# Delay Analysis of the Selective-Repeat ARQ with the Per Flow Resequencing

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***Abstract*— A SR (Selective-Repeat) ARQ (Automatic Repeat reQuest) protocol is used to recover packet errors on a satellite channel effectively. This SR ARQ has a problem of large delay due to the resequencing of received packets. To mitigate this problem, the PFRS (Per Flow ReSequencing) scheme was proposed, where the resequencing is performed independently for each upper layer flow, while the detection of lost packets and associated retransmissions are performed based on the whole flows multiplexed over the SR ARQ. This paper models the SR ARQ protocol, where the maximum number of retransmissions is limited, by a collection of simple stop-and-wait protocols; it shows calculation results on the delay distribution of retransmission and resequencing and proves the effectiveness of the PFRS scheme.**

## I. INTRODUCTION

The ARQ is important to recover lost packets due to transmission errors over a channel. So far, the Go-Back-N ARQ has been widely used because of its simple retransmission mechanism. However, as the transmission rate of wireless communication increases, there is a trend that the Selective Repeat ARQ, which is more complicated, is employed. This SR ARQ is effective, as it retransmits the minimum number of packets that actually encounter transmission errors. A receiving side of the SR ARQ has to perform the resequencing function, which retains correctly received packets that arrive after some packets received in error. This resequencing is needed to keep sequence integrity of packet communication. However, this resequencing incurs a large packet delay; since all packets correctly received after the lost packet have to be retained until the lost one is retransmitted and correctly received. There is another defect of the resequencing; when the lost packet is retransmitted and received correctly, all packets waiting for the lost one are released and transferred to the upper layer at the same time. A large burst of packets, which might cause undesirable effects to other communications, is generated by the resequencing.

So far, there are studies on the performance of the SR ARQ mainly on its queueing analysis of the sending side [1] [2]. As for the resequencing performed by the receiving side, numerical analysis on delay and buffer occupancy due to the resequencing is performed for the case where a transmission channel is fully loaded [3]. The RLC (Radio Link Control), which is a Layer 2 protocol defined by 3GPP, employs the SR ARQ [4]; there is a study on effect of out-of-order packets derived from the limit of hold time in resequencing by the RLC [5]. In order to mitigate the delay and bursty packet output due to the resequencing, the Per Flow ReSequencing (PFRS) scheme is proposed [6].

This paper shows the analysis on the resequencing delay of the PFRS scheme and proves that the delay is significantly reduced by the scheme. In the following, we will describe the PFRS scheme, assumptions and conditions of the analysis, and introduce a model and associated state probability. Then, we will show the analysis of the probability distribution on the pure resequencing delay as well as the sum of both retransmission delay and resequencing delay.

## II. THE PFRS SCHEME AND ITS ANALYTICAL MODEL

### A. The PFRS scheme

The basic idea behind the PFRS scheme is that there is no need to keep packet sequence integrity among different upper layer flows while the packet order has to be preserved for the same upper layer flow. The PFRS scheme performs the resequencing for each upper layer flow independently, while it detects and retransmits lost packets based on the whole packet flows.

The conventional SR ARQ, which preserves packet order for the whole packet flows on a transmission channel, has problems of unnecessary holds of packets and associated delay as illustrated in Fig. 1. In this figure, two flows, a and b, are multiplexed over the SR ARQ. Packets a1 and a2 are lost due to transmission errors and retransmitted. In case of the conventional full resequencing scheme, packets b1 and b2 of the flow b are unnecessarily retained until the lost packet a1 is retransmitted and received. This situation is a kind of HOL (Head of the Line) blocking for flow b. In case of the PFRS scheme, as illustrated in Fig. 2, the resequencing is performed for each flow independently, while the acknowledgment and retransmission of packets are done by the SR ARQ as the conventional way, and packets b1 and b2 are delivered to the upper layer without being retained. Thus, the PFRS scheme resolves the invalid suspension of packets due to the HOL.

### B. Analytical model and associated assumptions

To evaluate the resequencing delay of the PFRS scheme, analysis is performed, where assumptions are as follows:

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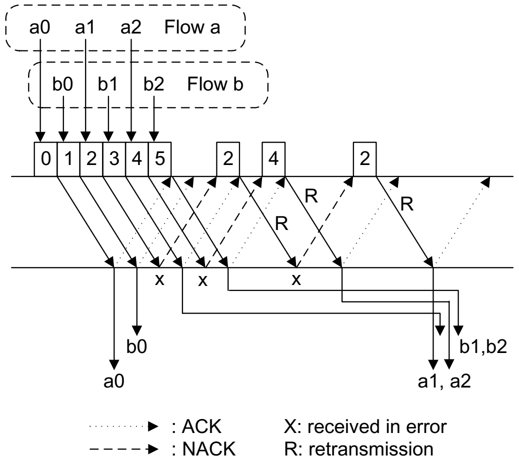

Fig. 1. An example sequence of the full resequencing scheme.

