QUEUES WITH RESEQUENCING, PART I: STRUCTURAL PROPERTIES

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ABSTRACT

Queues with resequencing arise as models in various applications, including distributed databases and computer communication networks. Most models are extremely difficult to analyze using traditional techniques. In this paper we obtain several structural properties of resequencing systems. In particular we investigate the variation of the end–to–end delay with the number of servers in certain resequencing systems, as well as provide a comparison between single–hop with multi–hop resequencing.

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1. Introduction

Queues with resequencing are used to model synchronization algorithms that arise in packet communication networks. For example consider the transmission group in IBM's SNA architecture, in which the source and destination nodes are linked together with multiple transmission links. Multiplicity of links helps in achieving higher throughput as well as increased reliability in the event of link failure. Messages are packetized and transmitted over the multiple links, so that they arrive at the destination in a different order than the one in which they were transmitted. This requires resequencing of the packets before they can be processed. The resequencing mechanism is also important in packet communication networks that provide datagram services between the source and destination nodes. In such systems messages are broken up into packets at the source and transmitted independently of one another over the network. They may follow different paths, and when they arrive at the destination, they may have to resequenced. Resequencing is also important in some concurrency control schemes in distributed databases [17], [29] and in some inter-connection network message switching schemes [21].

One of the first queueing models to incorporate resequencing was due to Kamoun et. al. [15], in which they analysed a resequencing system in which the disordering is due to an infinite server queue with exponential services, which is subject to Poisson arrivals. Harrus and Plateau [11] removed the restriction of exponential services, and analysed the system in which the infinite server queue has general service times. Baccelli, Gelenbe and Plateau [1] analysed a more complicated model in which the customers are sent into a single server queue after leaving the resequencing buffer. A number of results have also appeared in the literature regarding resequencing models in which the disordering is due to finite server queues. Iliadis and Lien [18], [19], [20] and Varma [24] analysed the case in which the disordering is due to a $M/M/2$ queue, Yum and Ngai [29] analysed the case when the disordering is due to a $M/M/K/B$ queue, while Gün and Jean–Marie [10] analysed the case when the disordering is due to K single server queues operating in parallel.

In this paper our objective is prove some structural properties for resequencing models. Central to all the analysis that is presented here, are the recursions that govern the sequence of delays in these systems (See Section 2). We use these recursions in making

sample path comparisons (Section 3), as well as in obtaining the heavy traffic limits [27]. These techniques that we use here are quite powerful due to the fact that a large class of resequencing models can be analysed in an unified manner with their help, and they lead to simple approximations for otherwise intractable systems.

2. Basic Representations of Resequencing Systems

In this section we introduce a generic resequencing model, from which specific resequencing structures can be recovered as special cases. There is a stream of customers which enter a disordering system, and leave in an order different from the one in which they entered it (Fig 1). After leaving the disordering system, they wait in a resequencing buffer until all customers who entered the disordering system prior to them, have left it.

We now define some RV's that are useful in discussing properties of this system. Let the sequences of RV's $\{a_n\}_0^\infty$ and $\{D_n\}_0^\infty$ be defined on some probability space $\{\Omega, I\!\!F, P\}$. Here, a_n and D_n represent the time of arrival of the nth customer into the system and its disordering delay respectively. We adopt the convention that the 0th customer comes at time $t = 0$, so that $a_0 = 0$. In terms of these RV's define the following quantities for all $n = 0, 1\ldots$,

d_n: Departure instant of the nth customer from the system.

Y_n: End-to-end delay of the nth customer (i.e., $Y_n = d_n - a_n$).

W_n: Waiting time of the nth customer in the resequencing box (i.e., $W_n = Y_n - D_n$).

u_{n+1}: Interarrival interval between the $(n + 1)^{rst}$ and the nth customer (i.e., $u_{n+1} = a_{n+1} - a_n$).

Various kinds of disordering systems can be realized by assuming different statistical structures on the sequence $\{D_n\}_0^\infty$. For example, if the delay sequence $\{D_n\}_0^\infty$ is an iid sequence which is independent of the interarrival sequence $\{u_n\}$, then the disordering system corresponds to an $GI/GI/\infty$ queue. Similarly we can realize the disordering system as a $GI/GI/K$ queue or a system of K parallel $GI/GI/1$ queues by imposing a particular structure on $\{D_n\}_0^\infty$.

We now proceed to prove Theorem 2.1, which provides a recursive relationship between

the sequences $\{Y_n\}_0^\infty$, $\{D_n\}_0^\infty$ and $\{u_n\}_0^\infty$ defined earlier.

Theorem 2.1 *Consider a resequencing system of the type shown in Fig 2.2.1. If there is no initial load on the system, the end-to-end delays $\{Y_n\}_0^\infty$ are given by the relations,*

$$Y_0 = D_0, \tag{2.1a}$$

and

$$Y_{n+1} = \max\{D_{n+1}, Y_n - u_{n+1}\} \qquad\qquad n = 0, 1, \ldots \tag{2.1b}$$

Proof. Since there is no initial load in the system by assumption, the first customer in the system will not undergo any resequencing delay and (2.1a) is therefore immediate.

In order to prove equation (2.1b), consider the $(n+1)^{rst}$ customer. His resequencing delay will be zero if the nth customer has left the system at the time when he leaves the *disordering* subsystem i.e.,

$$Y_{n+1} = D_{n+1} \quad \text{if} \quad a_{n+1} + D_{n+1} > a_n + Y_n \qquad\qquad n = 0, 1 \ldots \tag{2.2}$$

If the nth customer has not left the system at the time the $(n+1)^{rst}$ customer leaves the disordering subsystem, then the $(n+1)^{rst}$ customer will experience a resequencing delay of duration $a_n + Y_n - (a_{n+1} + D_{n+1})$, hence

$$Y_{n+1} = D_{n+1} + [a_n + Y_n - (a_{n+1} + D_{n+1})] \quad \text{if} \quad a_{n+1} + D_{n+1} < a_n + Y_n \tag{2.3}$$

By combining (2.2) and (2.3), it is plain that

$$Y_{n+1} = \max\{D_{n+1}, Y_n - (a_{n+1} - a_n)\} \qquad\qquad n = 0, 1 \ldots$$

since $u_{n+1} = a_{n+1} - a_n$, and this proves (2.1b). ∎

The recursion (2.1) was first derived by Baccelli, Gelenbe and Plateau [1] albeit in a different context since they were trying to estimate the end-to-end delay in an infinite server resequencing system followed by a single server queue. Equation (2.1) is very basic since it provides us with a relationship between the disordering delays and the end-to-end system delays.

