

## **Frequently Asked Questions:**

### **I get an error when I click the display button or download button?**

1. Make sure to uncheck the radio button if you enter a custom value.
2. Enter a float value (i.e., a decimal value like 0.5 or 1.0) in the custom value space.

### **I don't see SNPs in the output file?**

Change the input parameters like delta,  $F_{ST}$  etc., and try again.

### **Which databases are available?**

HapMap Database Phase III and HGDP-CEPH Human Genome Diversity Project are the current databases. In future we have plans to include 1000 Genomes project database.

### **Can I upload my own data to develop AIMs? In what format?**

Yes, look at the manual.

### **What format should I use when using the text query?**

Gene Symbols or SNP IDs separated by a new line.

### **I get blank output when I use Text query?**

SNP IDs are unique. So do select all the chromosomes by holding the shift key if you are not sure of the exact chromosome.

### **How long will it take if I run the application using all the chromosomes?**

The time varies depending upon the filters and attributes you select.

### **What is composite measure?**

Composite measure (*CompM*) is an approach that combines and rank informative markers from all the five measures [*delta*, *SIC*, *FIC*,  $F_{ST}$ , and *In*]. The rank was based on assigning a score for each marker in each measure and rank based on the average score of all the measures. We recommend using this measure as the combined measure of ranking outperformed all the five measures when used individually.

*SNPs among the output with composite measure 0.0 indicate most significant and 1.0 indicates least significant SNPs.*

### **What if I have different questions/problems?**

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