Correlations in ATM Cell Streams Exposed to Cell Delay Variation

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Abstract

In this paper the correlation structure of a constant bit rate (CBR) cell stream is investigated after it has passed through a FIFO queue in which it is multiplexed with a background traffic stream. The background stream arrives in the form of independent and identically distributed batches with general batch size distribution. An exact Markovian model and a computational simpler diffusion model are used to obtain the correlation between interdeparture times of the perturbated CBR stream at the output of the queue. Numerical results are provided to evaluate the accuracy of the diffusion approximation. For the diffusion approximation it is proven that the correlation is always negative and that it converges to zero with rate $O(n^{-1/2}exp(-\alpha n))$ as the lag n tends to infinity. α is a positive constant which is determined by the drift and variance in the diffusion model, together with the interarrival time of the CBR stream.

1 Introduction

In the new standards for the Broadband Integrated Service Digital Network (B-ISDN) and its switching and transport mechanism Asynchronous Transfer Mode (ATM), the connection set up procedure includes a negotiation of a traffic contract between the user and the network [14]. At the entrance to the network (UNI) and at the border between networks owned by different operators (NNI) an enforcement, called usage parameter control (UPC) at the UNI and network parameter control (NPC) at the NNI, of the traffic parameters in the traffic contract of each connection will take place.

The *peak cell rate* of the connection is the most important traffic parameter in the traffic contract and it is the only traffic parameter which is mandatory.

The definition and the use of the peak cell rate for UPC/NPC and other traffic controls is made complicated due to the phenomenon that different cells of the same connection experiences different delays between the source and the UPC/NPC device due to switching and multiplexing with other cell streams. This phenomenon is called Cell Delay Variation (CDV), and it has forced the standardization bodies to define the peak cell rate by means of *two* parameters.

- The peak emission interval T, which is the distance between two adjacent cells of the connection transmitted at peak rate. Equivalently $1/T$ is the *peak cell rate* of the connection.

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- The *CDV tolerance* τ. τ is to be interpreted as a measure of how much the instantaneous peak cell rate is allowed to deviate from the peak cell rate declared by T.

In ITU a UPC/NPC algorithm has not been standardized. However, it is standardized how to measure whether a cell stream is conforming to the traffic contract or not. The *Generic Cell Rate Algorithm* (GCRA) [14] characterized by the two parameters T and τ, is standardized for exactly this purpose. Essentially the GCRA works like a leaky bucket, that is, credits are generated at a rate of $1/T$ such that a maximum proportional to τ can be present simultaneous. Each arriving cell needs a credit to be declared conforming, and if too many cells arrive too close to each other all credits will be used, and cells arriving when no credits are present will be declared non-conforming.

Several models has been proposed for the setting of T and τ such that well behaving cell streams exposed to CDV does not suffer from a large amount of cells declared non-conforming by the GCRA.

The most frequently applied approach has modeled the CDV perturbated cell stream by a renewal stream. The variance of the time between adjacent cells of the CBR stream has been computed ([11], [5]) or measured/simulated, ([12]). A distribution matching the mean and variance has then been used and the associated GI/D/1 queue[3] has been solved yielding proper values for T and τ. However, it has turned out that this modeling approach predicts the τ value to diverge as the leak rate $1/T$ of the GCRA approaches the physical peak rate of the connection.

This important observation can be explained by the following way. The assumption of a renewal stream makes the number of credits available behave like a random walk with two barriers (0 and maximum number of credits) and with a drift equal to the difference between the credit generation rate $1/T$ and the cell arrival rate. When the credit generation rate approaches the cell arrival rate the associated random walk approaches a zero-drift random walk for which it is known that it will hit the barriers with a frequency inverse proportional to to the distance between the barriers. Therefore, in the limit where the credit generation rate equals the cell arrival rate, an enormous amount of credits (enormous τ) is needed in order to make the probability of non-conformance sufficiently small.