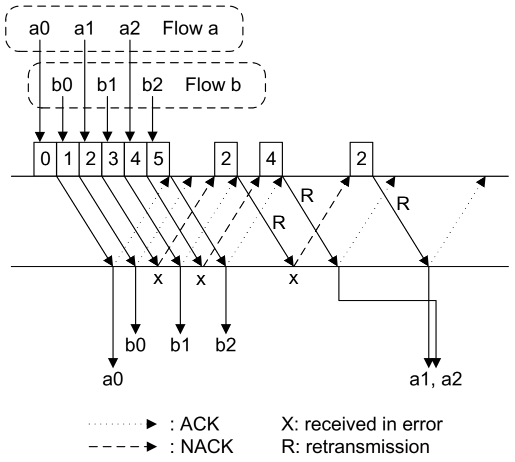

Fig. 2. An example sequence of the PFRS scheme.

1) Packet errors occur at random on a transmission channel with the error rate $\epsilon$.
2) If a packet is received without error, a positive acknowledgment (ACK) is returned to the sender; otherwise a negative acknowledgment (NACK) is returned. ACK or NACK is sent immediately when a packet is received correctly or in error.
3) There is no error for both positive and negative acknowledgments.
4) Retransmission has high priority compared to transmission of a new packet and is performed immediately after a NACK is returned to the sender.
5) The maximum number of retransmissions is limited to $N_r$. If a packet, retransmitted for $N_r$ times, is still received in error, packets waiting for this packet at the receiver are released and transfered to the upper layer.
6) Length of a packet is fixed and time is divided into slots based on the transmission time needed for sending one packet.
7) In each slot, if a channel is available (there is no retransmission), a new packet to be transmitted exists at the sender with the probability $\alpha$.
8) There are $m$ flows over the transmission channel. A new packet belongs to flow $j$ at random with the probability $\beta_j$ $(j = 1, \cdots, m)$, where $\sum_{j=1}^{m} \beta_j = 1$.
9) A collection of consecutive slots, from the beginning of a packet transmission time till a reception of the associated acknowledgment to this packet, is called a frame.
10) The number of slots in a frame is assumed to be M. Each slot in a frame is numbered from 0 to M-1.
11) The number M consists of the number of slots corresponding to the round trip delay and one slot for a packet transmission.
12) A collection of slots in the same position of consecutive frames is called a sub-channel. There are sub-channels from 0 to M-1 in a frame.

Based on the assumptions described above, once a new packet is sent on one of sub-channels, retransmission of the packet is always performed on the same sub-channel until the packet is successfully received or aborted due to the maximum number of retransmissions. Accordingly, the SR ARQ can be modeled by a collection of independent M sub-channels, on each of which a simple stop-and-wait protocol is performed. We introduced the probability $\alpha$ to change total load of the transmission channel. We also introduced the probability $\beta_j$ $(j = 1, \cdots, m)$, to study the effect of multiple flows over the transmission channel. When a sub-channel is available, transmission of a new packet is performed with the probability $\alpha$. The new packet belongs to one of flows, for example flow $j$, at random with the probability $\beta_j$.

We can analyze the collection of these sub-channels to obtain the distribution of resequencing delay. In the following analysis, we will focus on a single sub-channel. However, this never means any loss of generality in the analysis, as the phase of a frame is arbitrary.

### *C. State probability of a sub-channel*

We consider the case where a state of a sub-channel is defined by the number of consecutive receive failures of a packet. For example, Fig. 3 shows changes of sub-channel #2's state. When a packet is received in error, the state value is increased by one; otherwise state transfers to 0. If a packet is received in error after the maximum number of retransmissions, the state also returns to 0. If new packets are consecutively sent without transmission error, the value of the state remains at 0 in consecutive slots. When we define the state as the number of receive failures of a packet, the state transition is represented as in Fig. 4. The probabilities of the state $p_s(k)$ and the packet loss rate $p_L$ are given by,

$$p_s(0) = \frac{1-\epsilon}{1-\epsilon+\alpha\epsilon-\alpha\epsilon^{N_r+1}}, \tag{1}$$

$$p_s(k) = \frac{\alpha(1-\epsilon)\epsilon^k}{1-\epsilon+\alpha\epsilon-\alpha\epsilon^{N_r+1}}, 1 \le k \le N_r, \tag{2}$$

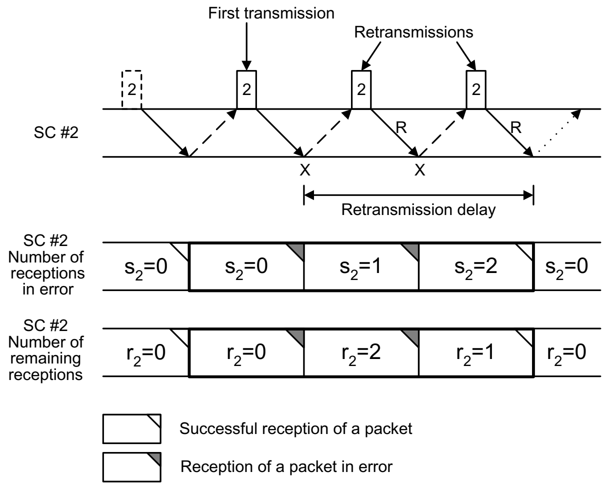

Fig. 3. An example of state transition on sub-channel #2.

