User Assisted Dynamic RAN Notification Area Configuration Scheme for 5G Inactive UEs

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Abstract. The new radio resource control inactive state has become the main status of user equipments (UEs) in 5G networks, because of its low power consumption and energy saving features. To deal with the massive signaling overhead in 5G networks, in this paper, we introduce a UE assisted dynamic RAN notification area (RNA) configuration scheme to effectively reducing the paging and the RNA update overhead of inactive UEs. Especially, UEs are divided into two categories, namely, the speed-priority type and the rate-priority type based on their communication rate, mobility, as well as the location. Accordingly, we further extensively investigate the dynamic RNA configuration update process in both the theoretical and the practical manner. The performance of proposed schemes is evaluated via simulations and the results demonstrate the effectiveness and the efficiency in achieving the design goals, which could achieve a considerable performance improvement with respect to schemes in literatures.

Keywords: Small cell · 5G · Inactive state · RAN notification area

1 Introduction

In order to satisfy the low-latency, high-reliability and low-power transmission performance requirements to support various scenarios in 5G networks, the ultra dense small cell network is considered as a feasible solution [1]. Recently a new state called RRC Inactive is designed as a main state for inactive UEs in 5G networks. The main characteristics of the inactive state is that the interface between the Radio Access Network (RAN) and Core Network (CN) is kept [2].

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However, the small coverage of cells increases the total number of paging and location update signaling messages due to the movement of Inactive User Equipments (UEs) [3]. Paging is a system access functionality that is triggered by the network to locate a UE when there is downlink packet for the UE.

In Long Term Evolution (LTE) networks, the location tracking of UEs is based on the tracking area (TA) and the tracking area list (TAL). Several works have been done for reducing the overhead due to the mobility of UEs during the last years [4–7]. In [4], an experience-based scheme was used to predict the movement trend of UEs, and the TAL is allocated to UEs according to movement type. An automatic scheme which could obtain the optimal TA update scheme and minimize network signaling was presented in [5], the scheme detected periods of similar trends of UEs that could share the same TA update scheme. In [6], the authors proposed an effective TAL design to reduce the overall signaling overhead while taking into account the TAL overlapping. In this case, a cell could be included in more than one TAL. When UEs moved from cell i to cell j, the location update is performed if cell j is in none of those TALs of UEs. The authors designed an effective tracking area list management scheme to optimize TAs in the form of TALs for each UE, which could minimize the number of the paging and tracking area updates signaling message [7].

The 3rd generation partnership project (3GPP) standard proposed three different granularity RNA configuration schemes for inactive UEs, that is, the cell list, the radio access network (RAN) area identification (ID) list and tracking area identity (TAI) list configuration scheme, respectively [8]. However, the small configuration granularity of the cell list-based RNA configuration scheme is only applicable to UEs with high paging rates and low-speed. The larger granularity of the RNA configuration scheme is based on the RAN area ID list/TAI list, which is only applicable to UEs with a high-speed and low paging rate.

In this paper, a UE assisted information-based dynamic RNA configuration scheme is proposed to minimize the total number of paging and RNA update signaling in 5G small cell network. The main contributions can be summarized as: First, UEs are divided into different categories based on their own state informations. In particular, UEs could recommend an appropriate RNA and report it to the anchor gNB as the RNA configuration assisted information. Finally, the anchor gNB will determine whether to reconfigure the recommended RNA based on assisted information from UEs. Second, we aim to minimize the total number of messages in paging and location tracking of UEs in Inactive mode. UEs could report the recommended RNA base on the state informations of UEs, thereby reducing the total overhead in the scheme we proposed. In addition, the RNA for a UE is dynamic update according to UEs activities. such as the current communication frequency and mobility, to further improve the performance of the network.

The rest of this paper is structured as follows: the system model is presented in Sect. 2. The detail procedure of the dynamic RNA configuration scheme is presented in Sect. 3. Section IV introduces the problem formulation of the proposed RNA configuration scheme. The simulation results are presented in Sect. 5. Finally, the paper is concluded in Sect. 4.