In reality a much smaller CDV tolerance value will be sufficient. Both simulation results [9], numerical results [4], and a simple worst case dimensioning scheme [20] which works when the peak and leak rate are equal, clearly shows a finite τ value also when the leak rate is put equal to the peak rate. The misleading behaviour of the renewal models can be explained by the fact that the CBR connection for which CDV has been introduced possesses negative correlations. Negative correlations implies that many arrivals presently will make likely few arrivals in near future which implies that as the number of credits decreases there is an increased tendency to fewer arrivals keeping the number of credits away from the zero barrier.

Thereby the correlation structure of the CDV perturbated CBR streams plays an important part in the description of the cell stream, and models which take this into account are needed. Can models which on one hand gives an accurate description of the correlated cell stream and on the other hand are applicable in practice be derived? Will it be possible to compute the correlation between two arbitrary chosen interdeparture intervals (intervals between adjacent CBR cells)? Is it possible to derive something about the range of the correlations, i.e how fast do they vanish? Are they always negative etc.? This paper is intended to answer these questions

[3] which can be viewed as equivalent to the GCRA, see [13]

by presenting an analysis of a CBR cell stream which is multiplexed with a background stream in a FIFO queue.

The analysis is based on two models. The first one is an exact Markovian model presented in [11] and generalized by the authors in [19] which provides a solution which is numerical in nature and computational non-trivial. The second one is an approximate diffusion model presented in [3] and further developed by the authors in [19] which enables the point process characteristics to be computed in closed form and also provides a simple tool for the performance evaluation of the multiplexed CDV affected CBR cell streams [18].

2 Exact Markovian Model

Consider a single server discrete time FIFO queue with infinite buffer capacity receiving the superposition of a CBR stream with interarrival time T and an interfering background stream which arrives to the queue in the form of independent and identically distributed batches with a general batch size distribution denoted by $b(k)$ (Figure 1). Time is slotted, with the slot size being equal to the cell transmission time. Choose the time such that cell no. n arrives at time nT to the queue. Let W_n denote the waiting time of cell no. n. Then $P\{W_n = k\}$ is the probability that cell no. n has a waiting time of k time units.

The sequence W_n is assumed stationary with distribution $w_k = P\{W_i = k\}$. Furthermore, due to the assumptions made, then the waiting time of successive CBR cells constitutes a discrete time Markov process in which the underlying transition matrix $\boldsymbol{Q}$ can be computed by the following way.

The element (j,k) of $\boldsymbol{Q}$ is defined as follows:

$$q_{j,k} = P\{W_i = k \mid W_{i-1} = j\} \quad j,k \geq 0 \tag{1}$$

and

$$q_{j,k} = Q(j,k-1) - Q(j,k) \tag{2}$$

where

$$Q(j,k) = P\{W_i > k \mid W_{i-1} = j\} = \sum_{n \geq 0} P_n(j,k) \tag{3}$$

with $P_n(j,k) = P\{W_i > k \mid W_{i-1} = j \text{ and } n \text{ arrivals in }]Ti-T,Ti]\ \} b^{T*}(n)$, where $b^{T*}(n)$ is the T-fold convolution of the batch size distribution, and evaluated in n it represents the probability of n arrivals in $]Ti-T,Ti]$. It can be shown, see appendix A in [19], that

$$P_n(j,k) = \begin{cases} 0 & j+1 \geq T \text{ and } n \leq T+k-j-1 \text{ or} \\ & \quad j+1 < T \text{ and } k \geq n \\ b^{T*}(n) & n > T+k-j-1 \\ \sum_{s=1}^{n-k} b^{s*}(k+s) \times & \\ \quad \times b^{(T-s)*}(n-k-s)\frac{T-n+k}{T-s} & j+1 < T \text{ and } k < n \leq T+k-j-1 \end{cases} \tag{4}$$

The stationary waiting time distribution can be found from solving the equilibrium system $\boldsymbol{w} = \boldsymbol{w}\boldsymbol{Q}$ where $\boldsymbol{w} = (w_0, w_1, ..., w_i, ...)$ and $\boldsymbol{Q} = \{q_{j,k}\}$. In numerical applications, a truncation of the state space is in general necessary.

