

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 100 pairs of twins. From these 200 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 monozygoty and dizygoty. 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 170.449 and a median of 135. For the KREC we have a mean of 117.571 and a median of 75.5. In the scatterplots we see a clear positive association, linear until the outliers started to act.

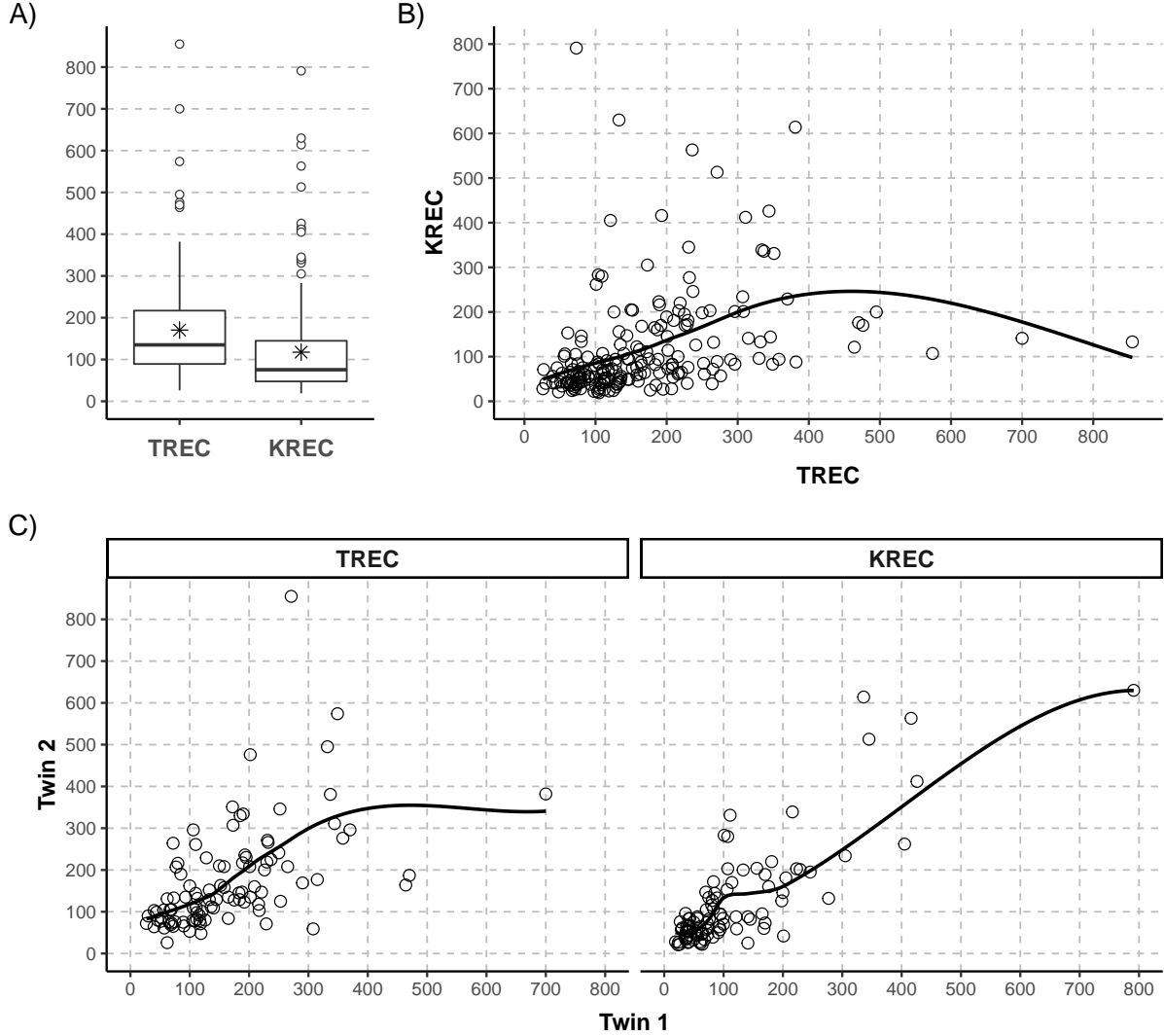


Figure 1: Graph A) TREC and KREC boxplots with their means in asterisks; Graph B) TREC and KREC scatterplot with tendency curve in solid black; Graph C) Twins scatterplots per TREC and KREC with tendency curves in solid black.