2 System Model

In this paper, we consider a 5G small cell network consists of the RAN and next generation core network (NGC), where RAN includes a set of small cell gNBs (i.e., base station of the 5G network), and UEs are randomly located in the coverage of gNBs. NGC includes the access and mobility management function (AMF), the user plane gateway (UP-GW) and the control plane gateway (CP-GW) as shown in Fig. 1. Each gNB covers a different number of cells and inter-gNBs are connected via the X_n interface. The anchor gNB maintains the connection of the user plane and the control plane with the NGC, which is in charge of the paging and location tracking of UEs. In order to avoid a large number of paging and RNA updates signaling message between gNBs, we assume there is a X_n interface between gNBs and the anchor gNB where the UE is located. Alternatively, when a UE moves to a gNB that does not have interface with the anchor gNB, the anchor gNB will be replaced by the gNB where the UE is currently located. In this case, the intra-gNB mobility is hidden from the anchor gNB enabling the tracking of the cell level location of UEs to minimize the signaling overhead.

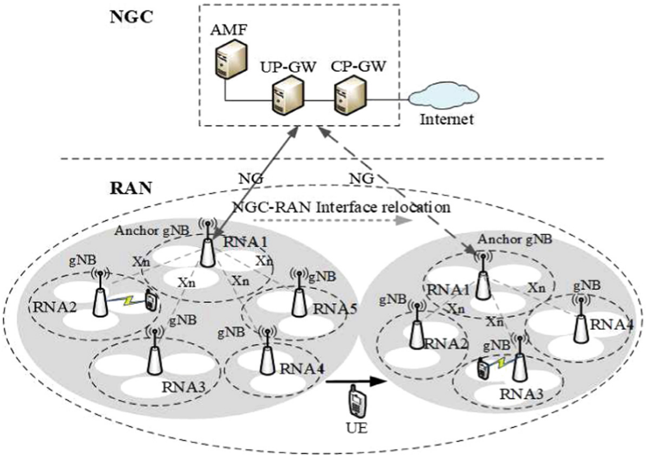


Fig. 1. System model

Generally, the initial configuration of the RNA is depended on the mobility of UEs as well as on their geographical distribution. gNBs will provide UEs with the initial configuration of the RNA when UEs firstly connect to the network. The initial RNA configuration varies from scene to scene and one RNA can contain multiple gNBs regions. We denote $R = \{1, 2...r\}$ as the set of RNAs, and $U = \{1, 2...u\}$ as the set of UEs. Let Υ denote the set of all possible RNA lists in the network, Υ_i denote the set of all possible RNA lists that can be assigned to UEs in RNA i. $m_{i\ell}$ represents the probability to assign RNA list in RNA i to UEs, h_{ij} represents the probability that UEs move from RNA i to RAN j. When UEs move to a new RNA does not belong to it is own RNA list, there is a RNA update procedure for UEs and a signaling message to the anchor gNB. Once the anchor gNB received the RNA update message, it would calculate and forward the set of possible RNA lists to UEs to generate new RNA. Symbols used in this paper are listed in Table 1.

Table 1. Notations of Symbols

Symbol	Description
R	The set of RNAs in the network
U	The set of UEs in the network
Υ	The set of all possible RNA lists
Υ_i	The set of RNA lists can be assigned to UEs in RNA i
$m_{i\ell}$	The probability to assign RNA list in RNA i to UEs
h_{ij}	The probability UEs move to RAN j from RNA i
τ	Signaling overhead of one paging process
λ_0	The necessary overhead generated by cells UE camped
λ_1	The unnecessary overhead generated by cells except UE camped
n_u^k	The cells of the RNA of UE other than the cell UE camped
α_u	The paging probability of UE i during period k
ρ	Signaling overhead of one RNA updating process
β_u	The RNA update probability of UE i during period k
t_{ui}	The duration time of UE u in RNA i

3 Dynamic RNA Configuration Scheme

3.1 Dynamic RNA Configuration

According to the dynamic changes of UEs, the initial RNA configuration needs to be reconfigured timely. The user assisted dynamic RAN notification area configuration scheme consists of two steps: the decision making step and the RNA adjustment step, as shown in Fig. 2. Firstly, in the decision making step, UEs will periodically collect their own state informations for time interval T, which include the paging rate, mobility rate and the time duration of UEs in the visited RNA etc. Based on these information UE could determine the categories of UEs, namely, rate-priority or speed-priority. Formally, the category of UE u is depended on the ratio of paging overhead and RNA update overhead in the network within the kth period T (T_k), which is given as follows:

