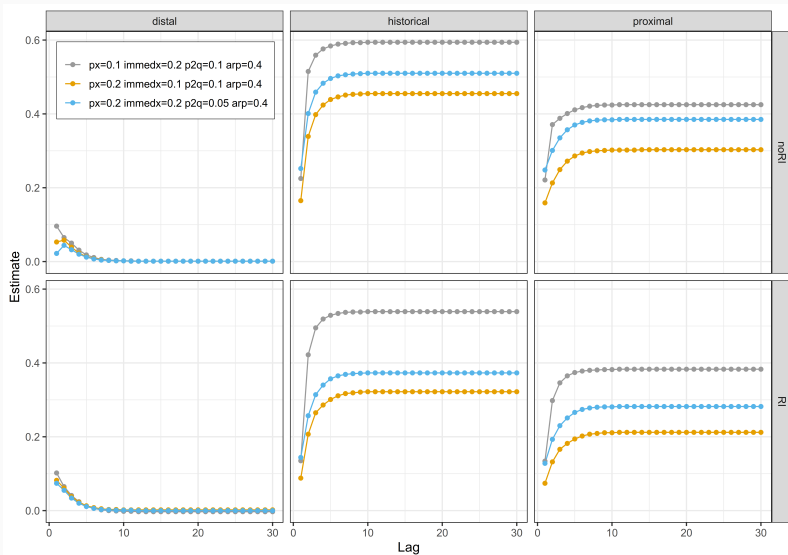
The model is identified as depicted (3 waves). It comprises 5 main elements: (A) the observed variables in green; (B) the between-person variances in orange; (C) the polygenic scores in blue; (D) the means in yellow; and (E) the random intercepts in red. Free paths are in black, and named. Fixed paths are marked with 1. The specific variances for the observed variables are equal across study waves, marked in green.



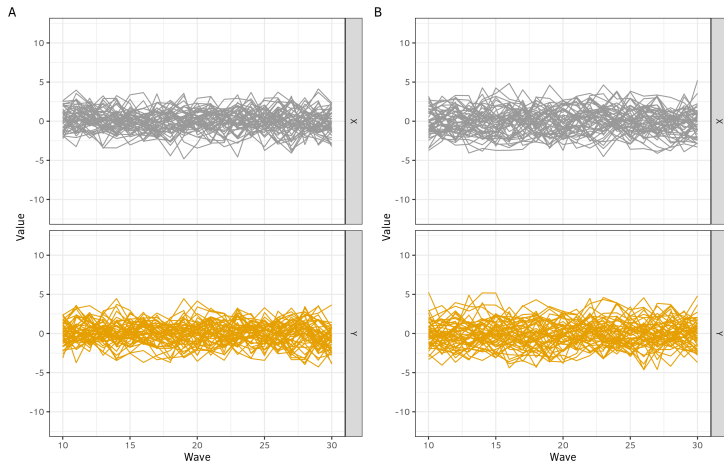
**Figure 2:** Correlation between  $X_t$  and  $Y_t$ , where  $t$  is the study wave up to 40. With the extension of the model, the correlations stabilize. This model reaches stationarity at wave 10.