For the steady state queue length distribution seen by an arbitrary CBR cell, [5] provide a closed form expression for the generating function. [5] also provide the generating function of the waiting time for cell no. $n+1$ conditioning on the event that waiting time for cell n is i. From this the entries in the transition matrix can in principles be found. However, this requires not only an inversion but also the determination of $T-1$ boundary probabilities, and we have found the direct approach more appealing.

Define $\tau_n = nT + W_n$. Thus τ_n denotes the departure time [4] of cell no. n. The interdeparture time between cell no. j and cell no. $j+1$ is denoted X_j and the distribution is independent of j due to the stationary assumption. Define the shifted interdeparture time of cell no. n as: $U_n = \tau_n - nT - \tau_0$ (see Figure 2). It is a fundamental random variable with zero mean from which all point process characteristics of interest can be derived. Let $f_n(k) = P\{U_n = k\}$ be the probability distribution of U_n for cell no. n. It can be seen [11] that

$$f_n(k) = \begin{cases} \sum_{i=0}^{\infty} w_i q_{i,i+k}^{(n)} & \text{if } k \geq -nT+1 \\ 0 & \text{otherwise} \end{cases} \tag{5}$$

where $q_{j,k}^{(n)}$ denotes entry (j,k) in the n'th power of the transition matrix $\boldsymbol{Q} = \{q_{j,k}\}$.

The *interdeparture time distribution* between cell no. 0 and n is simply obtained by the translation nT of the shifted interdeparture time distribution U_n i.e.

$$P\{\tau_n - \tau_0 = k\} = P\{U_n = k - nT\} = f_n(k - nT) \tag{6}$$

The variance of the interdeparture time between cell 0 and cell n denoted $V(n)$ is:

$$V(n) = Var(X_1 + .. + X_n) = Var(\tau_n - \tau_0) = \sum_{k=-nT+1}^{\infty} k^2 f_n(k) \tag{7}$$

From the basic formula $Var(X_1 + .. + X_n + X_{n+1}) = Var(X_1 + .. + X_n) + Var(X_{n+1}) + 2Cov(X_1 + .. + X_n, X_{n+1})$ it is straightforward by induction to prove that

$$\begin{aligned} C(n) &:= Cov(X_{n+1}, X_1) \\ &= \frac{Var(X_1 + .. + X_{n+1}) + Var(X_1 + .. + X_{n-1})}{2} - Var(X_1 + .. + X_n) \\ &= \frac{V(n+1) + V(n-1)}{2} - V(n) \end{aligned} \tag{8}$$

Since the sequence $\{X_n\}$ is assumed stationary the *correlation* is given as

$$\text{corr}(n) = \frac{\frac{V(n+1)+V(n-1)}{2} - V(n)}{V(1)} \tag{9}$$

i.e. in terms of the variance function alone.

[4] Strictly speaking, τ_n denotes the time cell no. n enters service. However, this has no effect when service time is deterministic.

3 Diffusion Approximation

The exact approach is in general computational hard and the numerical complexity increases without bounds when the load on the queue approaches one. Therefore an accurate approximation which maintain the important qualities of the exact model is desirable. The following diffusion model is suggested.

The main idea of the diffusion approach is to model the evolution of the unfinished work (or virtual waiting time) between CBR arrivals by a reflected Brownian motion. Markovian dependencies are assumed between successive CBR cell waiting times in the queue as in the exact case.