In Figure 2

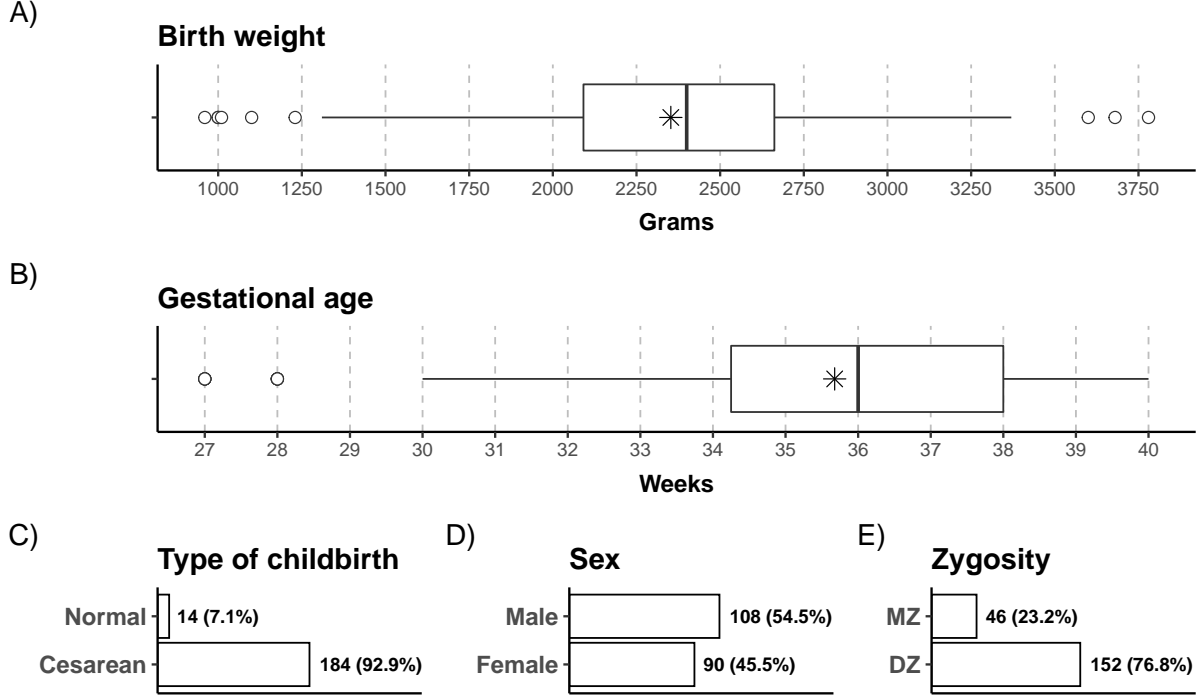


Figure 2: Graphs A) and B) are the boxplots of the numerical variables with their means in asterisks; Graphs C), D) and E) are the barplots of the categorial variables with their level frequencies and respective sample percentages.

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/regressors in it. In both mean and covariance structures we tested for the effect of six regressors.

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 regressors selection procedure.

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

	Estimate	SD	z-value	Pr(> z)
TREC				
Mean gestational age & female sex	-97.1912	127.8171	-0.7604	0.4470
A week in the gestational age	8.0203	3.5627	2.2512	0.0244
Male sex	-34.7133	15.0805	-2.3019	0.0213
KREC				
Mean gestational age	-160.7853	126.7882	-1.2681	0.2047
A week in the gestational age	7.7597	3.5385	2.1929	0.0283

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

About the covariance, what we do is decompose the TREC variance (13698.107), KREC variance (13787.069), and their covariance (4392.4173) in the manner described in Table 2.

At Table 3 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 regressors in the covariance. As a solution, we fitted univariate AE models with the same mean structure as in the bivariate scenario.

