Dear colleague,

We would like to bring to your attention the following two articles that might contain useful recommendations for the analysis of family-based samples. The first one is:

**Sandwich corrected standard errors in family-based genome-wide association studies** (attached, also available here: <http://www.tweelingenregister.org/nederlands/verslaggeving/NTR-publicaties_2014/Minica_EJHG_2014_epub.pdf>)

The paper answers the following practical question: Which is the most powerful procedure in conducting a family-based GWAS?

We compared several analytic strategies currently implemented in the GWAS-dedicated software (Plink, GCTA, FaSTLMM, EMMAX, Merlin).

We found that the efficiency of family-based analyses depends critically on the choice of the model for the familial covariance matrix. Families might be highly variable in size and composition, hence full correct modeling  of the conditional covariance matrix can be complicated and subject to misspecification.

We show that choosing a simpler model for the background (AE or CE) and using a sandwich correction is an efficient and computationally feasible analytic strategy. An example with annotated scripts for conducting such an analysis is available at <http://cameliaminica.nl/scripts.php>

The focus of this article is on family-based Genome-Wide Association Studies. However the analytic strategies we discuss are regression based approaches, hence,  relevant for any analysis involving family-data (i.e., the predictor can be a genetic variant, a polygenic score, or any other covariate one might be interested in).

The second article is:

**MZ twins or MZ singletons in population family-based GWAS? More power in pairs.** (attached, also available here: <http://www.tweelingenregister.org/nederlands/verslaggeving/NTR-publicaties_2014/Minica_MP_2014_epub.pdf>)

Occasionally in family-based GWAS, including monozygotic (MZ) twins, the data from one MZ twin are dropped, thus reducing the MZ pairs to singletons. We show that retaining data from both MZ twins does not affect type I error rate and reducing MZ pairs to singletons results in a loss of power.

I hope this information is useful.

best wishes,

Camelia Minica