Laird and Lange (2006).Family-based designs in the age of large-scale gene-association studes. Nature Reviews Genetics 7: 385-.

1. What is the difference between linkage analysis and association analysis?
2. What is a candidate gene?
3. Which factors affect the power of your GWA study?
4. How does subject design impact the power of an association study: family-based versus case-control?
5. Why is multiple testing correction important? What are some of the methods you can use? What are the pros and cons of these methods?
6. What is population substructure? How can it be dealt with? Name two main strategies. List some pros and cons of each.
7. What is a genetic effect size? Is it expressed differently depending on the measurement type of the trait?
8. What are the pros and cons of FBAT testing? How does the FBAT test generalize the TDT test? Is it robust against population substructure? Is it a conditional test? Can it deal with missing phenotypes? Can it deal with missing genotypes? Can it deal with missing parental genotypes?
9. What is population admixture? Is it different from population stratification?
10. Where do concepts like nuisance parameters and sufficient statistics fit into the picture of “fbat testing”?
11. What is the random variable in FBAT testing? Is it similar to the parametric regression setting?
12. What are informative families to the FBAT statistic? Do they play a role when pre-screening in a PBAT screening approach? Is screening independent from testing in this approach? Is the screening step affected by population stratification?
13. What is the alternative hypothesis for FBAT testing? What is the null hypothesis?
14. Can GWAs be more feasible when using family-data versus unrelated individuals?