We started with the same six regressors. In the TREC model, we end up with no significant regressors 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

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

	Estimate	SD	Percentage	z-value	Pr(> z)
Environment component (E)					
TREC	3712.4482	2751.5400	27.1019	1.3492	0.1773
KREC	1391.8790	4100.7340	10.0955	0.3394	0.7343
TREC & KREC	862.7034	490.8413	19.6407	1.7576	0.0788
Genetic component (A)					
TREC	8703.5756	3370.8550	63.5385	2.5820	0.0098
KREC	9990.1531	5750.4968	72.4603	1.7373	0.0823
TREC & KREC	2633.3467	1090.5257	59.9521	2.4147	0.0157

Table 3: Summary of the genetic components of the AE bivariate model.

	Estimate	SD	z-value	Pr(> z)
Environmentability				
TREC	0.299005	0.209571	1.426747	0.153653
KREC	0.122287	0.363368	0.336538	0.736465
TREC & KREC	0.246765	0.157990	1.561908	0.118310
Correlation	0.379516	0.594325	0.638567	0.523105
Heritability				
TREC	0.700995	0.209571	3.344908	0.000823
KREC	0.877713	0.363368	2.415491	0.015714
TREC & KREC	0.753235	0.157990	4.767623	0.000002
Correlation	0.282405	0.139745	2.020867	0.043293

is significant. In Table 4 and Table 5 we have a summary of the covariances decompositions in terms of the significant regressors for the TREC and KREC measures, respectively.

In the TREC measure (Table 4), 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 7.07% of the twins being born from normal childbirth.

In the KREC measure (Table 5), 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%,

Table 4: Summary of the covariance structure of the AE TREC model.

	Estimate	SD	Percentage
Environment component (E)	3534.162	2773.739	25.8004
Genetic component (A)			
Cesarean childbirth	9851.598	3647.523	71.9194
Normal childbirth	-10976.948	3140.646	-80.1348

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.

Table 5: Summary of the covariance structure of the AE KREC model.

	Estimate	SD	Percentage
Environment component (E)			
Cesarean childbirth & DZ zygosity	-8562.138	3940.7251	-62.1027
Normal childbirth	9185.825	4003.8748	66.6264
MZ zygosity	9829.275	609.2463	71.2934
Genetic component (A)			
Cesarean childbirth	22781.346	3823.2523	165.2371
Normal childbirth	-22636.617	3909.9002	-164.1873

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Appendix

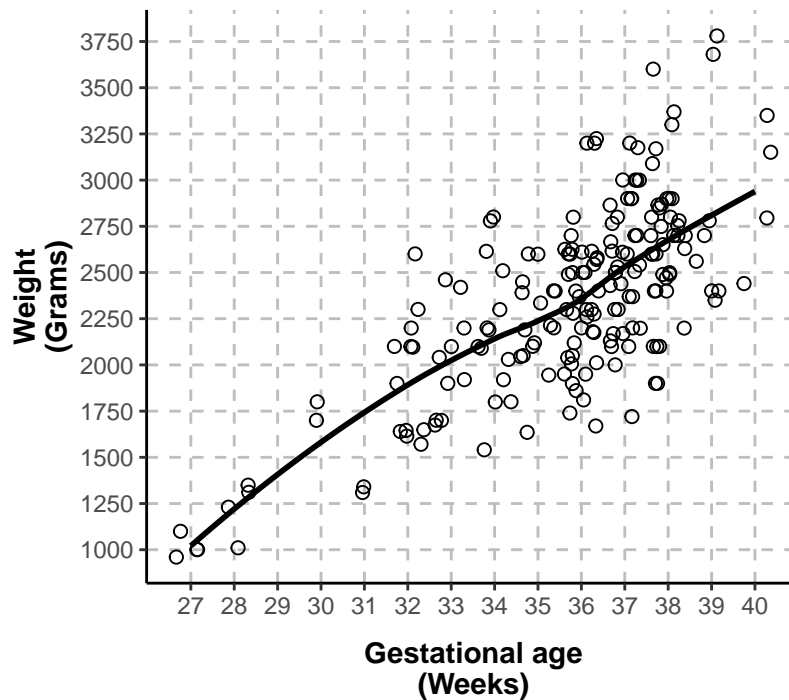


Figure 3: Gestational age and weight scatterplot with tendency curve in solid black.