Supplementary Material for:

Breastfeeding Mitigates the Association Between Prenatal Maternal Pandemic-Related Stress and Children's Sleep Problems at 24 Months of Age

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1 Study overview

The quality of sleep significantly influences the long-term functioning of children. This study aimed to examine whether the exclusive breastfeeding of infants during the first 6 months of life could moderate the link between maternal prenatal pandemic-related stress (PRS) and sleep issues in 24-month-old children born during the pandemic. The study also considered the influence of maternal postnatal anxiety. Complete data from birth to 24 months were provided by seventy-eight mother-infant dyads, with the majority being White and 50% males. Maternal PRS during pregnancy was reported retrospectively at birth, while maternal anxiety and exclusive breastfeeding were reported at delivery, 3, and 6 months. Infant sleep disturbances were documented at 24 months. Bayesian analyses uncovered a positive association between maternal PRS and sleep problems in children who were not exclusively breastfed from birth to 6 months. The present Supplementary Material aims at providing a further description of our plan of analysis including missing data analysis and prior evaluation.

2 Maternal pandemic-related stress questionnaire

At delivery (T0) mothers retrospectively reported on their pandemic-related stress (PRS) during pregnancy through an ad-hoc questionnaire (Provenzi et al., 2020). The questionnaire included six 5-point Likert scale items (1, not at all; 5, very much) on the emotional stress response to the COVID-19 emergency during pregnancy. An average maternal antenatal pandemic-related stress (PRS) score was obtained, ranging from 1 (low) to 5 (high). Items are: 1. How much worried were you about the risk of COVID-19 infection? 2. How much did you feel that your pregnancy was at risk due to COVID-19 pandemic? 3. How much did you fear for your health? 4. How much did you fear for your baby's health? 5. How much did you feel that you were losing confidence in your health? 6. How much did you feel you had lost faith in medicine?

3 Missing data analysis

Due to attrition over time, the sample at 24 month after delivery (t3; n = 85) included less subjects than the sample at delivery (t0; n = 320) (Grumi et al., 2022). Here, we compare initial and final samples in order to assess if the are differences between them. Figure S1 shows the percentages of missing data in each of the 11 variables considered meaningful and taken under consideration for the comparison. We used a Bernoullian logistic model to evaluate whether participants who attend and did not attend data collection at different time points differed on sociodemographic (i.e., maternal age and education as well as infants' gestational age and sex) and personological variables (i.e., maternal anxiety and depression) and variable of interest (i.e., maternal PRS, exclusive breastfeeding and infants' sleep problems). In this model, we included all variables without missing data as predictors and an indicator variable taking the value of 1 when a subject has at least one missing data as a dependent variable. With this model, we estimated the posterior probability of missing data as a function of those variables without any missing data. If the relations are small or close to null, the hypothesis that missing data do not depend on particular characteristics of the grouping variable is supported. Since we did not expect such effects, for all parameters we used a prior of the same type, namely Student's t(3, 0, 1), This implies that we hypothesized a 90% probability for the parameters to fall within the interval [-2.35, 2.35]. It should be noted that maternal state anxiety assessed at t0, t1 and t2 have been collapsed in one variable, i.e., maternal anxiety factor score, according to factor score computation (Revelle., 2023) and then included in the tested models. Moreover, in order to provide a graphical description of variables with missing data, we computed related density distributions for subjects with and without missing data. Density distributions are presented in Figure S2. Box 1 resumes model parameters while Figure S3 presents the model predictions, i.e. the estimated posterior probability that a subject presents a missing data in the response variables given the values in the predictors. The bands indicate the 90% credibility intervals. Both graphical representation and model expected suggest that there were no relevant differences related to any of these variables.

