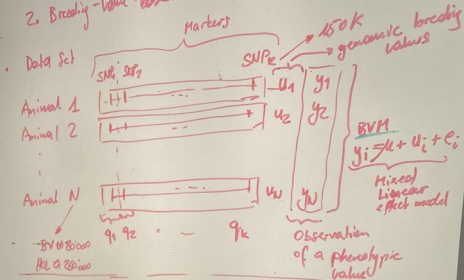


- Changes related to prediction of genomic breeding values
 - replace the infinitesimal model by the polygenic model

- Two statistical models that can be used

1. Marker effect-model (MEM)
2. Breeding-value-based model (BVM) \rightarrow equivalent



MEM: $y_i = \mu + q_1 + q_2 + \dots + q_k + e_i \Rightarrow$ Fixed linear effect model