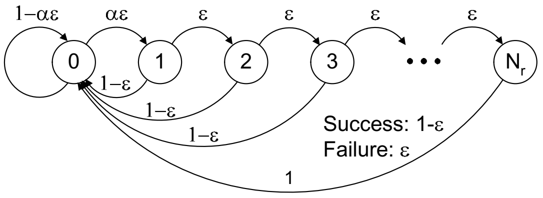

Fig. 4. A state transition diagram based on the number of consecutive receive failures of a packet.

$$p_L = \epsilon p_s(N_r) = \frac{\alpha(1-\epsilon)\epsilon^{N_r+1}}{1-\epsilon+\alpha\epsilon-\alpha\epsilon^{N_r+1}}. \tag{3}$$

In the analysis of the resequencing delay described in the subsequent section, the number of remaining receive failures till the end of current packet transmission is needed. We call this as the number of remaining receive failures. Fig. 3 also shows the change of state based on this number. In this case, when a packet is received in error at the first time, the state transits to the number of total receive failures till the end of this packet transmission. After that, the value of the state is decreased by one each time a packet is received in error. It should be noted that the end of packet transmission means either the packet is received successfully or aborted due to the maximum number of retransmissions. If we define the state as the number of remaining receive failures, its state probability $p_r(r)$ can be calculated based on the original state probability $p_s(k)$.

*a) In case of $r = 0$:*

$$\begin{aligned} p_r(0) &= \{1-\alpha+\alpha(1-\epsilon)\}p_s(0) \\ &\quad + \sum_{k=1}^{N_r}(1-\epsilon)p_s(k) + \epsilon p_s(N_r) \\ &= \frac{1-\epsilon}{1-\epsilon+\alpha\epsilon-\alpha\epsilon^{N_r+1}} \end{aligned} \tag{4}$$

*b) In case of $1 \le r \le N_r$:*

$$\begin{aligned} p_r(r) &= \alpha\epsilon^r(1-\epsilon)p_s(0) + \sum_{k=1}^{N_r-r}(1-\epsilon)\epsilon^r p_s(k) \\ &+ \epsilon^{r+1}p_s(N_r-r) \\ &= \frac{\alpha(1-\epsilon)\epsilon^k}{1-\epsilon+\alpha\epsilon-\alpha\epsilon^{N_r+1}} \end{aligned} \tag{5}$$

As indicated above, the state probability, based on the number of remaining receive failures, takes the same form as equations (1) and (2). We can intuitively explain this based on a cycle from the end of previous packet transmission to the end of current packet transmission. In each cycle, there is one-to-one mapping between the state value of the first definition (the number of receive failures) and the same state value of the second definition (the number of remaining receive failures) as depicted in Fig 3. Accordingly the probability of each state is the same between these two state definitions.

As mentioned before, we will study the case, where the load of the transmission channel is changed by parameter $\alpha$. The transmission channel becomes vacant with the probability $(1-\alpha)$ on condition that the state of a sub-channel is 0. Then the utilization factor $\rho$ of the transmission channel is given by,

$$\begin{aligned} \rho &= 1-(1-\alpha)p_s(0) \\ &= \frac{\alpha(1-\epsilon^{N_r+1})}{1-\epsilon+\alpha\epsilon-\alpha\epsilon^{N_r+1}}. \end{aligned} \tag{6}$$

## III. DELAY DISTRIBUTION DUE TO THE RESEQUENCING AND RETRANSMISSION

In this section we will calculate two types of delay. One is the pure resequencing delay and another is the delay including both the retransmission and the resequencing.

### A. Delay distribution of the pure resequencing

Let us define $P_{reseq}(w, i|\beta_j)$ as the probability that the resequencing delay is $wM + i$ slots, where a packet of flow $j$ is successfully received on sub-channel #0.

*a) In case of $i \neq 0$:* The delay due to the pure resequencing is from the time when a packet is correctly received to the time when it is delivered to the upper layer. We assume that a packet of flow $j$ is correctly received on sub-channel #0 after it was retransmitted $u$ times $(u = 0, 1, 2, \ldots, Nr)$.

Fig. 5 shows the case where a packet on sub-channel #0 is delayed due to waiting for reception of a packet, which belongs to the same flow $j$ on sub-channel #2. In Fig. 5, a packet on sub-channel #0 is received correctly after $u(u = 2)$ times receive failures; the first receive failure occurs at time $t_0$. When we observe states of other sub-channels at this moment, the resequencing delay occurs if there is at least one sub-channel of which state (the number of remaining receive failures) is larger than or equal to $u + 1$. In the figure, the states of sub-channel #2 and #4 are 4 and 3, respectively, at time $t_0$.

