

TREC & KREC of twins: Decomposing the covariance matrix

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Multivariate linear *regression* models built to handle multiple responses and with genetic and environmental interrelations of twins data (Bonat and Hjelmberg 2022) were applied to understand the dynamics from the TREC and KREC measures.

Keywords:

Introduction

Data

We have the TREC and KREC measures of 55 pairs of twins. From these 110 twins, we have five covariates, as follow:

- Birth weight (grams);
- Gestational age (weeks);
- Type of childbirth (normal or cesarean);
- Sex (male or female);
- Zygosity (MZ: monozygotic or DZ: dizygotic).

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Zygoty is a key term in our modeling framework since we need to inform how many twin pairs are monozygotic and dizygotic. Therefore, we drop a pair that do not present this information. We stay with 198 twins. Besides these five covariates, we may also consider the twin covariate (1 or 2), to verify a randomness supposition.

In Figure 1 we have some plots to see how our two responses behave. We can see that they are asymmetric with both having some upper outliers. For the TREC we have a mean of 110.78 and a median of 107.5. For the KREC we have a mean of 71.29 and a median of 58. In the scatterplots we see a clear positive association, linear until the outliers started to act.

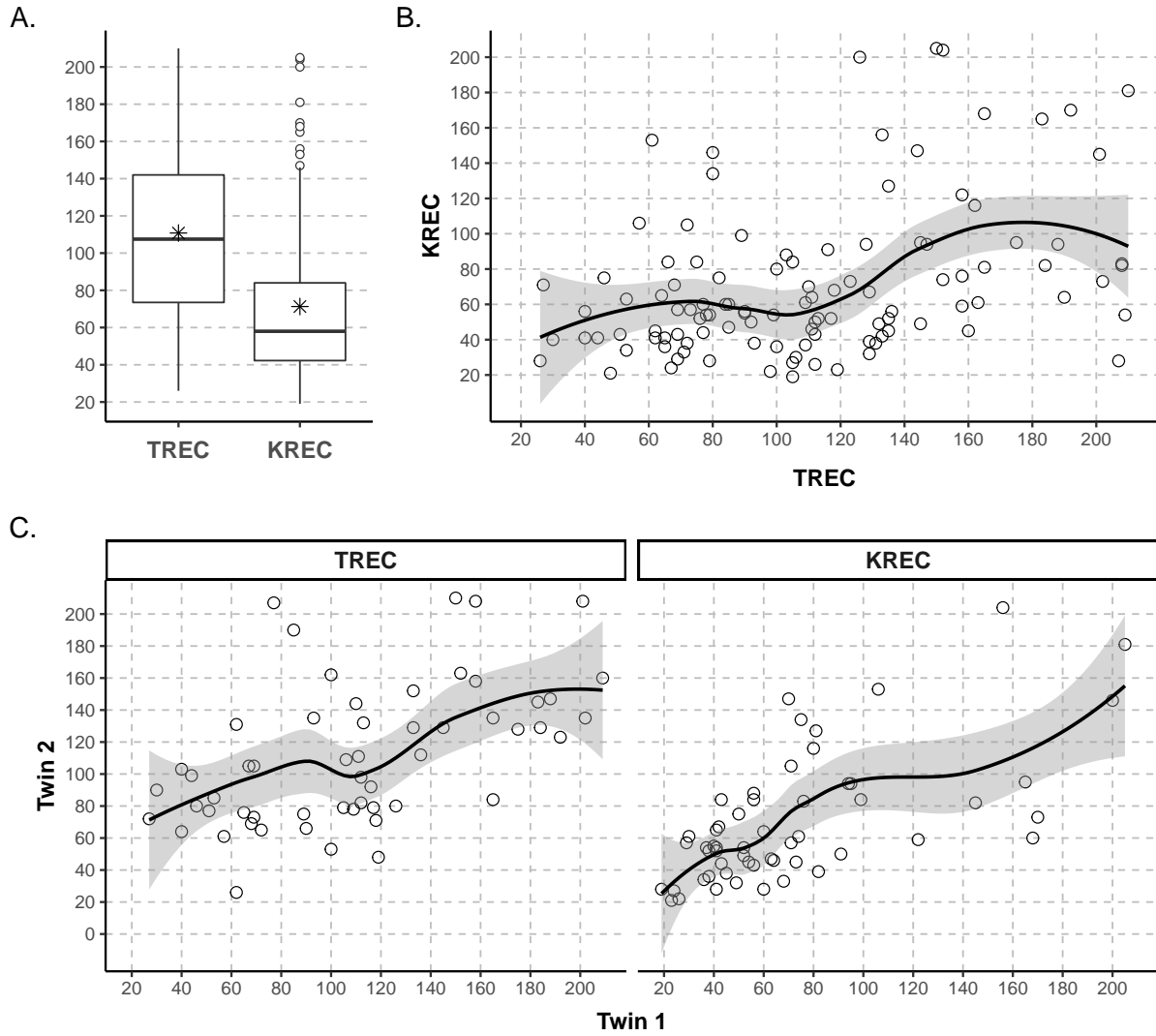


Figure 1: Graph A. TREC and KREC boxplots with their means in asterisks; Graph B. TREC and KREC scatterplot with tendency curve in solid black and 95% confidence band in gray; Graph C. Twins scatterplots per TREC and KREC with tendency curves in solid black and 95% confidence bands in gray.