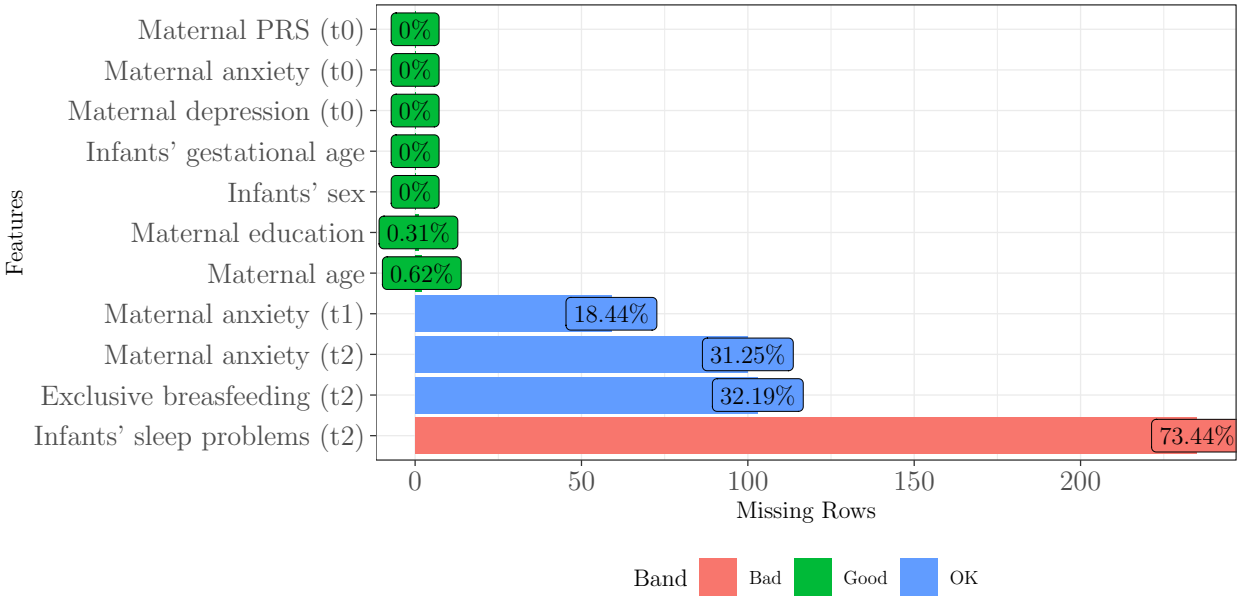

Figure S1: Missing values for variables of interest.