If the state (number of remaining receive failures) of sub-channel #$i$ is the largest among sub-channels from #1 to #$(M-1)$ and its value is $u + w + 1$ $(w = 0, 1, 2, \ldots, Nr - 1)$, the resequencing delay of the packet on sub-channel #0

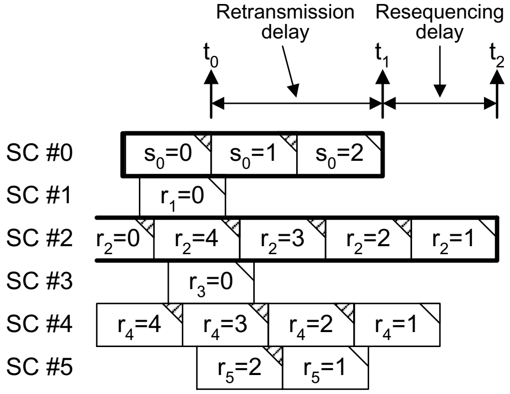

Fig. 5. An example of resequencing delay.

becomes $wM + i$ slots. In Fig. 5, the state of sub-channel #2 is the largest, then $i = 2$, $u + w + 1 = 4$, $w = 1$. The resequencing delay becomes $wM+i = 8$ slots. The probability $P_{reseq}(w, i|\beta_j)$ can be calculated by the subsequent equation.

$$P_{reseq}(w, i|\beta_j) = \sum_{u=0}^{N_r-w-1} p_t(u)R(w + u + 1, i|\beta_j), \quad (7)$$

where $p_t(u)$ corresponds to the case where a packet on sub-channel #0 is received correctly after $u$ times receive failures.

$$p_t(u) = \frac{(1-\epsilon)\epsilon^u}{1-\epsilon^{N_r+1}} \quad (8)$$

$R(w+u+1, i|\beta_j)$, which will be defined and calculated below, corresponds to the case where a packet on sub-channel $\#i$ belongs to flow $j$ and the state of sub-channel $\#i$ is the largest among sub-channels from #1 to $\#(M-1)$ with value $u + w + 1$.

More precisely, $R(n, i|\beta_j)$ is defined as the probability that the number of remaining receive failures on sub-channel $\#i$ is $n$, and the following conditions are satisfied.

- A packet on sub-channel $\#i$ belongs to flow $j$, on which we are focusing.
- Packets on sub-channels from #1 to $\#(i-1)$ do not belong to flow $j$, or if there is a packet of flow $j$, its number of remaining receive failures is larger than or equal to that of the packet on sub-channel $\#i$.
- Packets on sub-channels from $\#(i+1)$ to $\#(M-1)$ do not belong to flow $j$, or if there is a packet of flow $j$, its number of remaining receive failures is larger than that of the packet on sub-channel $\#i$.

As each sub-channel is independent, the probability that the numbers of remaining receive failures of sub-channels from #1 to $\#(M-1)$ are $r_1, \ldots, r_{M-1}$, respectively, is given by the products of each state probability.

$$P_{rob}(r_1, \ldots, r_i, \ldots, r_{M-1}) = \prod_{k=1}^{M-1} p_r(r_k) \quad (9)$$

Based on this equation, $R(n, i|\beta_j)$ can be calculated as follows;

$$\begin{aligned} R(n,i|\beta_j) &= \beta_j p_r(n) \prod_{k=1}^{i-1} \left(1-\beta_j+\beta_j \sum_{r_k=0}^{n} p_r(r_k)\right) \\ &\quad \cdot \prod_{k=i+1}^{M-1} \left(1-\beta_j+\beta_j \sum_{r_k=0}^{n-1} p_r(r_k)\right) \\ &= \beta_j p_r(n) U(n|\beta_j)^{i-1} U(n-1|\beta_j)^{M-1-i}, \end{aligned} \quad (10)$$

where $U(n|\beta_j)$ is the probability that a packet on a sub-channel does not belong to flow $j$ or, if it belongs to flow $j$, the number of remaining receive failures is less than or equal to $n$.

$$\begin{aligned} U(n|\beta_j) &= 1-\beta_j+\beta_j \sum_{k=0}^{n} p_r(k) \\ &= 1-\beta_j+\beta_j \frac{1-\epsilon+\alpha\epsilon(1-\epsilon^n)}{1-\epsilon+\alpha\epsilon-\alpha\epsilon^{N_r+1}} \end{aligned} \quad (11)$$

By using equations (7) and (10), we can calculate the distribution of the sequencing delay for the case of $i \neq 0$.