$$O_u^k = \frac{\tau(\lambda_0 + \lambda_1 n_u^k)\alpha_u}{\tau(\lambda_0 + \lambda_1 n_u^k)\alpha_u + \rho\sigma_u\beta_u} \tag{1}$$

where $0 < O_u^k < 1$, $\sigma_u = T_k/t_{ui}$. $\tau(\lambda_0 + \lambda_1 n_u^k)T_k\alpha_u$ denotes the paging overhead of UE u during T_k. $\rho T_k/t_{ui}\beta_u$ denote the RNA update overhead incurred by UE u during T_k. T_k/t_{ui} denotes the RNA update frequency of UE u in the T_k. UE with larger O_u^k causes larger number of the paging message than the RNA update message, which is considered as a rate-priority type UE. Consequently, the smaller the value of O_u^k the more RNA update message than the paging message, which is considered as a speed-priority type UE.

Secondly, in the dynamic adjustment step, according to the category of UEs determined by the previous step, the set of possible RNA lists can be assigned to UEs to generate a new RNA. In this step, rate-priority type UEs would select a RNA list with small number of RNAs to reduce the paging overhead. Similarly, speed-priority type UEs would select a RNA list with large number of RNAs to mitigate the impact of the RNA update on the network performance. Then, UEs report the assisted information to the anchor gNB to update the RNA configuration.

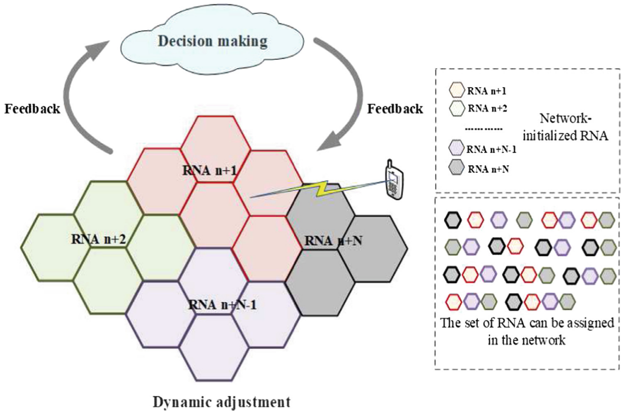


Fig. 2. Dynamic RNA configuration scheme

3.2 RNA Lists Update Process

We give an example to show the update process of the RNA of UEs. Assume that there are three RNAs in the network, named $R1$, $R2$ and $R3$, UEs can freely move in any RNAs. Notice that, when UEs are in one of RNAs, there would form a set of RNA lists that can be assigned to UEs with the neighboring RNAs. For example, if UEs camp in $R1$, all the RNA lists that can be assigned to UEs are denoted as Υ_1, Υ_1=$\{\{R1\}, \{R1, R2\}, \{R1, R3\}, \{R1, R2, R3\}\}$. Additionally, all the RNA lists in the network are denoted as Υ=$\bigcup_{i \in R} \Upsilon_i$, Υ=$\{\{R1\}, \{R2\}, \{R3\}, \{R1, R2\}, \{R1, R3\}, \{R2, R3\}, \{R1, R2, R3\}\}$.

Assume that each RNA list is assigned to UEs with a specific probability, denotes as $P_i(L)$. All RNA lists are in descending order by the number of included RNAs. Furthermore, the category of UEs should be taken into consideration during RNA update process. Speed-priority type UEs should be assigned to a large

RNA list as the notification area to reduce RNA update signaling. Otherwise, rate-priority type UEs should be assigned to a small RNA list as the notification area to reduce paging signaling. Thus, speed-priority type UEs has high probability to be assigned to $\{R1, R2, R3\}$, while $\{R1\}$ is probably be assigned to rate-priority type UEs.

We define a poisson cumulative distribution function $F(r_u, t_{ui})$, where $r_u = 1/(O_u^k) \geq 1$. Especially, the cumulative distribution probability of $\{R1, R2, R3\}$ is the smallest, while $\{R1\}$ is the biggest. UEs will select the appropriate RNA list when the following condition are satisfied:

$$\sum_{m=1}^{L-1} P_i(m) < F(r_u, t_{ui}) < \sum_{m=1}^{L} P_i(m) \tag{2}$$

From above, larger O_u^k results in smaller r_u and indicates that UE u, which called rate-priority type. It is better to assign a RNA list with small number of RNAs for this UE u. In contrast, smaller O_u^k results in bigger r_u and indicates that UE u, which called speed-priority type. It is better to assign a RNA list with a number of RNAs for this UE u.In addition, the small t_{ui} indicates the high speed of UEs, which will be assigned to a large RNA list. As shown in Fig. 3, when r_u is small, UEs have a higher probability to select a smaller RNA list. Otherwise, when r_u is large, UEs have a higher probability to select a larger RNA list. In addition, the time duration t_{ui} indicates the speed of UEs, the speed-priority type UEs will select a large RNA list.