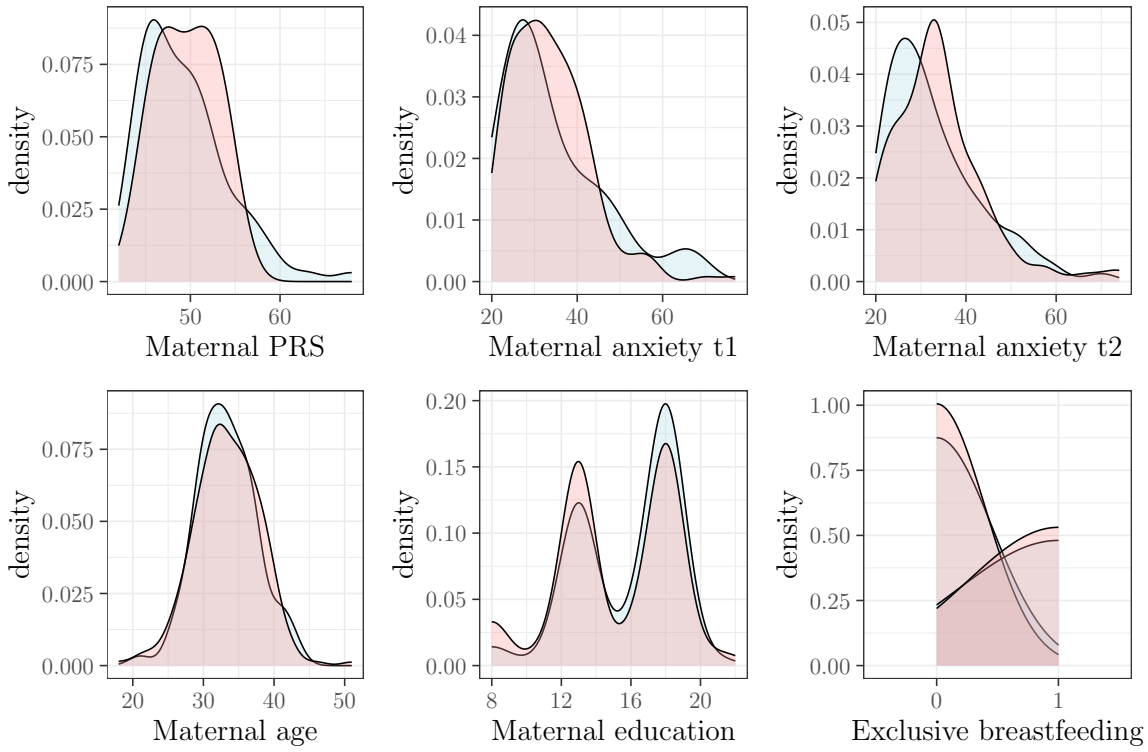

Figure S2: Empirical density of model variables depending on the presence of missing data. In red subjects with missing data, in blue subjects without.

```
 Family: bernoulli
  Links: mu = logit
Formula: missing ~ cov_str + stai_state_0 + bdi_0 + ga + sex
   Data: breast (Number of observations: 320)
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000

Population-Level Effects:
             Estimate Est.Error l-90% CI u-90% CI Rhat Bulk_ESS Tail_ESS
Intercept        7.63      4.85    -0.24    15.60 1.00     5357     2714
cov_str          0.00      0.20    -0.32     0.33 1.00     5337     3008
stai_state_0     0.01      0.02    -0.02     0.04 1.00     4393     3350
bdi_0           -0.01      0.03    -0.06     0.04 1.00     4547     3579
ga              -0.17      0.12    -0.37     0.02 1.00     5377     2761
sex             -0.18      0.25    -0.59     0.23 1.00     6405     3015

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
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Box 1: Logistic model. cov_str = Maternal PRS, stai_state_0 = Maternal anxiety t0, bdi_0 = Maternal depression t0, ga = Infants' gestational age, sex = Infants'sex.

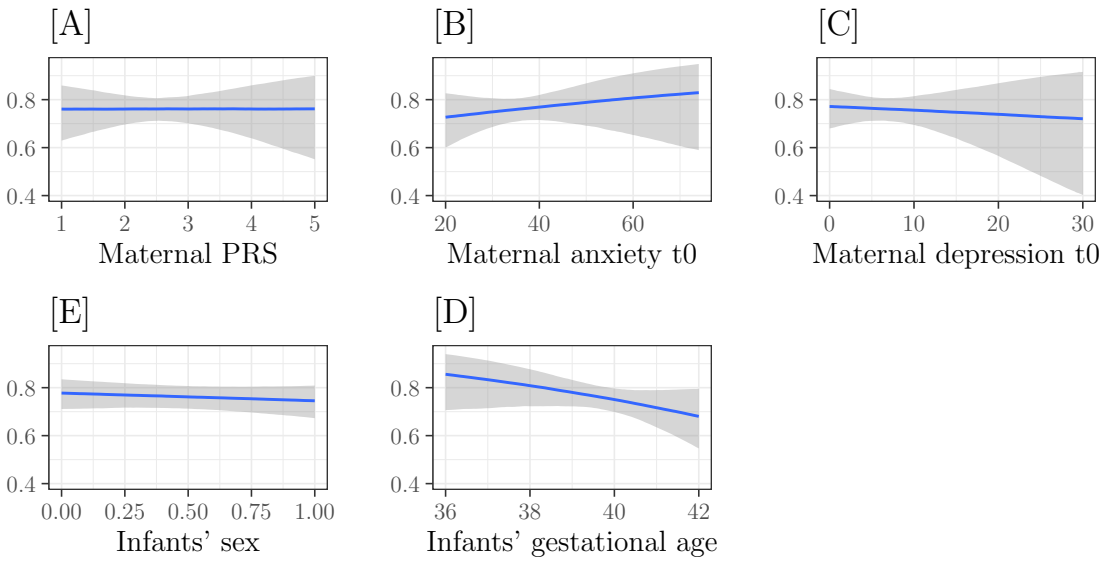

Figure S3: Missing data model predictions. Each panel presents the posterior probability of observing missing data as a function of maternal COVID-related stress assessed at T0 [A], maternal anxiety assessed at T0 [B], maternal depression assessed at T0 [C],infants' gestational age [D], infants' sex [E]. The bands indicate the 90% credibility intervals.

4 Descriptives of variable of interest