*b) In case of* $i = 0$*:* The resequencing delay occurs, if a packet on sub-channel #0, which has been received correctly, waits for a packet sent in one of other sub-channels. As $i = 0$ corresponds to the case where a packet on sub-channel #0 waits for another packet of the same channel, there is no possibility of such event, then the probability is 0 in case of $w \neq 0$. However, there is a possibility that the delay is 0 in case of $w = 0$, then the probability $P_{reseq}(0, 0|\beta_j)$ exists. Fig. 6 shows an example where packets on all other sub-channels belong to flow $j$ and the resequencing delay does not occur.

In this figure, a packet on sub-channel #0 is received correctly after receive failures of $u(u = 3)$ times. We observe states (the number of remaining receive failures) of other sub-channels at time $t_0$, which is the time when the first transmission of the packet is received. The resequencing delay never occurs if the state of each sub-channel, of which packet belongs to flow $j$, is less than or equal to the state of sub-channel #0.

$$P_{reseq}(w, 0|\beta_j) = \begin{cases} \sum_{u=0}^{N_r} p_t(u)U(u|\beta_j)^{M-1} & w = 0 \\ 0 & w \neq 0 \end{cases} \quad (12)$$

*c) Resequencing delay distribution for the case of multiple flows:* We can calculate the resequencing delay distribution for the whole packets sent over $m$ flows as follows,

$$P_{reseq}(w, i) = \sum_{j=1}^{m} \beta_j P_{reseq}(w, i|\beta_j). \quad (13)$$

If the packet generation probability is the same for the all $m$ flows, then the distribution is calculated as follows, where $\beta = 1/m$.

$$P_{reseq}(w, i) = P_{reseq}(w, i|\beta) \quad (14)$$

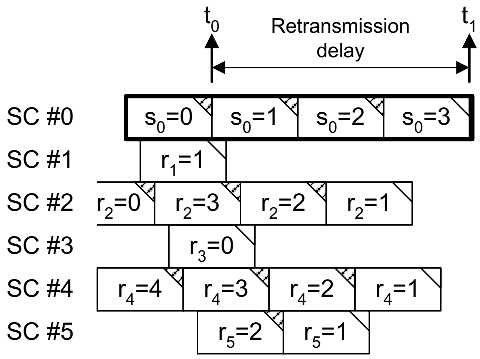

Fig. 6. An example of no resequencing delay.

### *B. Delay distribution of both retransmission and resequencing*

Let us define the probability $P_{delay}(u,i|\beta_j)$ as the sum of retransmission delay and resequencing delay is $uM+i$ slots in the case where a packet of sub-channel $\#0$ is successfully received after receive failures of $u$ times.

*a) In case of $i \neq 0$:* The sum of both retransmission and resequencing delay becomes $uM+i$ slots for the following case. A packet of sub-channel $\#0$ is received correctly after receive failures of less than or equal to $u$ times . We observe states (the number of remaining receive failures) of other sub-channels at time $t_0$, which is the time when the first transmission of the packet is received. The state of sub-channel $\#i$ is the largest among packets belonging to flow $j$ on other sub-channels, except sub-channel $\#0$, and its value is $u+1$.

$$\begin{aligned} P_{delay}(u,i|\beta_j) &= \left(\sum_{k=0}^{u} p_t(k)\right) R(u+1,i|\beta_j) \\ &= \beta_j q_t(u) p_r(u+1) U(u+1|\beta_j)^{i-1} U(u|\beta_j)^{M-1-i} \\ &= \beta_j q_t(u) p_r(u+1) \frac{U(u|\beta_j)^{M-1}}{U(u+1|\beta_j)} \left(\frac{U(u+1|\beta_j)}{U(u|\beta_j)}\right)^{i}, \end{aligned} \tag{15}$$

where $q_t(u)$ is the probability that a packet is received correctly after receive failures of less than or equal to $u$ times.

$$q_t \triangleq \sum_{k=0}^{u} p_t(k) = \frac{1-\epsilon^{u+1}}{1-\epsilon^{N_r+1}} \tag{16}$$

*b) In case of $i = 0$:* A packet on sub-channel $\#0$ is received correctly after receive failures of $u$ times. We observe states (the number of remaining receive failures) of other sub-channels at time $t_0$, which is the time when the first transmission of the packet is received. The resequencing delay is 0, if the state of each sub-channel, of which packet belongs to flow $j$, is less than or equal to the state of sub-channel $\#0$.

$$P_{delay}(u,0|\beta_j) = p_t(u) U(u|\beta_j)^{M-1} \tag{17}$$

*c) In case of multiple flows:* In the same manner as the case of the resequencing delay, the delay distribution of both retransmission and resequencing can be calculated by the following.

$$P_{delay}(u,i) = \sum_{j=1}^{m} \beta_j P_{delay}(u,i|\beta_j) \tag{18}$$

If the packet generation probability of each flow is the same, the delay distribution of both retransmission and resequencing can be calculated by the following.

$$P_{delay}(u,i) = P_{delay}(u,i|\beta) \tag{19}$$

## IV. RESULTS OF NUMERICAL CALCULATIONS

Numerical calculations and simulations are performed for the case where the SR ARQ is applied to a satellite channel of which transmission rate is 1.5Mbps and the length of a packet is 1500 bytes. The propagation delay of the satellite channel is assumed to be 0.25sec. Based on these conditions, calculated value of M becomes 64.