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3. A General Bounding Methodology

In this section we present the following simple result that will enable us to make stochastic comparisons between the end–to–end delay of different resequencing systems.

Theorem 3.1 *Given two resequencing systems governed by inter–arrival and disordering sequences $\{u_n^i\}_0^\infty$ and $\{D_n^i\}_0^\infty$ respectively, for $i = 1, 2$, defined on the same probability space $(\Omega, I\!F, I\!P)$. Assume that,*

$$u_n^1 = u_n^2 \qquad\qquad n = 1, 2 \dots (3.1)$$

$$D_n^1 \le D_n^2 \qquad\qquad n = 0, 1 \dots (3.2)$$

Then, it follows that

$$Y_n^1 \le Y_n^2 \qquad\qquad n = 0, 1 \dots (3.3)$$

Proof. The proof proceeds by induction. For the case $n = 0$, we have

$$Y_0^1 = D_0^1 \le D_0^2 = Y_0^2$$

so that (3.3) is satisfied. As the induction step, assume that

$$Y_m^1 \le Y_m^2 \qquad\qquad (3.4)$$

for some $m \ge 1$. We will show that $Y_{m+1}^1 \le Y_{m+1}^2$. Note that due to (3.1) and (3.4),

$$Y_m^1 - u_{m+1} \le Y_m^2 - u_{m+1} \qquad\qquad (3.5)$$

Combining (3.5) with (3.2), we conclude that

$$Y_{m+1}^1 = \max(D_{m+1}^1, Y_m^1 - u_{m+1}) \le \max(D_{m+1}^2, Y_m^2 - u_{m+1}) \le Y_{m+1}^2$$

thus completing the induction step. ∎

Note that (3.3) implies that the end–to–end delay in system 1 is smaller then the end–to–end delay in system 2, in the sense of strong stochastic ordering (see Appendix A). This is denoted by

$$Y_n^1 \le_{st} Y_n^2 \qquad\qquad n = 0, 1 \dots (3.6)$$

Proposition 3.1 is extremely useful, since it tells us that we can establish a strong stochastic ordering relation between the end–to–end delay of two resequencing systems, provide we can establish (3.2) that on some common sample space, the disordering delay of system 1 is smaller than the disordering delay of system 2. This idea is systematically applied in Sections 3.1, 3.2 and 3.3 to obtain some interesting structural properties.

3.1 Structural properties for finite server queues with resequencing

In this section we investigate the variation of the end–to–end delay with the number of servers, for the case when the disordering is due to $GI/GI/K$ queues. We also exhibit a result regarding the variation of the end–to–end delay with the service intensity. Consider two resequencing systems, such that the disordering in the first one is due to a $GI/GI/K_1$ queue, while the disordering in the second one is due to a $GI/GI/K_2$ queue (Fig 2). Define,

a_n^i: Time of arrival of the nth customer into the ith system, for $i = 1, 2$.

v_n^i: Service time of the nth customer to enter service in the ith system, for $i = 1, 2$.

d_n^i: Time instant of the nth departure from the ith system, for $i = 1, 2$.

z_n^i: Time instant of the nth departure from the servers of the ith queue, for $i = 1, 2$.

D_n^i: Disordering delay of the nth customer in the ith queue, for $i = 1, 2$.

Note that in case of $GI/GI/K$ queues, the nth customer to enter service is also the nth customer to enter the queue, since we assume that the queue operates under the FCFS discipline. Also note that the nth departure from either one of the queues is not necessarily the same as the nth arrival into that queue. Hence a_n^i and z_n^i may describe different customers.

We now state the main result.

Theorem 3.1 *Consider two resequencing systems, such that the disordering in the first system is due to a $GI/GI/K_1$ queue, while the disordering in the second system is due to a $GI/GI/K_2$ queue. If any of the following conditions hold, where*

(i) *If*

$$a_n^1 = a_n^2 \qquad\qquad n = 1, 2 \ldots (3.7a)$$

$$v_n^1 = v_n^2 \qquad\qquad n = 0, 1 \ldots (3.7b)$$

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$$K_2 = K_1 + 1. \tag{3.7c}$$

or,

(ii) *If*

$$a_n^1 = a_n^2 \qquad\qquad n = 1, 2 \dots \tag{3.8a}$$

$$K_1 = K_2 \tag{3.8b}$$

$$v_n^1 \le v_n^2. \qquad\qquad n = 0, 1 \dots \tag{3.8c}$$

then

$$Y_n^1 \le_{st} Y_n^2 \qquad\qquad n = 0, 1 \dots \tag{3.9}$$

Proof.

(i): Let $K = K_1$ and $N^1 = K$ and $N^2 = K + 1$ in what follows. In the following proof, quantities that are common to both systems are written without a super-script. As per Proposition 3.1, in order to prove (3.9) it sufficient to prove that

$$D_n^1 \le D_n^2 \qquad\qquad n = 0, 1 \dots$$

This was shown for multiple server queues by Wolff [30], from which our proof is adapted. We first prove that departure epochs from the buffer and the servers occur sooner in the $GI/GI/(K+1)$ system than in the $GI/GI/K$ system. For both systems,

$$z_0^i = \min_{j \ge 0} \{ d_j^i + v_j \}$$

$$= \min_{0 \le j < N^i} \{ a_j + v_j \} \tag{3.10}$$

and, in general

$$z_j^i = j^{th} \text{ order statistic from } \{ d_k^i + v_k : 0 \le k < j + N^i \} \tag{3.11}$$