In Figure 2 we have the plots of the covariates. We have a mean birth weight of 2266.28 grams and a mean gestational age of 34.98 weeks. 92.9% of the twins were born from cesarean childbirth and 76.8% are zygotes. In terms of sex, the sample is balanced.

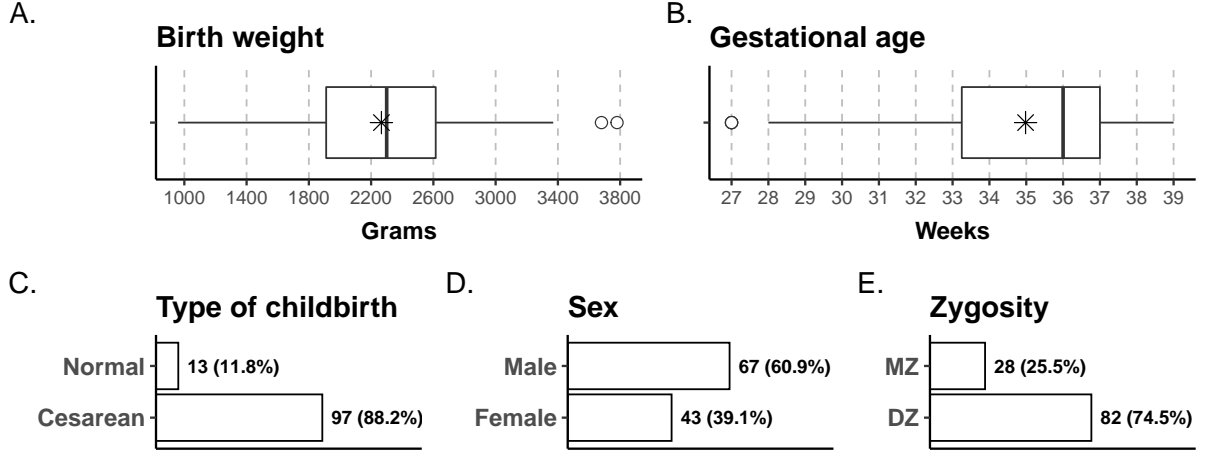


Figure 2: Graphs A. and B. are the boxplots of the numerical variables with their means in asterisks; Graphs C., D. and E. are the barplots of the categorical variables with their level frequencies and respective sample percentages.

Modeling framework

The statistical analysis was performed through the R (R Core Team 2022) language and environment for statistical computing. Besides the model fitting performed through the `{mgglm4twin}` (Bonat 2022, 2018; Bonat and Hjelmberg 2022; Bonat and Jorgensen 2016) package, the leading R packages used are: `{dplyr}` (Wickham et al. 2022), `{tidyr}` (Wickham and Girlich 2022), `{ggplot2}` (Wickham 2016), `patchwork` (Pedersen 2020), `{kableExtra}` (Zhu 2021) and `{Matrix}` (Bates, Maechler, and Jagan 2022).

Results

We model the TREC and KREC measures in a bivariate fashion and in two fronts, in the mean and covariance structures. We use a model called ACE to study heritability and the genetic and environmental relationships. Basically, we decompose the covariance matrix into three:

- A: genetic/heritability effect or component;
- C: common environment effect or component;
- E: unique environment effect or component.

Besides the covariance decomposition itself, we can also insert covariates in it. In both mean and covariance structures we tested for the effect of six covariates. With a bivariate model, we are able to handle the TREC and KREC measures jointly. We started with the ACE model,

however, the C component presented to be non-significant. Thus, we stayed with an AE model and from this performed a covariates selection procedure.

Table 1: Summary of the mean structure of the AE bivariate model.

	Estimate	SD	z-value	Pr(> z)
TREC				
Cesarean childbirth (intercept)	106.9038	5.1533	20.7446	0.0000
Normal childbirth (add to intercept)	36.6523	14.5258	2.5233	0.0116
KREC				
Cesarean childbirth (intercept)	67.8584	4.8132	14.0984	0.0000
Normal childbirth (add to intercept)	28.3342	13.2053	2.1457	0.0319

Starting from the mean structure, from the six covariates we end up with two. The significant ones, for each response, are presented in Table 1. For the TREC measures, the statistically significant covariates are the gestational age and the twin sex. For KREC, only the gestational age is significant.

About the covariance structure, what we do is decompose the TREC variance (13698.107), KREC variance (13787.069), and their covariance (777.2108) in the manner described in Table 2.