Let $\tilde{W}_t$ denote the waiting time a fictitious observer would experience if he joined the diffusion queue at time t (the unfinished work at time t). The probability of $\tilde{W}_t \leq x$ conditioned on $\tilde{W}_0 = y$ is, for a Brownian motion with drift m (m assumed smaller than zero in order to ensure a stable queue), variance σ^2 and a reflection in zero, in section 2.8 of [16] derived to be:

$$P\{\tilde{W}_t \leq x \mid \tilde{W}_0 = y\} = \begin{cases} \Phi(\frac{x-y-mt}{\sigma\sqrt{t}}) - e^{2\frac{mx}{\sigma^2}}\Phi(\frac{-x-y-mt}{\sigma\sqrt{t}}), & \text{for } x \geq 0 \\ 0, & \text{for } x < 0 \end{cases} \tag{10}$$

where Φ denotes the standard Gaussian probability distribution. The right hand side of formula (10) is a distribution function in x for all $y \geq 0$ and all $t > 0$, and it converges towards the exponential distribution with mean $\frac{-\sigma^2}{2m}$, independent of initial condition y, when t tends to infinity.

The waiting time of CBR cell no. n, is approximated by:

$$W_n = \tilde{W}_{nT} \tag{11}$$

that is *the waiting time that CBR cell no. n experience in the queue is approximated by the virtual waiting time in the diffusion queue at time nT.*

The diffusion approximation is used for modeling the arrivals of cells belonging to both the CBR stream and the background stream, i.e. both the CBR arrivals as well as the background arrivals and the departures are taken into account by a proper choice of drift and variance.

As in the diffusion model for the M/G/1 queue (see section 2.8 in [16]) the drift is $m = \rho - 1$. The key idea of choosing the most appropriate variance is that *we match the decay rates of the stationary waiting time distribution in the diffusion approximation with the asymptotic decay rate of the $D + GI^{[x]}/D/1$ queue.*

It is known from [6] that the queue length seen by an arriving CBR cell is asymptotically geometric i.e. $P(Q > r) \approx (1/z_\infty)^r$, where z_∞ is the dominant root of the corresponding z-transform which is found by solving the equation

$$B(z)^T - z^{T-1} = 0. \tag{12}$$

The root z_∞ is the root with smallest module outside the unit disk, and it is unique and real (see Appendix A3 in [6]).

Since the diffusion decay rate is $\frac{-2m}{\sigma^2}$ we get:

$$\sigma^2 = -\frac{2m}{\ln(z_\infty)}. \tag{13}$$

3.1 The distribution of the interdeparture time

The shifted interdeparture time in the diffusion context is: $\tilde{U}_t = \tilde{W}_t - \tilde{W}_0$ (think of $t = nT$), and

$$\begin{aligned} P\{\tilde{U}_t \leq x\} &= \int_0^\infty P\{\tau_t - \tau_0 - t \leq x \mid \tau_0 = y\} dP\{\tau_0 \leq y\} \\ &= \int_0^\infty P\{\tilde{W}_t \leq x + y \mid \tilde{W}_0 = y\} dP\{\tilde{W}_0 \leq y\} \end{aligned} \tag{14}$$

The computation carried out in [3] shows that the time dependent shifted interdeparture time distribution function is given as:

$$\tilde{F}_t(x) = P\{\tilde{U}_t \leq x\} = \begin{cases} \frac{1}{2} + \frac{1}{2}\Phi(\frac{x-mt}{\sigma\sqrt{t}}) - \frac{1}{2}e^{\frac{2mx}{\sigma^2}}\Phi(-\frac{x+mt}{\sigma\sqrt{t}}), & \text{for } x \geq 0 \\ \frac{1}{2}e^{-\frac{2mx}{\sigma^2}}\Phi(\frac{x-mt}{\sigma\sqrt{t}}) + \frac{1}{2}\Phi(\frac{x+mt}{\sigma\sqrt{t}}), & \text{for } x < 0 \end{cases} \tag{15}$$

From this expression it is seen that the probability distribution function $\tilde{F}_t$ for $\tilde{U}_t$ fulfills the relation: $\tilde{F}_t(x) + \tilde{F}_t(-x) = 1$, thus implying that the density function for $\tilde{U}_t$ is symmetric.