Since the service initiation of the nth customer coincides with the departure epoch of the $(n - N^i)^{th}$ customer from the system (provided the nth customer arrives before the $(n - N^i)^{th}$ customer has departed the system), the following equation holds

$$d_n^i = \max\{ a_n, z_{n-N^i}^i \} \qquad\qquad n = 0, 1 \dots \tag{3.12}$$

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where $z_j^i = 0$ if $j < 0$. We now show that

$$d_n^1 \geq d_n^2 \qquad\qquad n = 0, 1 \ldots (3.13)$$

From (3.12) it follows that $d_n^1 = d_n^2$, for $0 \leq n < leqK$, since the first K customers in either system, do not suffer any queueing delays. However note that

$$d_K^1 = \max\{a_K, z_0^1\} \geq a_K = d_K^2$$

The proof proceeds by induction with an induction step which assumes that for some $n \geq K$,

$$d_j^1 \geq d_j^2 \quad 0 \leq j < n \qquad\qquad (3.14)$$

From (3.11), it follows that

$$v_{j+1}^1 \geq v_j^2 \quad 0 \leq j \leq n - K - 1 \qquad\qquad (3.15)$$

and (3.12) now yields

$$\begin{aligned} d_n^1 &= \max\{a_n, z_{n-K}^1\} \\ &\geq \max\{a_n, z_{n-(K+1)}^1\} \qquad\qquad (3.16) \\ &= d_n^2 \end{aligned}$$

which completes the induction step and the proof of (3.13). We now obtain an ordering for the total time spent in the queue in the following way. It is clear that ,

$$D_n^i = d_n^i - a_n + v_n \qquad\qquad n = 0, 1 \ldots (3.17)$$

for every $i = 1, 2$.

From (3.13) and (3.17), it is now clear that

$$D_n^1 \geq D_n^2 \qquad\qquad n = 0, 1 \ldots (3.18)$$

From (3.18), using well known techniques, we can prove that

$$Y_n^1 \geq Y_n^2 \qquad\qquad n = 0, 1 \ldots (3.19)$$

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and (3.9) follows directly from (3.19).

(ii): Using (3.8), it can be shown as in [13] that

$$D_n^1 \leq D_n^2 \qquad\qquad n = 0, 1 \ldots (3.20)$$

from which it follows that

$$Y_n^1 \geq Y_n^2 \qquad\qquad n = 0, 1 \ldots (3.21)$$

and (3.9) is now a direct consequence of (3.21).

∎

Part (i) of Theorem 3.1 reveals an interesting structural feature of multiple server resequencing systems. It states that the system delay decreases if we add an additional server to the multiserver system. However note that the resequencing delay clearly does not decrease because more customers may go out of sequence as result of the presence of the additional server. Hence the crux of the result is that the decrease in queueing delay due the presence of the additional server, outweighs the increase in synchronization delay due to the resequencing constraint. Hence it permissible to increase the amount of parallelism in the system as much as possible without worrying about resequencing delays. An interesting open problem is to characterize the behavior of the resequencing delay as the number of servers is increased. Clearly, since it increases as more servers are added and yet does not go to infinity in an infinite server system, its distribution must converge to stable distribution at infinity. This situation is in direct contrast to the behavior of a fork-join queue, whose system time increases logarithmically with the number of servers in the queue [3].

3.2 Finite Server Queues in Tandem with Resequencing

The short survey of the literature given in the introduction, revealed a paucity of results concerning multistage resequencing systems, which is not surprising considering their extremely complex nature. However, as shown in this section and the next one, interesting properties of these systems can be deduced by using stochastic comparison techniques.

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Consider a system consisting of a $GI/GI/K$ queue in tandem with a $GI/GI/L$ queue (without resequencing and with $K, L \geq 2$). If there is an increase in the number of servers or the service rate at the $GI/GI/K$ queue, then classical results due to Jacobs and Schach [13], tell us that the system time of a customer decreases sample-pathwise in that queue. However this decrease does not carryover to the end–to–end delay of a customer due to both the queues, in other words a decrease in system time at the first queue does not imply a decrease in end–to–end delay [22]. However, in this section we show that if the customers are resequenced after each queue, then a decrease in system time at the first queue does imply a decrease in the end–to–end delay (Fig 3). This property is further extended to an arbitrary number of $GI/GI/K$ queues in tandem, with resequencing after each stage. However it does not seem to apply to end–to–end resequencing systems.

The model is now introduced with the appropriate notations. The first disordering system is allowed to be arbitrary, while the second disordering system is assumed to be a $GI/GI/K$ queue. Resequencing is carried out after each disordering stage. In the next theorem we show that a decrease in the system time at the first disordering system, implies a samplepathwise decrease in the end–to–end delay. In what follows we use the super-script $i = 1, 2$ to refer to the two systems. For all $n = 0, 1 \ldots$, and $i = 1, 2$ pose,

Y_n^i: End-to-end delay of the nth customer in the ith system.

u_{n+1}^i: Inter-arrival time between the $(n+1)^{rst}$ and the nth customer into the ith system.

X_n^i: Delay of the nth customer in the first disordering system in the ith system.

Z_n^i: Delay of the nth customer in the ith system due to the first disordering system and the following resequencing box.

a_n^i: Arrival instant of the nth customer in the ith system.

τ_n^i: Arrival instant into the $GI/G/K$ queue, of the nth customer to enter the ith system.

J_n^i: Departure instant from the $GI/G/K$ queue buffer of the nth customer to enter the ith system.

d_n^i: departure instant from the system of the nth customer to enter the ith system.

$\bar{\sigma}_n^i$: service time in the $GI/G/K$ queue, of the nth customer to enter the ith system.

We now state the main result in this section.

Theorem 3.2 *Consider the two double stage disordering systems, in which the first system*

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is allowed to be arbitrary, while the second system corresponds to a $GI/G/K$ queue. If on some sample space $(\Omega, \mathbb{F}, P)$, the following relations hold

$$u^1_{n+1} = u^2_{n+1}$$
$$X^1_n \geq X^2_n \qquad\qquad n = 0, 1 \ldots (3.22)$$
$$v^1_n = v^2_n$$

then the inequalities

$$Y^1_n \geq_{st} Y^2_n \qquad\qquad n = 0, 1 \ldots (3.23)$$

hold true.

