# Related Analysis

Because there is a subset that sem particularly outbred and seem to have replated (at least trioml) inflating their relatedness (r) value; these two subsets may need to be treated separately.

Additionally it is worth experimenting with the mean of all algorithms, rather than relying on one. Similarly the inbreeding coefficient (f) might be better averaged for the four algorithms that can calculate it. (The two likelihood methods, lynchrd, and ritland.)

## Munge

### LarvalPeeliiSnps (all) #238

### larvalPeeliiSAnps(noOutbreds) #195 if cutoff at (-0.4)

### larvalPeeliiSnps(outbreds) #43 “ “

## run Related on each set (for all algorithms) and with inbreeding coefficient.

### Create mean of r for each dyad and add to df

### Create mean for each inbreeding coefficient and add to df

## Run simulation for each related