### *A. In case where $\alpha$ is changed.*

Table I shows utilization factor, average retransmission delay, average resequencing delay, and average delay due to both retransmission and resequencing for various values of $\alpha$. In this table, we select $\beta = 1$, which corresponds to the case where full resequencing is performed or the number of upper layer flows is one. The parameter $\alpha$ is introduced to change the utilization factor $\rho$ of the satellite channel; as $\alpha$ decreases, the utilization factor $\rho$ also becomes small and takes almost the same value as $\alpha$. However, if the bit error rate becomes large, the utilization factor $\rho$ becomes larger than $\alpha$ because of additional traffic due to retransmissions. From Table I it is clear that the average resequencing delay is dominant as compared to the average retransmission delay. The reason is as follows; only a packet, which is lost and retransmitted, experiences the retransmission delay, while a large number of correctly received packets that follow retransmitted one experience the resequencing delay. As shown in the table, if the bit error rate is fixed, resequencing delay decreases as the utilization factor $\rho$ of the channel becomes small, since the number of packets involved in the resequencing decreases as the utilization factor $\rho$ becomes small. Fig. 7 shows the delay distribution due to the resequencing alone, where $\epsilon$ is 0.1 and $\alpha$ is 0.9, while Fig. 8 shows the delay distribution due to both retransmission and resequencing for the same condition. In these figures, the simulation results are also plotted. As the results of the simulations and numerical calculations well overlap, this proves the validity of the calculations described above. The probability of the delay decreases in steps as the delay increases due to the change of retransmission times. In case of the same retransmission times, for example from 0 to 63 slots, the probability increases as the delay becomes large. This is due to the fact that a packet, of which distance from a retransmitted packet is large, takes the small resequencing delay and probability of being involved in the resequencing is also small.

TABLE I

UTILIZATION FACTOR, AVERAGE RETRANSMISSION DELAY (SLOT), AVERAGE RESEQUENCING DELAY (SLOT), AND AVERAGE DELAY DUE TO BOTH RETRANSMISSION AND RESEQUENCING (SLOT).

| $N_r = 3, \beta = 1.0$ | | | retrans. delay | reseq. delay | total delay |
|---|---|---|---|---|---|
| $\alpha$ | $\epsilon$ | $\rho$ | | | |
| 1.00 | 0.0001 | 1.0000 | 0.0064 | 0.2012 | 0.2076 |
| | 0.0010 | 1.0000 | 0.0641 | 1.9770 | 2.0410 |
| | 0.0100 | 1.0000 | 0.6465 | 16.7627 | 17.4092 |
| | 0.1000 | 1.0000 | 7.0855 | 71.8210 | 78.9065 |
| 0.90 | 0.0001 | 0.9000 | 0.0064 | 0.1811 | 0.1875 |
| | 0.0010 | 0.9001 | 0.0641 | 1.7831 | 1.8472 |
| | 0.0100 | 0.9009 | 0.6465 | 15.3821 | 16.0286 |
| | 0.1000 | 0.9091 | 7.0855 | 69.4644 | 76.5499 |
| 0.80 | 0.0001 | 0.8000 | 0.0064 | 0.1610 | 0.1674 |
| | 0.0010 | 0.8002 | 0.0641 | 1.5884 | 1.6524 |
| | 0.0100 | 0.8016 | 0.6465 | 13.9441 | 14.5906 |
| | 0.1000 | 0.8163 | 7.0855 | 66.7985 | 73.8840 |
| 0.70 | 0.0001 | 0.7000 | 0.0064 | 0.1409 | 0.1473 |
| | 0.0010 | 0.7002 | 0.0641 | 1.3928 | 1.4569 |
| | 0.0100 | 0.7021 | 0.6465 | 12.4459 | 13.0923 |
| | 0.1000 | 0.7216 | 7.0855 | 63.7298 | 70.8153 |

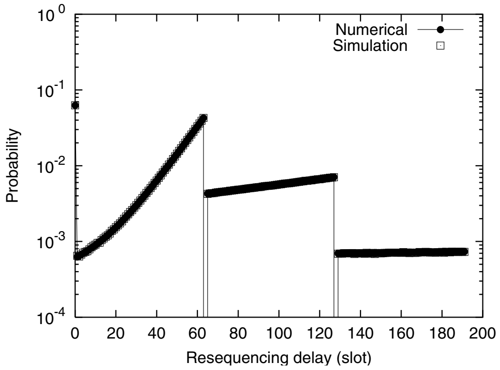

Fig. 7. Distribution of the resequencing delay ($\epsilon = 0.1, M = 64, N_r = 3, \alpha = 0.9, \beta = 1.0$).

