



Statistical comparison of methods of association mapping with three-way admixture

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Introduction

- Incorporating ancestry into association testing has the potential to improve the ability to detect associations between certain genes and traits or illnesses
- Association mapping is a method used to locate genetic variations that cause diseases. These variations may differ in frequency across populations

Methods

- I compared 9 methods of association mapping
 - 7 were designed for 2 populations of ancestry
- Extended methods to three populations in two ways
 - Each population vs other two (3 sep)
 - 3 populations in a single analysis (2 covariate)
- To compare the powers of the methods named above, I used a proportion test in R with a significance level of 0.05

Results

- QATT and Liu2 (both 2covar) were among the most powerful in each model, and were the most powerful of the combined methods
- Generally, the power of each individual method ranged from 0 to .92, with varied performance throughout each model
- Simulations with higher genetic effect yielded greater power
- Generally, the methods that used a 2 covariate extension tended to perform better

Conclusion

- In the future, it would be beneficial to try using QATT and Liu2 to analyze real data
- Excellent performance of QATT suggests that global ancestry is more informative than local ancestry alone
 - Possibly due to reduced “noise”
- Because QATT and Liu2 performed with the highest power throughout each model of simulated data that was used, these would be recommendable for similar models

Figure 1

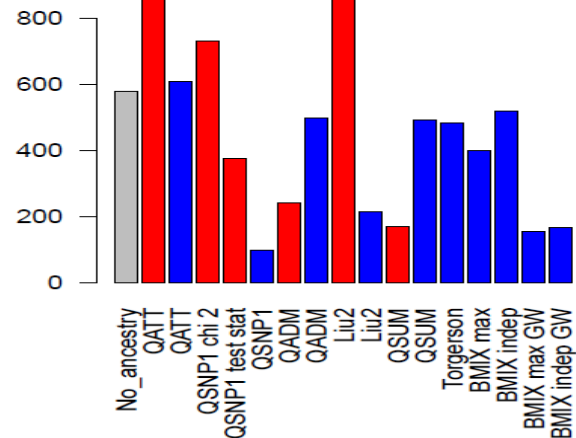


Figure 1: This figure displays the frequency with which each method displayed significantly better power than another method. The maximum possible frequency is 1200. The bars that are red are representatives of 2 covariate methods, while the blue are 3 sep. The gray model is one that did not use either.

Figure 2

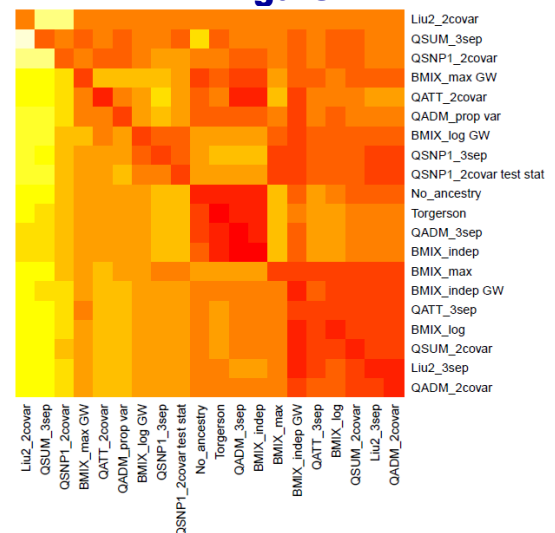


Figure 2: This is a visual representation of how the models performed against each other. The color yellow indicates that the method in that column is frequently more powerful than the method in that row.

References

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- Shriner, Daniel, Adebawale Adeyemo, and Charles N. Rotimi. "Joint Ancestry and Association Testing in Admixed Individuals." *PLoS Computational Biology* 7.12 (2011): e1002325. *PMC*. Web. 18 Apr. 2016.

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