18.4.4 Compound CMPs -- the interlaboratory environment

When a measurement process consists of two or more segments, it can be properly characterized as a *compound (chemical) measurement process*. Specification of the Performance Characteristics of a compound or hierarchical CMP depends upon one's viewing point or position in the hierarchy. That is, at least for the "tree" structure, all segments below the viewing (or "null") node consist of multiple branches or replicates. For the CMP that is in a state of statistical control these replicates yield a crucial measure of random error. (The CMP that is *not* in a state of control is undefined!) Only a single path lies above the null node; this path necessarily fixes the bias of the CMP. By moving up in the hierarchy, one has an opportunity to convert bias into imprecision -- put another way, what is viewed as a fixed (albeit unknown) error at one level of a compound CMP, becomes random at a higher level. This is very important, for random error may be estimated statistically through replication, but bias may not; yet inaccuracy (total error) necessarily comprises both components. Figure 18.4.3 presents these concepts schematically.

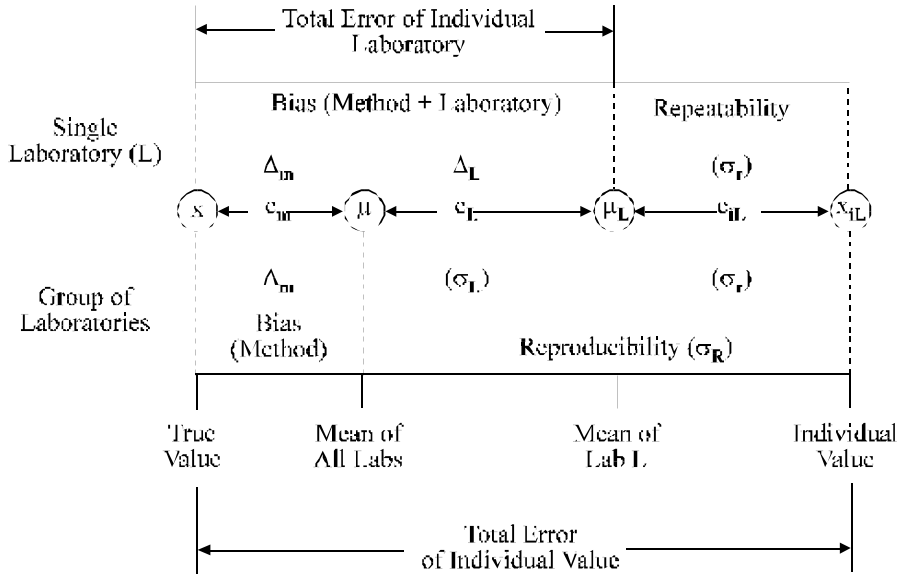

Fig. 18.4.3 Partitioning of method, interlaboratory, and intralaboratory error.

Collaborative or interlaboratory tests, which under the best of circumstances may be found at the uppermost node of the Compound CMP, provide one of the best means for accuracy assessment. In a sense, such intercomparisons can give us a direct

experimental (statistical) measure of inaccuracy. The basic concept, as indicated in Fig. 18.4.3, is that fixed intralaboratory biases are converted into random errors from the interlaboratory perspective. If the overall interlaboratory mean is free from bias, then the observed interlaboratory dispersion is the measure of *both* imprecision and inaccuracy.

Sampled Population [*S*] vs Target Population [*T*]. These represent, respectively, the population (of potential measurements) actually sampled, and that which would be sampled in the ideal, bias-free case. They are shown schematically in Fig. 18.4.4, for a two-step measurement process. When only the *S* population is randomly sampled (left side of the figure), the error e_1 from the first step is systematic while e_2 is random. In this case, the estimated uncertainty is likely to be wrong, because a) the apparent imprecision (σ_S) is too small, and b) an unmeasured bias (e_1) has been introduced. Realization of the *T*-Population (right side of the figure) requires that all steps of the CMP be random -- ie, e_1 and e_2 in the figure behave as random, independent errors; *T* thus represents a Compound Probability Distribution. If the contributing errors combine linearly and are themselves normal, then the *T*-distribution also is normal. The concept of the *S* and *T* populations is absolutely central to all hierarchical measurement processes (Compound CMPs), whether intralaboratory or interlaboratory.

Fig. 18.4.4 Sampled [S] and Target [T] Populations.

From the interlaboratory perspective, the first population in Fig. 18.4.4 (e_1) would represent the distribution of errors among laboratories; the second [*S*] would reflect intralaboratory variation ("repeatability"); and the third [*T*], overall variation ("reproducibility"). If the sample of collaborating laboratories can be taken as unbiased, representative, and homogeneous, then the interlaboratory "process" can be treated as a compound CMP. In this fortunate (doubtless asymptotic) situation, results from individual laboratories are considered random, independent variates from the compound CMP population. For parameter estimation (means, variances) in the interlaboratory environment it may be appropriate to use weights -- for example, when member laboratories employ different numbers of replicates.

Types of Interlaboratory (Collaborative) Tests. Interlaboratory studies commonly have one of the following objectives: (1) method evaluation, (2) method comparison, (3) proficiency testing, or (4) establishment of reference values. Each must have its own design and approach to evaluation of the resulting data. See sections 18.7 and 18.8.