Considering exclusive breastfed and non-exclusive breastfed groups, we had 30 and 48 subjects respectively. Figure S4 represents bivariate associations between variables of interest (i.e., variables included in tested models) while Figure S5 represents bivariate associations between participants descriptives considering exclusive breastfeeding groups. As evident from Figure S5, no differences between exclusive breastfeeding groups were found.

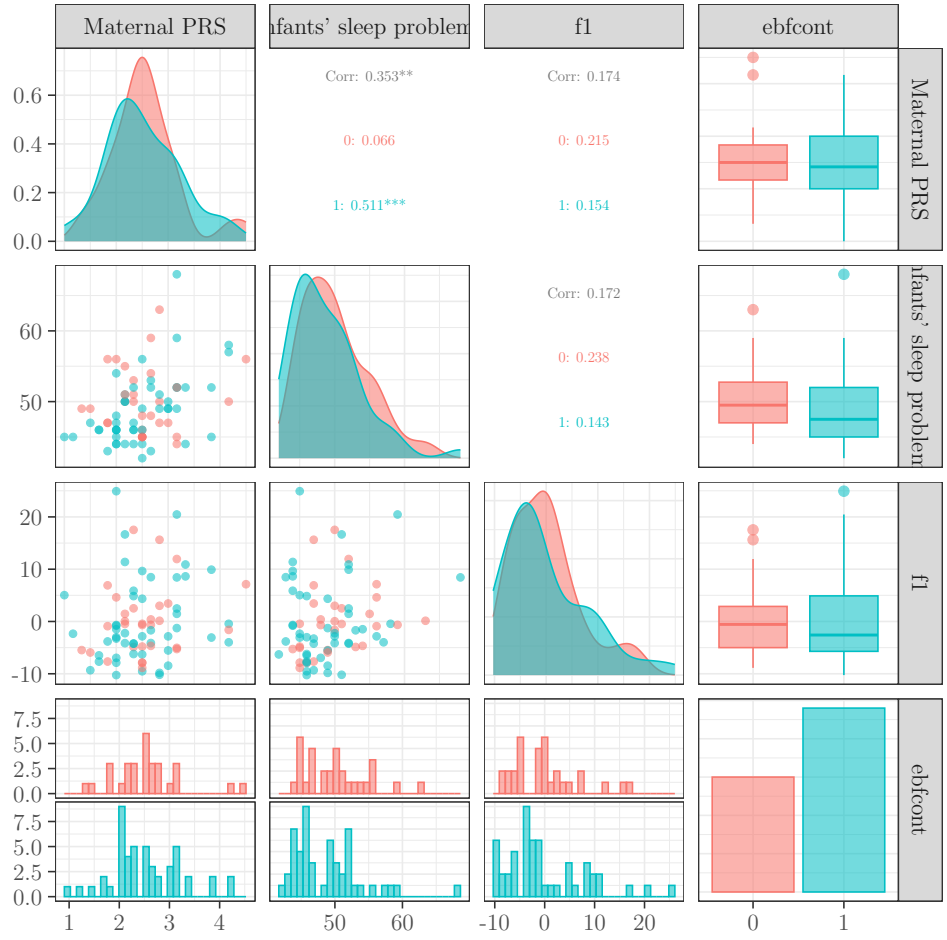

Figure S4: Distributions of variables of interest. Maternal PRS = maternal prenatal pandemic-related stress; Infants' sleep problems = infants' sleep problems assessed at t3; f1 = maternal anxiety factor score; ebfcont = exclusive breastfeeding groups (0 = yes, 1 = no)

Figure S5: Distributions of participants descriptive variables in exclusive breastfeeding groups. Maternal edu = maternal education expressed in years; Infants ga = infants gestational age expressed in weeks; Infants' bw = infants' birth weight expressed in grams; ebfcont = exclusive breastfeeding groups (0 = yes, 1 = no)

5 Prior Specification

5.1 Prior distribution

For each models parameter, we defined a prior probability distribution, chosen with the aim of formalizing our prior hypotheses. In particular, we adopted the Student's t for intercepts

and regression coefficients. Table 1 reports in detail all the priors defined for the target model [M04]. The "parameter" column indicates the specific model coefficient name while column "Prior" reports priors' degrees of freedom, mean and sd. Credible Interval column shows corresponding intervals within which we hypothesized that model parameters would fall with a 90% of probability. Figure S6 represents prior distributions.

