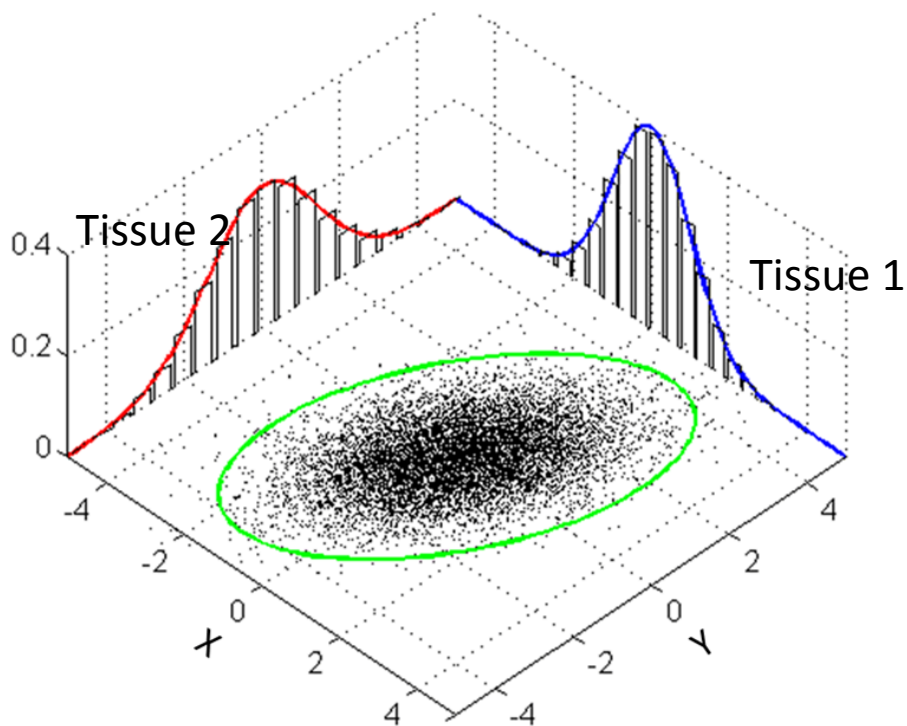


In the two tissue case, all b_{j1} (i.e., the effect of each gene snp pairs in tissue 1) lie along the blue curve, while all b_{j2} lie along the red curve. The off-diagonal entries of the covariance represent the 'tightness of the ellipse', where a large correlation (or covariance) means ellipse is very narrow and expression in tissue 1 perfectly dictates expression in tissue 2.



A 'mixture' of multivariate normals means that we seek to find an optimal combination of these ellipse and marginal width plots to maximize the likelihood across all gene-snp pairs, assuming again that all b_j lie somewhere along the contour of the resulting function.

