Study Questions for "Improving polygenic prediction in ancestrally diverse populations" by Ruan et al.

1. What type of statistical model is used to compute a polygenic risk score (PRS)? Start with the most basic one–without LD adjustment, Bayesian priors or multi-ancestry–and then talk about innovations since the earliest PRS studies. Some early papers you might want to consult include PMID: 26430803 and PMID: 19571811.
2. What factors contribute to health care inequities in the context of PRS?
3. How do "mult" approaches to PRS differ from the "meta" approach?
4. What does PRS-CSx do differently from other "mult" approaches? When is this an advantage?
5. What statistic do the authors use to assess method performance?
6. Discuss the different populations involved in a PRS study: the GWAS population, the discovery population, and the target population. What are the effects of different sample sizes and ancestries for each of these?
7. **Challenge question:** If GWAS were equally large and well-powered across ancestries, how do you think the results in this paper would change?