Table 2: Summary of the covariance structure of the AE bivariate model.

	Estimate	SD	Percentage	z-value	Pr(> z)
Environment component (E)					
TREC	817.7266	132.5380	37.7230	6.1698	0.0000
KREC	487.8804	660.9370	26.7987	0.7382	0.4604
TREC & KREC	265.9359	159.3236	34.2167	1.6692	0.0951
Genetic component (A)					
TREC	1115.7542	317.5889	51.4715	3.5132	0.0004
KREC	1124.9519	626.5544	61.7923	1.7955	0.0726
TREC & KREC	358.6664	241.5068	46.1479	1.4851	0.1375

At **?@tbl-AE-bivariate-model-genetic-components** we have the environment and heritability measures. The heritability is statistically significant in all scenarios, marginally; jointly; and its correlation.

Given the small sample size and the inferential level of complexity involved in the bivariate

model, we were not able to obtain numerical convergence by inserting covariates in the covariance structure. As a solution, we fitted univariate AE models with the same mean structure as in the bivariate scenario.

We started with the same six covariates. In the TREC model, we end up with no significant covariates in the environmental E component and with the type of childbirth as significant in the genetic A component. In the KREC model, the type of childbirth and zygosity are statistically significant in the E component, and in the A component, only the type of childbirth is significant. In **?@tbl-TREC-AE-model-covariance** and **?@tbl-KREC-AE-model-covariance** we have a summary of the covariances decompositions in terms of the significant covariates for the TREC and KREC measures, respectively.

In the TREC measure (**?@tbl-TREC-AE-model-covariance**), 26% of the observed variance has its explanation attributed to the environment component. In a twin born from a cesarean, 72% of the observed variance is explained by the genetic component. Together, both components explain 98% of the variance. In a twin born from normal childbirth, the explanation by means of the genetic component decreases by 80% - no variance explanation. We can justify that by the low representation in our data, with only 11.82% of the twins being born from normal childbirth.

In the KREC measure (**?@tbl-KREC-AE-model-covariance**), in a twin born from a cesarean and dizygotic, nothing of the observed variance is explained by the environment component (-62%). Nevertheless, if we change to a twin born from normal childbirth the attributed explanation grows by 66%, i.e. 4% (-62 + 66) of variance explanation. In a monozygotic twin, the explanation by the environment component is 9% (-62 + 71). In the genetic component, the difference in terms of variance explained by the type of childbirth is abysmal. In a twin born from cesarean, we have 103% (-62 + 165) of variance explained. The effect is so big and uncertain that it blows up. In a twin born from normal childbirth, we have the opposite. The unbalance in the data frequencies ends up generating these unrealistic results.

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Appendix

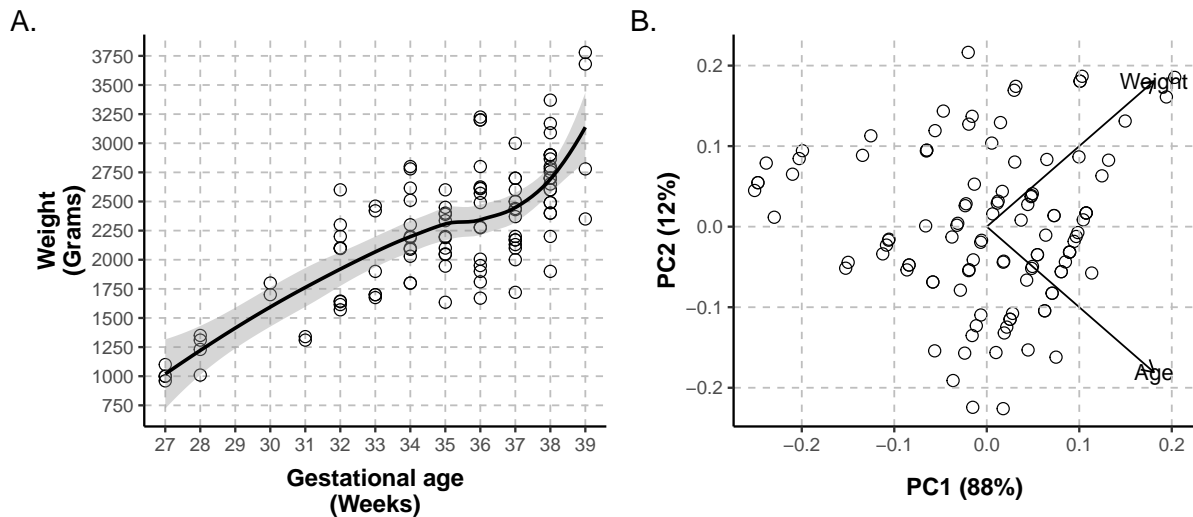


Figure 3: Graph A. Gestational age and weight scatterplot with tendency curve in solid black and 95% confidence band in gray; Graph B. Gestational age and weight biplot from a Principal Components Analysis (PCA).