### *B. In case where $N_r$ is changed*

Table II shows delay and packet loss rate $p_L$ for the cases where $\alpha = 0.9$ and the maximum number of retransmissions $N_r$ is changed to 1, 3, and 5. Other conditions are the same as the case of Table I. When $N_r$ is small (=1), though the delay becomes small, the packet loss rate $p_L$ is non-negligible for large bit error rates. When $N_r$ is larger than 3, the packet loss rate becomes small and delay is almost the same for cases where $N_r$ is 3 and 5.

### *C. In case where $\beta$ is changed*

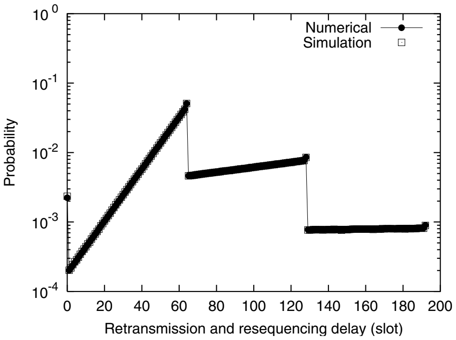

Fig. 8. Distribution of delay including both the retransmission and resequencing ($\epsilon = 0.1, M = 64, N_r = 3, \alpha = 0.9, \beta = 1.0$).

TABLE II

PACKET LOSS RATE, AVERAGE RETRANSMISSION DELAY (SLOT), AVERAGE RESEQUENCING DELAY (SLOT), AND AVERAGE DELAY DUE TO BOTH RETRANSMISSION AND RESEQUENCING (SLOT).

| $\alpha = 0.9, \beta = 1.0$ | | | retrans. delay | reseq. delay | total delay |
|---|---|---|---|---|---|
| $N_r$ | $\epsilon$ | $p_L$ | | | |
| 1 | 0.0001 | 1.00e-008 | 0.0064 | 0.1811 | 0.1875 |
| | 0.0010 | 1.00e-006 | 0.0639 | 1.7778 | 1.8417 |
| | 0.0100 | 1.00e-004 | 0.6337 | 14.9246 | 15.5583 |
| | 0.1000 | 1.00e-002 | 5.8182 | 47.2160 | 53.0342 |
| 3 | 0.0001 | 1.00e-016 | 0.0064 | 0.1811 | 0.1875 |
| | 0.0010 | 1.00e-012 | 0.0641 | 1.7831 | 1.8472 |
| | 0.0100 | 1.00e-008 | 0.6465 | 15.3821 | 16.0286 |
| | 0.1000 | 1.00e-004 | 7.0855 | 69.4644 | 76.5499 |
| 5 | 0.0001 | 1.00e-024 | 0.0064 | 0.1811 | 0.1875 |
| | 0.0010 | 1.00e-018 | 0.0641 | 1.7831 | 1.8472 |
| | 0.0100 | 1.00e-012 | 0.6465 | 15.3822 | 16.0287 |
| | 0.1000 | 1.00e-006 | 7.1107 | 70.3243 | 77.4350 |

Table III shows average retransmission delay, average resequencing delay, and average delay due to both retransmission and resequencing for changes of values $\beta$, where $\alpha = 0.9$. $\beta = 1.0, 0.5, 0.2$, and 0.1 correspond to the cases where the number of homogeneous upper layer flows are 1, 2, 5, and 10 respectively. It is clear that the resequencing delay decreases as the number of upper layer flows increases. The reason is that the number of packets in one flow becomes small, then the number of packets involved in the resequencing also decreases. The conventional full resequencing corresponds to the case of $\beta = 1$, where order of all packets are preserved irrespective of the number of upper layer flows. The significant advantage of the PFRS scheme is well observed by comparing the delay of a small $\beta$ case to the delay of $\beta = 1$. The number of flows that are simultaneously active over a transmission channel depends on the number of users and applications. It is reported that some web browser opens up to 8 TCP connections per web-server using HTTP/1.0 and 2 TCP connections using HTTP/1.1 [7]. This implies that the advantage of the PFRS scheme can be normally expected even in a single user case. Fig. 9 shows the delay probability distribution due to the retransmission and resequencing, where the number of upper layer flows is 5 and $\beta = 0.2$ in each flow. Other conditions are the same as the case of Table III. Fig. 10 shows the delay probability distribution due to the retransmission and resequencing for the case where conditions are the same as Fig. 9, except that $\epsilon$ is 0.01. The results of the simulations and numerical calculations also well overlap, this proves the validity of the calculations. In these figures, peaks due to retransmission delay (multiple of M slots) becomes outstanding, as the probability of resequencing delay decreases because of the per flow resequencing.