Proof. It is plain from (3.22) that

$$\tau^1_n \geq \tau^2_n \qquad\qquad n = 0, 1 \ldots (3.24)$$

since by definition

$$\tau^i_n = a^i_n + X^i_n \qquad\qquad n = 0, 1 \ldots (3.25)$$

for all $i = 1, 2$.

We now focus our attention on the $GI/GI/K$ queue. The first thing to note is that

$$J^1_n \geq J^2_n \qquad\qquad n = 0, 1 \ldots (3.26)$$

A little thought will convince the reader that (3.26) follows directly from (3.22) and (3.24) since the order in which customers are sent into service in the $GI/GI/K$ queue is the same as the order in which they entered it. However this statement does not hold for K $GI/GI/1$ queues in parallel.

Our next step is to show that

$$d^1_n \geq d^2_n \qquad\qquad n = 0, 1 \ldots (3.27)$$

To that end, using the basic recursion of Theorem 2.1, it is not very difficult to see that,

$$d^i_{n+1} = \max\{d^i_n, J^i_n + v^i_n\} \qquad\qquad n = 0, 1 \ldots (3.28)$$

for $i = 1, 2$. We now prove (3.27) by induction. It is plain from (3.22) that

$$d^1_0 = X^1_0 + v^1_0 \geq X^2_0 + v^2_0 = d^2_0 \qquad\qquad (3.29)$$

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and (3.27) is thus satisfied for $n = 0$. Assume that (3.27) is true for some $n = m \geq 0$. i.e.,

$$d_m^1 \geq d_m^2 \qquad (3.30)$$

it immediately follows

$$d_{m+1}^1 \geq d_{m+1}^2 \qquad (3.31)$$

and this completes the induction.

Since

$$Y_n^i = d_n^1 - a_n^i \qquad n = 0, 1 \ldots (3.32)$$

for $i = 1, 2$, it directly follows that (3.23) holds. ∎

The next corollary follows directly from the above result and Theorem 3.1.

Corollary 3.1 *Consider a two stage disordering system, with hop–by–hop resequencing, in which the first stage is a $GI/GI/K_1$ queue and the second stage is $GI/GI/K_2$ queue. If any of the following changes (i)-(iii) are made to the system, where*

(i) The number of servers in either or both disordering systems is increased to $K_j + k_j$, $k_j \geq 0$, while keeping the service distribution of the additional servers the same as those of the original servers,

(ii) The service processes in either or both the disordering systems is changed to $\{v_{nj}^2\}_0^\infty, j = 1, 2$, such that

$$v_{nj}^2 \geq v_{nj}^1 \quad j = 1, 2, \qquad n = 0, 1 \ldots (3.33)$$

then

$$Y_n^1 \geq_{st} Y_n^2 \qquad n = 0, 1 \ldots (3.44)$$

Proof. (i) Consider the case when the $GI/GI/K_1$ queue is altered. For $i = 1, 2$, let X_n^i denote the system delay in this queue of the nth customer to enter it, before and after alteration. It is clear from Theorems 3.1 that in each of the cases (i)-(iii) above, the following equation

$$X_n^1 \geq X_n^2 \qquad n = 0, 1 \ldots (3.45)$$

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is satisfied. Hence the conditions of Theorem 3.2 are satisfied in this case, so that (3.44) follows directly from (3.23).

Now consider the case when the $GI/GI/K_2$ queue is altered. In this case

$$u_n^1 = u_n^2 \quad \text{and} \quad X_n^1 = X_n^2 \qquad\qquad n = 0, 1 \ldots$$

For case (i) (3.44) follows from the fact that $J_n^1 \geq J_n^2$ for all $n = 0, 1 \ldots$ while for case (ii), (3.44) follows from the fact that $v_n^1 \geq v_n^2$ for all $n = 0, 1 \ldots$. The details are left to the interested reader.

■

The next result extends Corollary 3.1, to any number N, of multi-server queues in tandem.

Corollary 3.2 *Consider a N stage disordering system, with hop–by–hop resequencing, in which the ith stage corresponds to a $GI/GI/K_i$ queue $1 \leq i \leq N$. If any of the following changes are made, where*

(i) The number of servers in the ith queue is increased to $K_i + k_i$ with $k_i \geq 0, \leq i \leq N$, while keeping the service distribution of the additional servers the same as those of the original servers,

(ii) The service process in the ith queue, $1 \leq i \leq N$, is changed to $\{\sigma_{ni}^2\}_0^\infty$, such that

$$\sigma_{ni}^2 \geq \sigma_{ni}^1, \qquad\qquad n = 0, 1 \ldots (3.36)$$

then

$$Y_n^1 \geq_{st} Y_n^2 \qquad\qquad n = 0, 1 \ldots (3.37)$$

Proof. A short sketch of the proof is provided, the details of which are left to the reader. Suppose that the ith queue is altered. Then the delay of a customer in the first $(i-1)$ queues is unchanged, however the departure epoch of a customer from the ith queue will be earlier in the altered system. This in turn implies that the departure epoch of that customer will be earlier in each of the downstream queues, and ultimately the system, for the altered case. This can be proved in exactly the same way as Theorem 3.3.1, and implies (3.50).

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3.3 The Optimality of End–to–End Resequencing

Given a multi-stage disordering system, a problem of considerable interest is the effect of various resequencing strategies on system delay. Yum and Ngai [31], presented simulation results on the comparison of resequencing delays for the two kinds of resequencing strategies in a two hop disordering system (Fig 4). The disordering in both stages was carried out by $M/M/K$ queues. In the first case, resequencing was done after a customer had traversed both queues, while in the second case, resequencing was implemented after each queue. We shall hereafter refer to the first strategy as *end–to–end* resequencing, and to the second strategy as *hop–by–hop* resequencing. The simulation results showed that the average hop–by–hop resequencing delay was greater than the average end–to–end resequencing delay for two stage disordering systems.

