**Potential Topics for future research:**

1. The heritability estimate for binary traits using GWAS data instead of sibling pair data; The current GWAS method for the estimation of heritability of binary trait is controversial

*( I feel a long-term possible project is the heritability estimate for binary traits using GWAS data. (You should create a file/system to track all possible future directions with as detailed notes as possible. You will be surprised how often we don't recall the details that seemed obvious now.*

*Visscher's group is big on this and there are also two very recent AJHG paper on this:*

*Hivert, V., Sidorenko, J., Rohart, F., Goddard, M. E., Yang, J., & et al. (2021). Estimation of non-additive genetic variance in*

*human complex traits from a large sample of unrelated individuals. American journal of human genetics, 108(5), 786-798.*

*Pazokitoroudi, A., Chiu, A. M., Burch, K. S., Pasaniuc, B., & Sankararaman, S. (2021). Quantifying the contribution of*

*dominance deviation effects to complex trait variation in biobank-scale data. American journal of human genetics, 108(5),*

*799-808.*

*There have been some criticism of this type of approach for analyzing and interpreting binary traits.*

*I recall Rosset had a earlier paper on this, but couldn't pinpoint the paper. But you should be able to infer it from his other paper:*

*https://www.pnas.org/content/111/49/E5272*

*Finally, a number of Rosset's paper on h2 estimates appeared in PNAS. So you could take a closer look at the writing style, and we could consider first trying PNAS, depending on Professor Lawless's honest opinion of your work*

*https://www.pnas.org/content/pnas/116/1/local/information-for-authors.pdf*

***Here are another two papers suggested by Lei during the meeting:***

*[昨天 上午11:05] Lei Sun*

[*Estimating SNP-based heritability and genetic correlation in case-control studies directly and with summary statistics*](https://www.sciencedirect.com/science/article/pii/S0002929718301952)

*Estimating SNP-Based Heritability and Genetic Correlation in Case-Control Studies Directly and with Summary Statistics*

*Methods that estimate SNP-based heritability and genetic correlations from genome-wide association studies have proven to be powerful tools for invest…*

*www.sciencedirect.com*

*​[昨天 上午11:05] Lei Sun*

*Mixed models for case-control genome-wide association studies: major challenges and partial solutions*

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