When the demand for diagnostic testing for medical conditions, such as infections due to the COVID-19 virus, is extensive, testing facilities can resort to the testing of samples from multiple individuals all at once, so-called pooled testing, instead of testing samples individually. Specifically, under a pooled testing regime, mixed samples from a group of individuals are tested for the presence of infection. A negative test implies that none of the individual samples show the presence of infection (assuming the tests are sufficiently accurate). A positive test implies that at least one individual sample within the sample group is testing positive. The individual samples within the group are then retested individually to identify which ones are positive.

Pooled testing has the advantage of reducing the number of samples that have to be tested individually but can increase the number of sample retests. Hence, it is important to identify the sample group size that can balance this tradeoff and maximize the performance objective of the testing facility.

There is a long history of pooled testing, both in practice and in the literature, dating back to Dorfman (1943) who appears to be the first to suggest pooled testing as a strategy to improve available testing capacity. The literature that followed is extensive (see for example Sobel and Groll (1959), Du et al. (2000), Aldridge et al. (2019) and the references therein). However, most of this literature focuses on pooling strategies that maximize throughput (the number of test requests that can be fulfilled per unit time) and does not take into account how this may affect the delay experienced by individuals in getting back test results. In other words, much of the existing literature does not study the relationship between the sample group size and congestion.

In this paper, we study the operation of a testing facility that diagnoses infected individuals. In particular, we focus on how the facility should select the sample pooling size that minimizes the total waiting time for testing results. We model the testing process as a two-stage tandem queueing system with batch service and re-entry. Requests for individual tests arrive to the first stage of the system, where testing samples are collected and formed into batches (i.e. a mixture of samples) with a pre-determined pooling size. Batches once formed exit the first stage and enter the second stage for virological testing. Samples in a batch that tests negative leave the system. Otherwise, samples individually rejoin the second stage for another test to identify each positive sample in this batch.

We provide conditions on the disease prevalence rate and the arrival intensity that guarantee system stability (i.e. a finite expected waiting time). We provide analytical expressions for estimating expected time spent in the system by each sample. We also develop an algorithm to obtain the batch size that minimizes the delay in delivering test results. We show that this batch size is different from the batch size suggested by the traditional pooled testing strategy originally developed by Dorfman in the 1940s, which minimizes the overall testing requirement instead of time in the system. We show that, in general, the optimal batch size decreases in the prevalence rate and increases in the testing times.

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