In the present section we shall compare different kinds of resequencing strategies in tandem systems, when the disordering is due to infinite server queues. Our results are stronger than the simulation results in [31] in two respects. The ordering we get is strict sample path ordering for each customer, and secondly it holds for any number of disordering stages. However we have been able to prove the result only for infinite server queues.

The discussion starts with the two hop resequencing systems depicted in Figs 4.1 (a) and 4.2 (b) above. For all $n = 0, 1 \ldots$, pose

$\overline{Y}_n$: Delay of the nth customer in the end–to–end resequencing system.

Y_n: Delay of the nth customer in the hop–by–hop resequencing system.

X_n: Delay of the nth customer in the first disordering system of the hop–by–hop resequencing tandem system.

$\overline{X}_n$: Delay of the nth customer in the first disordering system of the end–to–end resequencing tandem system.

u_{n+1}: Inter-arrival time the $(n + 1)^{rst}$ and the nth customers in the hop–by–hop tandem resequencing system.

$\overline{u}_{n+1}$: Inter-arrival time between the $(n + 1)^{rst}$ and the nth customer in the end–to–end resequencing tandem system.

v_n: Delay of the nth customer in the second disordering system of the hop–by–hop resequencing tandem system.

$\overline{v}_n$: Delay of the nth customer in the second disordering system of the end–to–end resequencing system.

D_n: Delay of the nth customer in the hop–by–hop resequencing scheme, due to the two disordering systems and the first resequencing box.

Z_n: Delay of the nth customer in the hop–by–hop resequencing system, due to the first disordering stage and the first resequencing box.

Since our aim is to understand how the system times vary with the resequencing strategy, we assume that the two disordering systems and the inter-arrival time statistics are identical in both cases. More precisely, if all these sequences are defined over some common sample space $(\Omega, I\!F, P)$, then the following equations

$$u_{n+1} = \overline{u}_{n+1} \qquad\qquad n = 0, 1 \ldots (3.38a)$$

$$X_n = \overline{X}_n \qquad\qquad n = 0, 1 \ldots (3.38b)$$

$$v_{n+1} = \overline{v}_{n+1} \qquad\qquad n = 0, 1 \ldots (3.38c)$$

are assumed to hold. Note that in writing (3.38c), we have made a subtle assumption which restricts the class of disordering systems considered here. Condition $v_n = \overline{v}_n$, does not hold true in general as we now show. Consider the situation where the second disordering system is a $GI/GI/K$ queue, in which case the nth customer to enter the system may undergo different queueing delays at this queue, depending on whether the resequencing is done hop–by–hop or end–to–end. This is because of the first resequencing box which drastically changes the nature of the arrival process into the $GI/GI/K$ queue. Hence (3.38c) is applicable only to those systems in which the *second* disordering delay is not affected by the arrival process into it. One class of disordering systems to which this is applicable, is the class of systems having an infinite number of servers provided the delays in this system are generated independently of the arrival process $\{u_{n+1}\}_0^\infty$ as well as the delays $\{X_n\}_0^\infty$ in the first disordering system. In all the results presented in this section, we shall restrict ourselves to this case.

Theorem 3.3 *Consider a two stage disordering system with resequencing, in which the*

second stage has an infinite number of servers, then the system delay for the end–to–end resequencing system is stochastically upper bounded by the system delay of the hop–by–hop resequencing system, i.e.,

$$\overline{Y}_n \leq_{st} Y_n. \qquad\qquad n = 0, 1 \ldots (3.39)$$

Proof. From the statement of the theorem we can assume that (3.38) holds on some probability space $(\Omega, I\!\!F, P)$.

First consider the end–to–end resequencing system. Application of Theorem 2.1 gives

$$\overline{Y}_{n+1} = \max\{X_{n+1} + v_{n+1}, \overline{Y}_n - u_{n+1}\} \qquad\qquad n = 0, 1 \ldots (3.40)$$

for the end–to–end resequencing system, and

$$Y_{n+1} = \max\{D_{n+1}, Y_n - u_{n+1}\} \qquad\qquad n = 0, 1 \ldots (3.41)$$

for the hop–by–hop resequencing system.

We now derive a recursive expression for the sequence $\{D_n\}_0^\infty$. Application of Theorem 2.1 to the first disordering stage followed by resequencing in the hop–by–hop resequencing system yields

$$Z_{n+1} = \max\{X_{n+1}, Z_n - u_{n+1}\} \qquad\qquad n = 0, 1 \ldots (3.42)$$

with $Z_0 = X_0$. Since

$$D_n = Z_n + v_n \qquad\qquad n = 0, 1 \ldots (3.43)$$

it follows from (3.42) that

$$D_{n+1} = v_{n+1} + \max\{X_{n+1}, D_n - v_n - u_{n+1}\} \qquad\qquad n = 0, 1 \ldots (3.44)$$

with $D_0 = v_0 + X_0$.

Next we use induction to prove that

$$\overline{Y}_n \leq Y_n, \qquad\qquad n = 0, 1 \ldots (3.45)$$

in which case (3.39) immediately follows.

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For $n = 0$, under the zero initial loading assumption in both systems, it is plain that

$$Y_0 = D_0 = v_0 + X_0 = \overline{Y}_0,$$

whence (3.45) is satisfied for the 0th customer. The induction step assumes that (3.45) holds for the mth customer so that

$$\overline{Y}_m \leq Y_m \tag{3.46}$$

or equivalently,

$$\overline{Y}_m - \overline{A}_{m+1} \leq Y_m - A_{m+1} \tag{3.47}$$

Since the inequality

$$\overline{X}_{m+1} \leq \max\{X_{m+1}, D_m - v_m - u_{m+1}\} \tag{3.48}$$

always holds, it follows that

$$\overline{S}_{m+1} + \overline{X}_{m+1} \leq S_{m+1} + \max\{X_{m+1}, D_m - v_m - u_{m+1}\} \tag{3.49}$$

by (3.44), this is equivalent to

$$\overline{v}_{m+1} + \overline{X}_{m+1} \leq D_{m+1} \tag{3.50}$$

By combining (3.47) and (3.50), it follows that

$$\max\{\overline{Y}_m - \overline{u}_{m+1}, \overline{v}_{m+1} + \overline{X}_{m+1} \leq \max\{Y_m - u_{m+1}, D_{m+1}\} \tag{3.51}$$

and we now easily obtain from (3.40)-(3.41) that

$$\overline{Y}_{m+1} \leq Y_{m+1}$$

i.e., (3.45) holds for $n = m + 1$. Since (3.45) holds for $n = 0$, it follows by induction that it is true for all $n = 0, 1 \ldots$.