Fig. 11 shows the delay probability distribution where rates

TABLE III

AVERAGE RETRANSMISSION DELAY (SLOT), AVERAGE RESEQUENCING DELAY (SLOT), AND AVERAGE DELAY DUE TO BOTH RETRANSMISSION AND RESEQUENCING (SLOT).

| $N_r = 3, \alpha = 0.9$ | | retrans. | reseq. | total |
|---|---|---|---|---|
| $\beta$ | $\epsilon$ | delay | delay | delay |
| 1.00 | 0.0001 | 0.0064 | 0.1811 | 0.1875 |
| | 0.0010 | 0.0641 | 1.7831 | 1.8472 |
| | 0.0100 | 0.6465 | 15.3821 | 16.0286 |
| | 0.1000 | 7.0855 | 69.4644 | 76.5499 |
| 0.50 | 0.0001 | 0.0064 | 0.0906 | 0.0970 |
| | 0.0010 | 0.0641 | 0.8998 | 0.9639 |
| | 0.0100 | 0.6465 | 8.3823 | 9.0288 |
| | 0.1000 | 7.0855 | 52.0038 | 59.0893 |
| 0.20 | 0.0001 | 0.0064 | 0.0363 | 0.0427 |
| | 0.0010 | 0.0641 | 0.3619 | 0.4260 |
| | 0.0100 | 0.6465 | 3.5375 | 4.1839 |
| | 0.1000 | 7.0855 | 29.7156 | 36.8011 |
| 0.10 | 0.0001 | 0.0064 | 0.0181 | 0.0245 |
| | 0.0010 | 0.0641 | 0.1813 | 0.2454 |
| | 0.0100 | 0.6465 | 1.8012 | 2.4477 |
| | 0.1000 | 7.0855 | 17.2001 | 24.2856 |

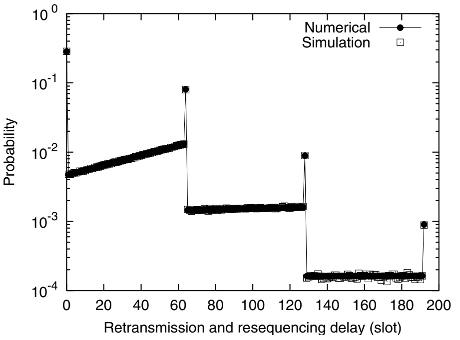

Fig. 9. Distribution of resequencing delay ($\epsilon = 0.1, M = 64, N_r = 3, \alpha = 0.9, \beta = 0.2$).

of flows are not the same. In this figure, the number of upper layer flows is 6. The probability of one flow ($\beta_1$) is 0.5 and the probability of other five flows ($\beta_i, i = 2, 3, 4, 5, 6$) is 0.1. Other conditions are the same as the case of Table III. As the results of simulations are consistent with numerical calculations, it is clear that the calculation method in this paper can also be applied to mixture of different flow rates.

## V. CONCLUSIONS

In this paper we have presented a calculation method on the delay probability distribution of the resequencing delay by the SR ARQ. In this calculation method, the maximum number of retransmissions is limited, and the utilization of a transmission channel as well as multiple upper layer flows are considered. The calculation results are well consistent with those of simulations. The method in this paper can be applied to both the conventional full resequencing and newly proposed PFRS schemes. Based on the calculation results, it is made clear that the resequencing delay is dominant as compared to the retransmission delay, and this delay can be reduced by the PFRS scheme as the number of flows over the SR ARQ increases.

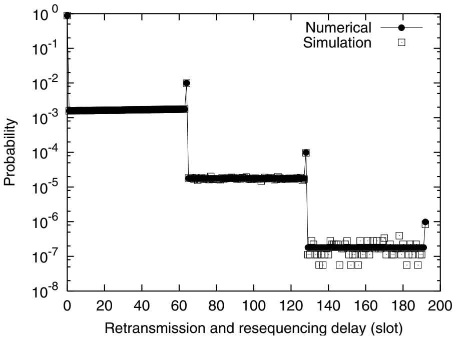

Fig. 10. Distribution of delay including the retransmission and resequencing ($\epsilon = 0.01, M = 64, N_r = 3, \alpha = 0.9, \beta = 0.2$).

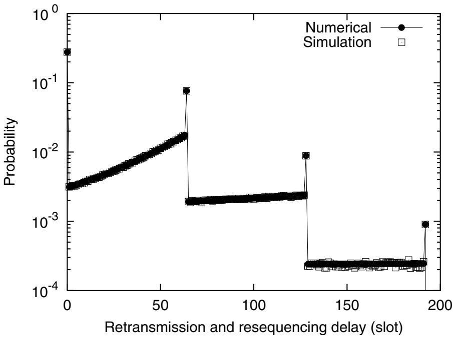

Fig. 11. Distribution of delay including both the retransmission and resequencing for multiple flow rates ($\epsilon = 0.01, M = 64, N_r = 3, \alpha = 0.9, \beta_1 = 0.5, \beta_i = 0.1, i = 2, 3, 4, 5, 6$).

Although we presented numerical calculations and simulations for a satellite channel, the PFRS scheme and the calculation method are also useful for high speed terrestrial wireless communications, where efficient SR ARQ is essential to recover transmission errors due to poor channel quality.

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