

and \hat{v} are of the form $\sum_{i=1}^n c_i r_i^2$, where the constants c_i depend on X but not on the σ_i^2 . For the situation in Section 10, the vectors $\mathbf{c} = (c_1, c_2, \dots, c_{12})$ are

$$v_{J(1)}: \quad (0.67, 0.28, 0.12, 0.04, 0.00, 0.00, 0.01, 0.06, 0.08, 0.06, 0.02, 0.46)$$

$$v_{H(1)}: \quad (0.52, 0.28, 0.13, 0.04, 0.01, 0.00, 0.02, 0.09, 0.09, 0.06, 0.02, 0.12)$$

$$\hat{v}: \quad (0.11, 0.11, 0.11, 0.11, 0.11, 0.11, 0.11, 0.11, 0.11, 0.11, 0.11, 0.11)$$

This raises several interesting questions, some of which are considered in the MINQUE literature:

- (i) For a given vector of variances $(\sigma_1^2, \sigma_2^2, \dots, \sigma_n^2)$, what is the best choice of the vector \mathbf{c} , say to minimize rms error?
- (ii) Given a set of possible variance vectors, is there a preferred general choice of \mathbf{c} ?
- (iii) Is there an adaptive way of selecting \mathbf{c} from the observed data, as suggested at the end of remark D?
- (iv) Wu's estimators $v_{J,r}$, $r > 1$, involve quadratic forms $\sum_i \sum_j c_{ij} r_i r_j$. Is there any real advantage to using the cross-terms $r_i r_j$, or does this just add to the variability of the estimator?

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The emphasis the author places on using nonstandard subset sizes in jackknife procedures is important for at least one other reason. In some applications of resampling methods we are estimating an entity that lives in a space in which extrapolation is essentially impossible. Wu's equation (4.4) takes the estimate obtained from analysis of a sample and extrapolates its deviation from the overall estimate. However, if the space does not admit of extrapolation, then a choice of a subset size of $(n + k - 1)/2$ eliminates the extrapolation entirely. The value of $\tilde{\beta}_s$ is then the same as $\hat{\beta}_s$. By resampling and collecting a set of values of $\hat{\beta}_s$ we get variation that we take to be typical of the sampling variation in the estimate.

The example that brings this to mind is placing confidence intervals on phylogenies (evolutionary trees), to which I have applied a bootstrap technique