Optimal group sizes for dynamic group screening

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Classification of items as good or bad can often be achieved more economically by screening the items in groups rather than individually. The underlying reason is that when a test on a group returns good, it can be concluded (after one test only) that all items within the group are good. Dorfman was the first to introduce the paradigm of group screening and he found an immediate application in the detection of syphilitic men drafted into military service during WWII. He suggested to apply this procedure also to manufacturing processes where the defective goods have to be eliminated from the collection of all produced goods. Later on, many researchers applied this paradigm to screen blood for the presence of HIV, Influenza and West Nile Virus (group screening is in this context generally referred to as blood pooling). The range of application even streches further, among which DNA screening and drug discovery.

When group screening is feasible, the *selection of the group size is crucial* : the larger a group size, the more items can be screened by only one test, but the more likely it becomes that one or more items of the group are bad, inferring that retesting becomes necessary. This can, for instance, be achieved by retesting all items of the group individually, which is often referred to as group-individual screening policy. However, in many occasions, a group-subgroup screening policy is adopted, whereby the group is divided into subgroups which are each subjected to a new group test.

For several decades, a mathematical model from Robert Dorfman was the de facto standard to determine the optimal group size. This model is essentially *static* : it postulates that a population consisting of a predetermined very large number of items has to be screened whereby all items are present from the beginning. However, the practical context is usually *dynamic* : items are not all present from the start, and arrive at random moments in time, possibly in groups of variable sizes. For instance, vans from various regions arrive at a blood screening laboratory at random moments of the day, with a variable number of blood samples to be screened. Also, in manufacturing processes, when goods have to be checked for their quality, they arrive at the screening facility when they are produced, which is a process that is spread over time.

An important disadvantage of dynamic models and analyses however, is that they are *much harder to implement* and the *processing time is slow* due to the *numerical work* that is involved, such as repeatedly calculating zeroes of func-

tions and solving sets of equations. A natural question, crucial to practitioners, is thus the following : *under which circumstances does the static model yield correct results in a dynamic context* ? This is the question we wish to answer. More specifically, we examine under which circumstances the optimal group size in the static model from Dorfman remains optimal in a dynamic context. However, when the conclusion is that, in some situation, static results cannot be applied, we still suffer from long processing times. This leads to the second objective : to *develop algorithms that decrease the processing time drastically* in such situations.

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