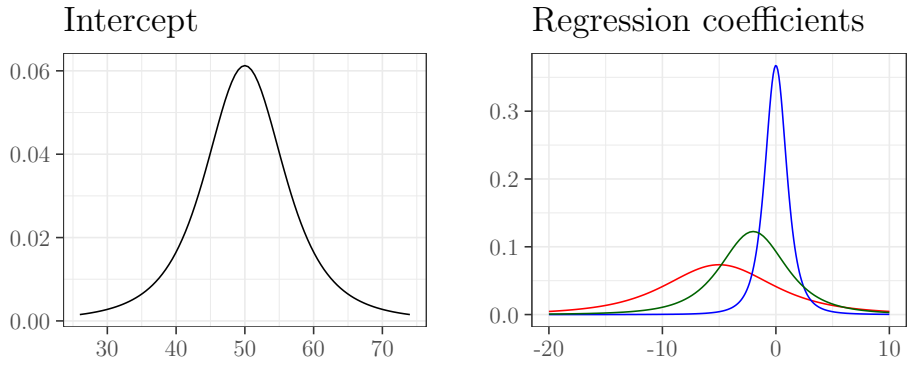

Figure S6: Prior distribution. Intercept = intercept; red = exclusive breastfeeding groups; blue = maternal prenatal pandemic-related stress; dark green = interaction between exclusive breastfeeding and maternal prenatal pandemic-related stress

Parameter	Prior	90% Credible Interval
Intercept	Student_t(3, 50, 6)	[35.88, 64.12]
b_ebfcont	Student_t(3, -5, 5)	[-16.77, 6.77]
b_cov_str	Student_t(3, 0, 1)	[-2.35, 2.35]
b_ebfcont_cov_str	Student_t(3, -2, 3)	[-9.06, 5.06]

Table S1: Priors of the target model [M04]. Parameter = model coefficient name; Prior = priors' degrees of freedom, mean and sd; 90% Credible Interval = intervals within which we hypothesized that model parameters would fall with a 90% of probability

5.2 Prior Predictive Check

The Prior Predictive Check (PrPC; Gelman et al., 2020) is crucial for appropriately selecting sensible priors in the models we are going to test, especially given the limited sample size (van de Schoot & Miocevic, 2020). While the posterior predictive check (PPC) generates replicated data following the posterior predictive distribution, PrPC generates data according to the prior predictive distribution. PrPC is similar to the PPC but without any observed

data. Executing this process mechanically involves simulating parameters based on the priors, followed by simulating data according to the sampling distribution given the simulated parameters. The outcome is a simulation from the joint distribution, and consequently, it represents a simulation from the prior predictive distribution. In other words, after selecting prior