1. Software note to Bioinformatics on Eagle – include new function to plot results (I don’t think I can integrate this into the GUI but can have it as a stand alone function)
2. Produce a GPU vesion of Eagle (includes Josh’s svd function). Look at performance with only CPU, 1GPU, 2GPU, 3GPU, - limitations – how large a data can we handle. Software note to I’m Not Sure?? Need to find a good journal . Could Journal of Statistical Software be an option? Maybe.
3. Produce cluster based version of Eagle – full paper. Could cluster have better way of transferring data – say break it up and keep each chunk temporarily on a node and access it locally when needed.
4. Look at parallel processing ideas of data but before this, need to profile code to see where bottlenecks are – maybe it is not from the reading of data but calculation of a and vara for full data. (i.e change in dimension).

Does genotype file need to be reformatted (could it just be read in as is).

Do I need Mt. Could I just calculate M\*A\*B and use it on both sides of the equation (take transpose).