Quadratically Asymmetric Distributions and Their Application to Chromosome Classification

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1 Quadratically Asymmetric Distributions

A distribution on Euclidean space \mathbf{R}^d is called *spherically symmetric* if it is invariant with respect to the orthogonal group SO(d) and an \mathbf{R}^d -valued random vector is *elliptically symmetric* if it is the affine image of a spherically-symmetric random variable S (cf., e.g., Fang et al., 1990). The successes of elliptical symmetry in the context of high-dimensional classification problems suggest to consider also more complex functions of spherically-symmetric random variables S, e.g., quadratic ones. This leads to several types of stochastic models which we call *quadratically asymmetric* (cf. Ritter). One of them is of the form

(1)
$$X = g(S) = b + AS + QS^2$$
,

where $S^2=(S_1^2,...,S_d^2)$, b is an element of \mathbf{R}^d , and A>0 and Q are $d\times d$ -matrices. We call the matrix Q the quadratic asymmetry of the model X.

It can be proved that g is one-to-one on the open centered ball of radius $(2\|A^{-1}Q\|_{1,2})^{-1}$, where $\|\cdot\|_{1,2}$ denotes the norm of a matrix as a linear operator $(\mathbf{R}^d, \|\cdot\|_1) \to (\mathbf{R}^d, \|\cdot\|_2)$. Therefore, the quadratically asymmetric model can be reasonably handled if one assumes $r := ess \, sup \|S\| < (2\|A^{-1}Q\|_{1,2})^{-1}$. (In practical applications, observations of X lying outside the g-image of the centered ball of radius r must be considered as outliers with respect to the quadratically asymmetric model.)

2 Estimation of the Parameters b, A, and Q

As in the normal model, the overall number of real parameters to be estimated is again quadratic in the dimension d. For estimating the vector b and the matrix A, the following relations, which are easily proved, can be used

- (2) EX = b + Q1
- $(3) \quad Var X = A^2 + Q(Var S^2)Q^T;$

here, 1 is the constant vector one. Assuming that the radial function φ of S is chosen in advance, for estimating the quadratic asymmetry several algorithms are available. We sketch here an algorithm based on the third central moment $E\hat{X}(\hat{X}^2)^T$. Writing $R \in \mathbf{R}^{d^2 \times d^2}$ for the matrix defined by

$$R_{(ij)(kl)} = 2\delta_{jk}ES_iS_j(S_l^2 - 1) + \delta_{ik}E(S_j^2 - 1)(S_l^2 - 1)$$

and abbreviating $B = A^{-1}Q$, we have

(4)
$$E[A^{-1}\hat{X}][(A^{-1}\hat{X})^2]^T = RB + E[B(S^2 - 1)][(B(S^2 - 1))^2]^T$$

if $ES^6 < \infty$. Moreover, from (??) we infer

(5)
$$A^{-1}(Var X)A^{-1} = I + B(Var S^2)B^T$$
.

We have the following statements:

- (a) If S is not zero then R is invertible and, under mild conditions on S, A, and B, the parameters A and Q in (??) are essentially the only solutions of the nonlinear equations (??), (??).
- (b) If the central moments of X appearing in (??) and (??) are replaced by estimates based on an iid-sequence (X_k) of observations of (??) then the resulting sequence of estimators for A und B (and hence A and Q) is strongly consistent.

If B is small the second and third powers of B appearing in (??) and (??) can be neglected. Then we have

(6)
$$A \approx \sqrt{Var X}, B \approx R^{-1} E[A^{-1} \hat{X}][(A^{-1} \hat{X})^2]^T,$$

i.e., estimation of A und Q is reduced to operations of linear algebra.

Applied to the large Copenhagen data set Cpr, the quadratically asymmetric model reduces the error rate of automatic chromosome classification by 20 % relative to the best-fitting elliptically-symmetric models (cf. Ritter and Gaggermeier, Ritter et al., 1995).

References

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