distributions, the model predictions are generated based on values sampled from these priors. By analyzing these model predictions and comparing them with the observed data, we can assess their reasonableness and whether they align with the expectations dictated by the hypotheses. PrPC and PPC of the target model are represented in Figure S7 [A] and [B] respectively.

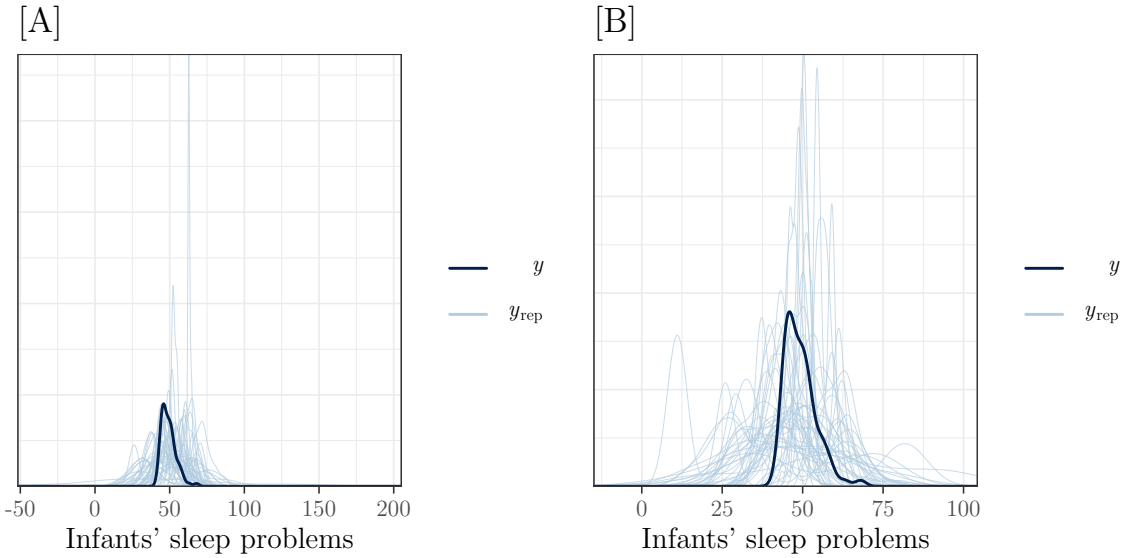

Figure S7: PrPC [A] and PPC [B] of simple interaction model.

6 Target Model Summary

Model coefficients of the target model are resumed below.

```
 Family: gaussian
  Links: mu = identity; sigma = identity
Formula: cshq_tot ~ ebfcont * cov_str
   Data: data_stai (Number of observations: 78)
  Draws: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup draws = 4000

Population-Level Effects:
                Estimate Est.Error l-90% CI u-90% CI Rhat Bulk_ESS Tail_ESS
Intercept          56.67     13.46    36.27    78.54 1.00     2814     2163
ebfcont1           -5.09      8.11   -16.78     6.38 1.00     2813     1591
cov_str             0.01      1.59    -2.24     2.29 1.00     3691     1837
ebfcont1:cov_str   -2.04      4.46    -8.92     4.91 1.00     3664     1958

Family Specific Parameters:
      Estimate Est.Error l-90% CI u-90% CI Rhat Bulk_ESS Tail_ESS
sigma     4.68      5.51     0.33    13.59 1.00     3217     1466

Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
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Box 2: Target model. cshq_tot = Infants' sleep problems; ebfcont = exclusive breastfeeding groups (0 = yes, 1 = no); cov_str = Maternal PRS.

7 References

7.1 R packages

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