# ESTIMATES WITH INCREASING LAG

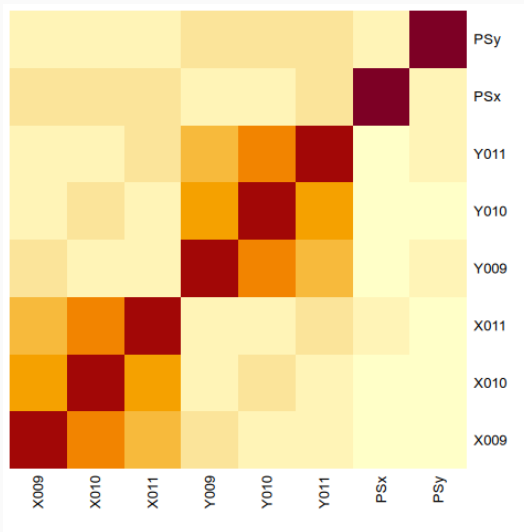


# WIREFRAME OF THE MEANS OF THE MEASURED VARIABLES ACROSS WAVES



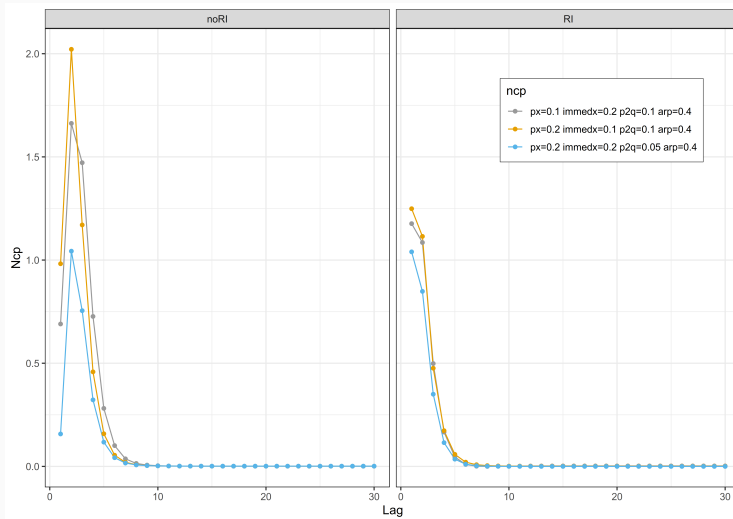
The means of the observed variables are plotted individually for both  $X_t$  and  $Y_t$ , when  $t$  is the study wave, starting in  $t = 20$ . The panel B depicts the means when the model with random intercepts. Panel A depicts the model without random intercepts. Panel B shows more spread than panel A. Theta ( $p_x = p_y = 0.1$ ;  $p_{t\_qt+1} = q_{t\_qt+1} = 0.05$ ;  $p_{t\_qt+1} = q_{t\_qt+1} = 0.1$ ;  $p_{t\_pt+1} = q_{t\_pt+1} = 0.4$ )

## HEATMAP FOR THE EXPECTED COV

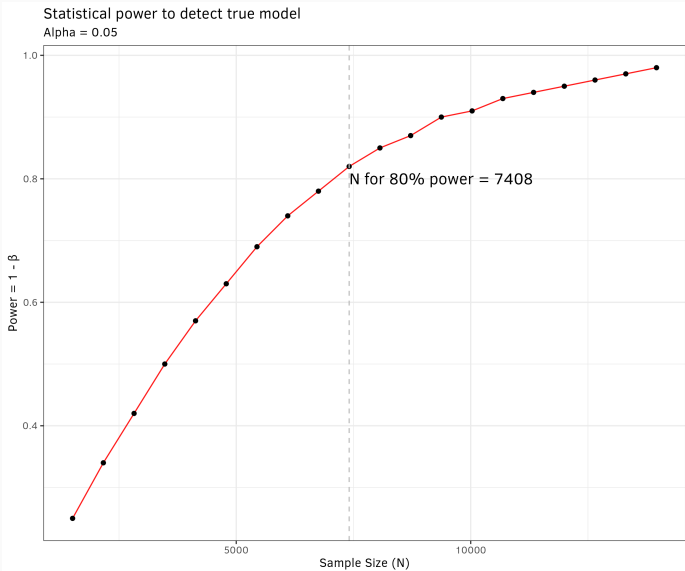


**Figure 4:** The expected covariance matrix for the observed variables.

# POWER WITH INCREASING LAG



# POWER AT THE FIRST STATIONARY WAVE



List of changed paths: 'p010' to 'q011'



## Team

- Joshua Pritkin.
- Rob Kirkpatrick.
- Michael C Neale.
- NIH grant no R01 DA049867 and 5T32MH-020030

## Contact



- **THANK YOU**