$\blacksquare$

Note that the assumptions of Theorem 3.3 can be weakened to

$$u_{n+1} \leq \overline{u}_{n+1}$$

$$X_n \geq \overline{X}_n \qquad\qquad n = 0, 1 \ldots \tag{3.52}$$

$$v_n \geq \overline{v}_n$$

without changing the conclusion of the theorem. The reader might expect that in order to extend the theorem to the case when the second disordering system has a finite number of servers, it is sufficient to verify that

$$v_n \geq \bar{v}_n \qquad\qquad n = 0, 1 \ldots \text{(3.53)}$$

However there is some reason to believe that (3.53) might not hold for this case, as intuitively argued below.

Let us consider a system in which the disordering is carried out by a $GI/GI/2$ queue in both stages. Consider the nth customer C_n which is in the process of receiving service from one of the servers in the first $GI/GI/2$ queue in the hop–by–hop resequencing system. If his service time is inordinately long, then customers who had arrived after him into the first queue, will complete their service before him and wait in the resequencing box for C_n to complete service. Assume that customers C_{n+1} to C_{n+k} have gone out of sequence with respect to C_n, and are waiting in the resequencing box for C_n. After C_n completes service, he will immediately join the second queue (before C_{n+1} to C_{n+k}), since he does not suffer any resequencing delay in the first resequencing box. On the other hand, for the case of end–to–end resequencing, C_{n+1} to C_{n+k} would immediately join the buffer of the second queue after getting served in the first queue. Consequently, after C_n finishes service in the first queue he would find a bigger queue length in the second queue, than for the case of hop–by–hop resequencing. Thus we would expect the delay of C_n in the end–to–end resequencing system to be greater than his delay in the hop–by–hop resequencing system. The delays of C_{n+1} to C_{n+k} though would be smaller in the end–to–end resequencing system. Hence it is not unlikely that the average delay for end–to–end resequencing is smaller than the average delay for hop–by–hop resequencing, even though sample path ordering is not possible, in fact *false* and comparison results can only be expected in a weaker sense.

Corollary 3.3 extends the result of Theorem 3.3 to any number, say N, of infinite server queues in tandem. For all $n = 0, 1, \ldots$, pose

v_n^N: Delay of the nth customer due to the Nth disordering stage in the hop–to–hop resequencing system.

$\bar{v}_n^N$: Delay of the nth customer due to the Nth disordering stage in the end–by–end resequencing system.

Y_n^N: delay of the nth customer in the hop–by–hop resequencing system consisting of N disordering stages.

$\bar{Y}_n^N$: delay of the nth customer in the end–to–end resequencing system consisting of N disordering stages.

Corollary 3.3 *Given $N (\geq 2)$ $GI/GI/\infty$ queues in tandem, the hop–by–hop resequencing delay for a customer is stochastically no smaller than the end–to–end resequencing delay for that customer, i.e.,*

$$\bar{Y}_n^N \leq_{st} Y_n^N \qquad\qquad n = 0, 1 \ldots (3.54)$$

Proof. Since we are only interested in comparing system times due to the difference in resequencing strategies, we will assume that

$$\bar{v}_n^N = v_n^N \qquad\qquad n, N = 0, 1 \ldots (3.55a)$$

$$\bar{u}_{n+1} = u_{n+1} \qquad\qquad n = 0, 1 \ldots (3.55b)$$

The proof proceeds by a double induction on the number of customers as well as the number of stages. By Theorem 3.3, it is clear that that (3.54) is true for $N = 2$. We will show that (3.54) holds for an arbitrary value of $N = M$.

Applying Theorem 2.1, we obtain the relations

$$Y_{n+1}^M = \max\{Y_{n+1}^{M-1} + v_{n+1}^M, Y_n^M - u_{n+1}\} \qquad\qquad n = 0, 1 \ldots (3.56)$$

and

$$\bar{Y}_{n+1}^M = \max\{\sum_{i=1}^{M} v_{n+1}^i, \bar{Y}_n^M - u_{n+1}\} \qquad\qquad n = 0, 1 \ldots (3.57)$$

We have to show that

$$\bar{Y}_n^M \leq Y_n^M \qquad\qquad n = 0, 1 \ldots (3.58)$$

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Assume that (3.58) is true for $n = m$

$$\overline{Y}_m^M \le Y_m^M \tag{3.59}$$

which implies that

$$\overline{Y}_m^M - u_{m+1} \le Y_m^M - u_{m+1} \tag{3.60}$$

Next by an induction on the number of disordering stages, we demonstrate that

$$\sum_{i=1}^{M-1} \overline{v}_{m+1}^i \le Y_{m+1}^{M-1} \tag{3.61}$$

From (3.48), it is clear that (3.61) holds for $M = 2$. As the induction step assume that (3.61) holds for $M = L$, i.e.,

$$\sum_{i=1}^{L-1} \overline{v}_{m+1}^i \le Y_{m+1}^{L-1} \tag{3.62}$$

It is clear that

$$Y_{m+1}^L = \max\{Y_{m+1}^{L-1} + v_{m+1}^L, Y_m^L - u_{m+1}\} \tag{3.63}$$

Hence it is immediate to see that

$$Y_{m+1}^L \ge Y_{m+1}^{L-1} + v_{m+1}^L \ge \sum_{i=1}^{L-1} \overline{v}_{m+1}^i + \overline{S}_{m+1}^L$$

$$= \sum_{i=1}^{L} \overline{v}_{m+1}^i \tag{3.64}$$

Hence (3.62) holds for $M = L + 1$ as well, completing the induction step. Hence from (3.60)–(3.61), it follows that

$$\overline{Y}_{m+1}^M \le Y_{m+1}^M \tag{3.65}$$

thus completing the induction step and the proof. ∎

APPENDIX A

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Some useful properties of the strong stochastic ordering are stated in this appendix without proof. For proofs the reader may consult [24], [25].