The interdeparture time distribution between cell no. k and $k + n$ is obtained from the shifted interdeparture time distribution as

$$F_n(x) = P\{\tau_{k+n} - \tau_k \leq x\} = P\{\tau_n - \tau_0 \leq x\} = P\{\tilde{U}_{nT} \leq x - nT\} = \tilde{F}_{nT}(x - nT) \tag{16}$$

3.2 The Variance Function

The variance function of $\tilde{U}_t$ is in [3] found to be:

$$\begin{aligned} Var(\tilde{U}_t) &= \frac{\sigma^4}{2m^2}(2\Phi(-\frac{m}{\sigma}\sqrt{t}) - 1) + (2\sigma^2 t + m^2t^2)\Phi(\frac{m}{\sigma}\sqrt{t}) \\ &+ (\frac{\sigma^3}{m}t^{1/2} + m\sigma t^{3/2})\varphi(\frac{m}{\sigma}\sqrt{t}) \end{aligned} \tag{17}$$

where φ is the standard normal density function. By applying the expansion $\Phi(-x) = \frac{\varphi(x)}{x}(1 - \frac{1}{x^2} + O(x^{-4}))$, for $x \to \infty$, see e.g. problem 7.7.1 in [8], we obtain

$$Var(\tilde{U}_t) = \frac{\sigma^4}{2m^2} + (3\frac{\sigma^5}{m^3}t^{-1/2} + O(t^{-3/2}))\varphi(\frac{m}{\sigma}\sqrt{t}) \quad \text{for } t \to \infty \tag{18}$$

3.3 The Covariance

From the approximation $W_n \approx \tilde{W}_{nT}$ we get $Var(X_1 + .. + X_n) \approx Var(\tilde{U}_{nT})$ from which

$$\tilde{C}(n) = \frac{Var(\tilde{U}_{(n+1)T}) + Var(\tilde{U}_{(n-1)T})}{2} - Var(\tilde{U}_{nT}) \tag{19}$$

Applying formula (17) it is seen that the covariance and therefore the correlation of any lag can be given in closed form.

Proposition 1: The correlation of any lag is negative.

Proof: From formula (8) it is seen that it suffices to prove that the function $[t \rightarrow Var(\tilde{U}_t)]$ is concave. Two times differentiations of (17) with respect to t yields

$$\frac{d^2Var(\tilde{U}_t)}{dt^2} = 2m^2\Phi(\frac{m}{\sigma}t^{1/2}) + 2\sigma m t^{-1/2}\varphi(\frac{m}{\sigma}t^{1/2}) \tag{20}$$

From the classical inequality $\Phi(-x) < \frac{\varphi(x)}{x}$ valid for $x > 0$ it is seen that $\frac{d^2Var(\tilde{U}_t)}{dt^2} < 0$ implying $Var(\tilde{U}_t)$ is concave.

Proposition 2: The correlation decays as $O(n^{-1/2}e^{-\frac{m^2}{2\sigma^2}Tn})$ as the lag n tends to infinity.

Proof: When the lag tends to infinity we may apply equation (18) which together with equation (8) yields

$$\begin{aligned}\tilde{C}(n) &= \frac{3\sigma^5}{m^3(2\pi T)^{1/2}}n^{-1/2}e^{-\frac{m^2}{2\sigma^2}Tn}[\frac{1}{2}(\frac{n}{n+1})^{1/2}e^{-\frac{m^2}{2\sigma^2}T} + \frac{1}{2}(\frac{n}{n-1})^{1/2}e^{\frac{m^2}{2\sigma^2}Tn} - 1 + O(n^{-3/2})] \\ &= \frac{3\sigma^5}{m^3(2\pi T)^{1/2}}n^{-1/2}e^{-\frac{m^2}{2\sigma^2}Tn}[\frac{1}{2}e^{-\frac{m^2}{2\sigma^2}T} + \frac{1}{2}e^{\frac{m^2}{2\sigma^2}T} - 1 + O(n^{-1})] \end{aligned} \tag{21}$$

proving the proposition.

