## A NOTE ON CLASSIFICATION

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Consider the multivariate complex Gaussian distribution  $\Pi_j$  (j = 1, 2) as defined by Goodman [3].

$$\Pi_i: p_i(\xi) = \Pi^{-p} |\Sigma|^{-1} \exp \left[-(\overline{\xi - \mu_i})' \Sigma^{-1} (\xi - \mu_i)\right],$$

where  $E(\xi) = \mu_j$  and  $\cos \xi = \Sigma$  (Hermitian positive definite complex covariance matrix). Any observation  $\xi$  will be a point in the space  $R^2$ , where R is the p-dimensional space. Partition  $R^2$  into two subspaces  $R_1$  and  $R_2$  such that  $R_j$  identifies  $\Pi_j$ . Now if  $q_j$  is the a priori probability of drawing  $\xi$  from  $\Pi_j$ , the conditional probability (after the individual is drawn) of the same will be  $q_j p_j(\xi) / \sum_{j=i}^2 q_j p_j(\xi)$ . The expected loss to be minimized (which is also the probability of misclassification when the costs of misclassification are unity) is

$$q_1 \int_{R_2} p_1(\xi) d\xi + q_2 \int_{R_1} p_2(\xi) d\xi.$$

Then the Bayes solution, which consists of assigning the individual to the population with higher conditional probability, gives the subspaces as

$$R_1:q_1p_1(\xi) > q_2p_2(\xi),$$

and

$$R_2: q_1p_1(\xi) \leq q_2p_2(\xi).$$

When the costs of misclassification are not unity, these will be modified as

$$R_1: [q_1C(2/1)]p_1(\xi) > [q_2C(1/2)]p_2(\xi),$$

$$R_2: [q_1C(2/1)]p_1(\xi) \leq [q_2C(1/2)]p_2(\xi).$$

Where C(j/i); (i, j = 1, 2) is the cost of misclassification of the individual from the *i*th population. Using  $\Pi_j$  as defined above

$$R_1: U > \log k$$

$$R_2: U \leq \log k$$
.

Where  $U = \bar{\xi}' \Sigma^{-1}(\mu_1 - \mu_2) + (\overline{\mu_1 - \mu_2})' \Sigma^{-1} \xi - \overline{\mu_1}' \Sigma^{-1} \mu_1 + \overline{\mu_2}' \Sigma^{-1} \mu_2$  and k is a constant depending upon  $q_j$  and C(j/i). It is easily seen that U is real valued. The distribution of U is ordinary univariate normal with  $E(U) = (-)^{j+1} \nu$  and  $\operatorname{var}(U) = 2\nu$  where  $\nu = (\overline{\mu_1 - \mu_2})' \Sigma^{-1}(\mu_1 - \mu_2')$ , according as  $\xi \in \Pi_j$ , (see [1]).  $\nu = (\overline{\mu_1 - \mu_2})' \Sigma^{-1}(\mu_1 - \mu_2)$  is termed as the "distance" between the two populations. If the parameters are estimated from sample of size  $N_j$  from  $\Pi_j$ , then

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