Definition. *A RV X is stochastically smaller than a RV Y, written as $X \leq_{st} Y$, if*

$$P[X > a] \leq P[Y > a] \qquad \text{for all a} \tag{A1}$$

(1) If f is a non-decreasing function, then $X \leq_{st} Y$, if and only if,

$$E[f(X)] \leq E[f(Y)] \tag{A2}$$

(2) (Lehmann [16]) F and G are distributions such that $F \leq_{st} G$, if and only if there exist RV's X and Y defined on the same probability space $(\Omega, I\!\!F, P)$ for which

$$X(\omega) \leq Y(\omega) \qquad \text{for all } \omega \in \Omega \tag{A3}$$

and

$$\begin{aligned} P(\{\omega : X(\omega) \leq x\}) &= F(x) \\ P(\{\omega : Y(\omega) \leq y\}) &= G(y) \end{aligned} \tag{A4}$$

(3) Let $\{X_n\}_1^n$ and $\{Y_n\}_1^n$ be independent sequences of iid random variables. If $X_i \leq_{st} Y_i, 1 \leq i \leq n$, then for any non-decreasing function f,

$$f(X_1, \ldots, X_n) \leq f(Y_1, \ldots, Y_n) \tag{A5}$$

(4) The weak convergence property.

Assume that the sequences $\{F_n\}$ and $\{G_n\}$ converge weakly to F and G and that $F_n \leq_{st} G_n$, then

$$F \leq_{st} G \tag{A6}$$

(5) A non-negative RV is defined to be *new better than used* (NBU) if

$$P[X - a \leq x \mid X \geq a] \leq P[X \geq x] \tag{A7}$$

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for all $a \geq 0$. If F is a NBU distribution having mean μ, then

$$F \leq_{st} \exp(\mu) \qquad (A8)$$

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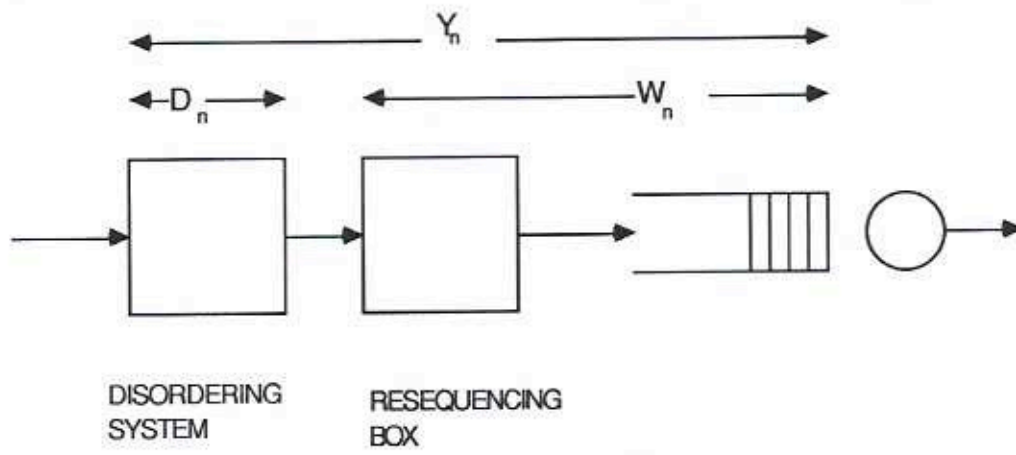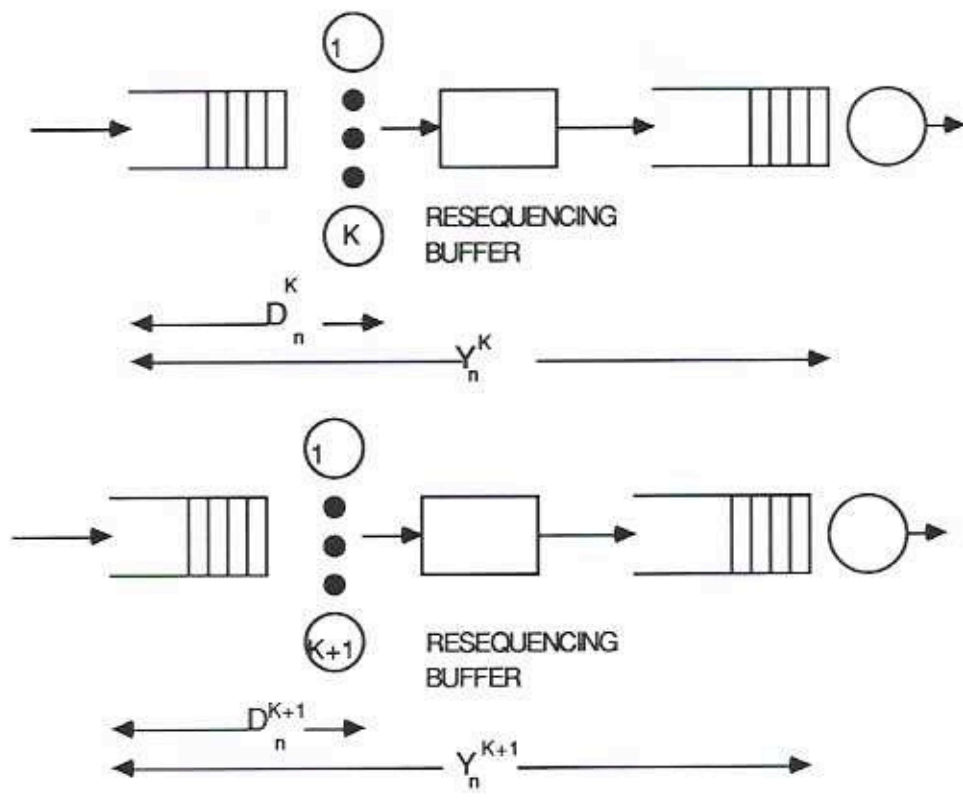
Fig. 1. A generic resequencing model