In many cases $\frac{m^2}{2\sigma^2}T$ is smaller than 1, and a second order Taylor expansion of the exponential can be applied yielding

$$\tilde{C}(n) \approx [\frac{3}{4}\frac{\sigma m}{(2\pi)^{1/2}}T^{3/2}n^{-1/2} + O(n^{-1})]e^{-\frac{m^2}{2\sigma^2}Tn} \quad \text{when } \frac{m^2}{2\sigma^2}T \text{ is small and } n \text{ is large} \tag{22}$$

Based on the above analysis it should be noticed:

- The correlations are negative, which implies that ignoring them yield results in queueing applications which overestimates waiting times, CDV tolerance etc.
- The rate at which the correlations decay to zero in the lags has been obtained such that it is possible to set the range within which correlations should not be neglected.

4 Numerical Examples

In this section some numerical examples are presented to illustrate the behaviour of both models. First we investigate the effect of the background burstiness and load on the shifted interdeparture time distribution. In the background burstiness study the interarrival time of the CBR traffic and the load on the multiplex are $T = 20$ and $\rho = 0.8$, respectively. For the analysis of the influence of the background traffic burstiness the following cases have been considered:

- *Smooth background traffic*: 2 *Bernoulli* streams each with probability $p = 0.375$ of submitting a cell to the present time slot. Thereby the peakedness of the background traffic is 0.625.
- *Poisson background traffic* with intensity 0.75.
- *Bursty background traffic*: a *negative binomial* batch size distribution with peakedness 2 and mean 0.75.

Figure 3 and 4 depict the effect of the burstiness of the background traffic and the effect of the multiplexer load on the shifted interdeparture time distribution, respectively.

By comparing Figure 3 and 4 it can be observed that the burstiness of the background traffic has a stronger influence on the shifted interdeparture time distribution than the load. Since it is the load which can be controlled or estimated, while the burstiness is highly unknown, this gives rise to practical difficulties in the dimensioning of the UPC parameters.

The diffusion approximation performs reasonable well, but for the smooth background traffic case the inaccuracy is slightly larger than for the other cases.

Finally, we compare the correlation obtained through the exact model with the results obtained by the diffusion model for lags less than 10 for two different values of the CBR peak rate in case of Poisson background traffic.

Table 1: The correlation as a function of the lag n. $T = 20$ and $\rho = 0.8$

lag n	1	2	3	4	5	6	7	8	9
exact corr.	-0.358	-0.0836	-0.0316	-0.0137	-0.0064	- 0.0031	-0.0016	-0.0008	-0.0004
diff corr.	-0.347	-0.0874	-0.0344	-0.0155	-0.0075	- 0.0038	-0.0020	-0.0011	-0.0006

Table 2: The correlation as a function of the lag n. $T = 10$ and $\rho = 0.8$

lag n	1	2	3	4	5	6	7	8	
exact corr.	-0.285	-0.0947	-0.0474	-0.0267	-0.0160	- 0.0100	-0.0065	-0.0042	-0.0028
diff corr.	-0.273	-0.0964	-0.0496	-0.0286	-0.0176	- 0.0112	-0.0074	-0.0050	-0.0034

As the examples indicate, then the diffusion approximation seem to have an overall acceptable accuracy for quick and effective computation of correlations in CDV perturbated CBR cell streams.

5 Conclusion

In this paper we have studied the Cell Delay Variation which a CBR cell stream is exposed to when it is multiplexed with a background cell stream in a FIFO queue. Two models, an exact Markovian model and an approximate diffusion model has been applied to obtain detailed information on the correlation structure of the CDV affected CBR stream after departure from the multiplexing queue.

Explicit computational methods for the correlations has been provided in the exact case while closed form expression are derived in the diffusion model which e.g shows that the correlation is always negative and gives the exponential decay rate as the lag tends to infinity.

It has been found that the burstiness of the background traffic has a significant influence on CDV, and that the diffusion approximation is sufficient accurate for fast but reliable performance evaluation of quantities related to CDV.

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