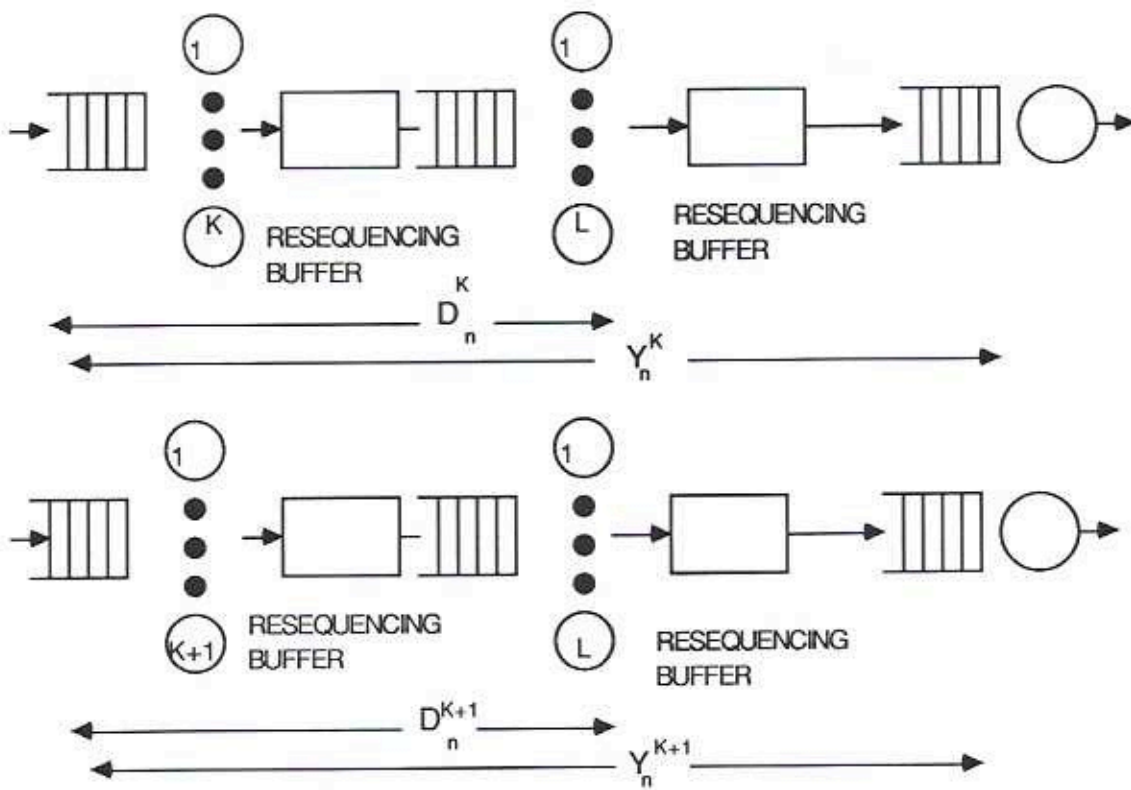Fig. 2. Variation of end-to-end delay with number of servers

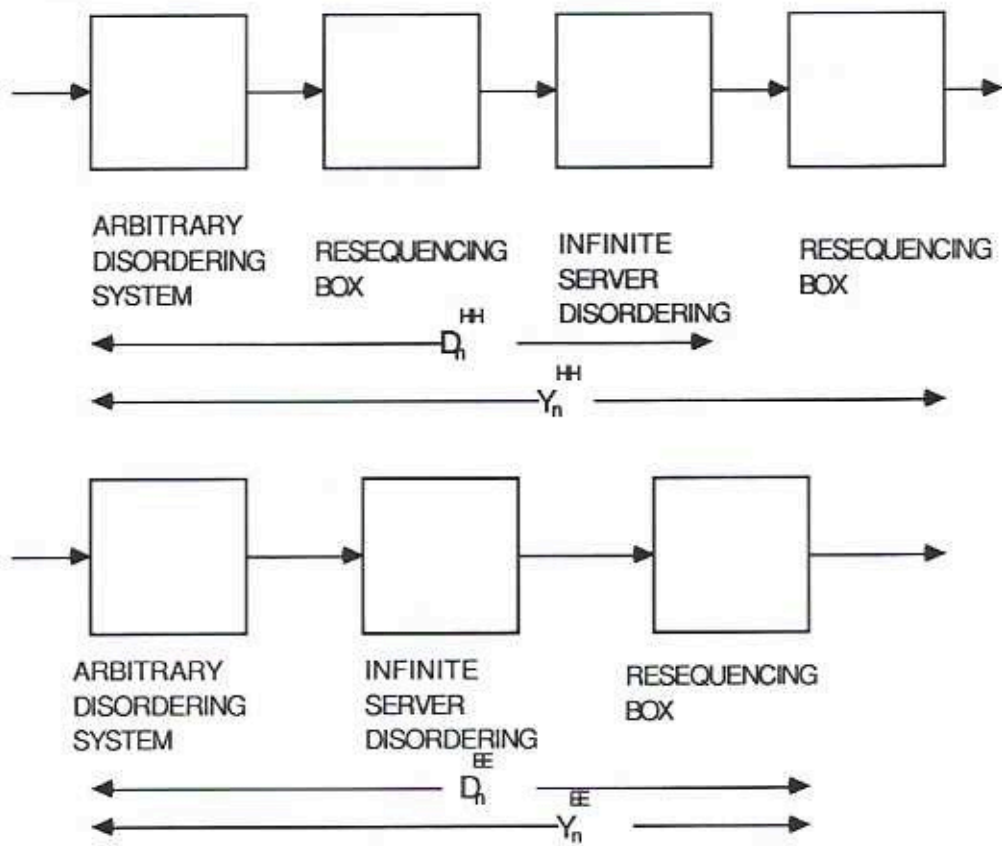Fig. 3. The multi-hop case: Variation of end-to-end delay with no. of servers

Fig. 4. Comparison of hop-by-hop vs end-to-end resequencing