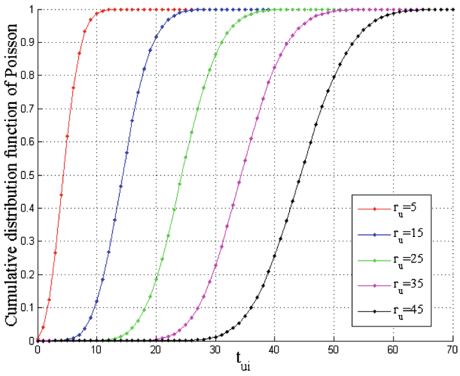


Fig. 3. t_{ui} versus the cumulative distribution function of poisson

4 Problem Formulation

In this paper, we consider a UE assisted information-based dynamic RNA configuration scheme to minimize the total number of paging and RNA update signaling message in 5G small cell network. The multi-objectives optimization technique is used to minimize both the paging and the RNA update overhead, find the optimal distributions of the RNA, and find a fair tradeoff of these two overhead. The RNA update overhead which generates in RNA i and j (not in the same RNA list) can be expressed as follows:

$$f_{RNAU(i,j)} = \rho \sum_{\ell\in\gamma_i\wedge\ell\notin\gamma_j} h_{ij}m_{i\ell} + \rho \sum_{\ell\in\gamma_j\wedge\ell\notin\gamma_i} h_{ji}m_{j\ell} \tag{3}$$

where ℓ is the current RNA list of UEs. The overhead of paging generated in RNA i can be expressed as:

$$f_{paging(i)} = \tau m_{i\ell} \sum_{u\in U} \alpha_u t_{ui} \tag{4}$$

where $\sum_{u\in U} \alpha_u t_{ui}$ is a constant that represents the paging overhead in RNA i. When there is data transmission requirement, the anchor gNB will send paging message to gNBs in the RNA of UE u. Based on the above discussion, the optimization problem can formulate as:

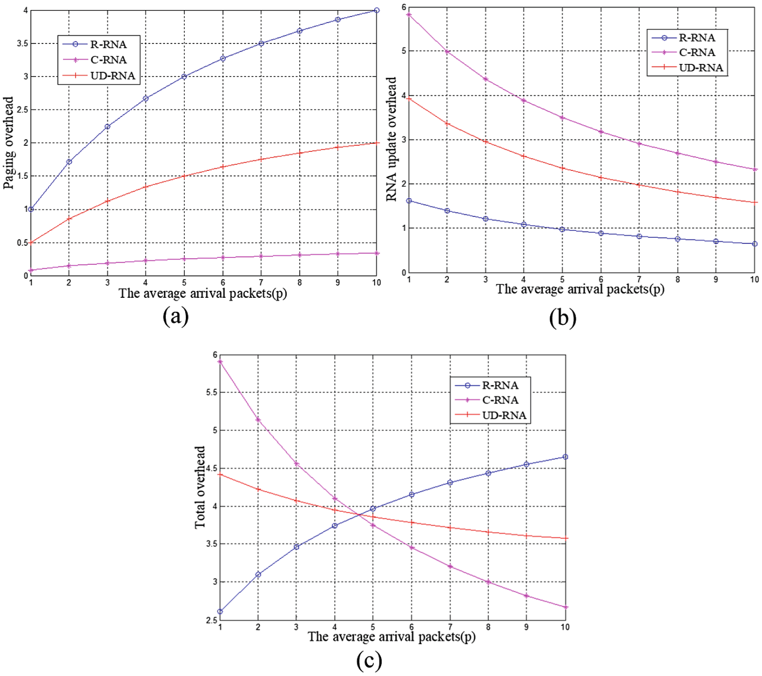
$$\begin{aligned}
\min \quad & \omega \sum_{i\in R} \sum_{j\in R\wedge i\neq j} f_{RNAU(i,j)} + (1-\omega) \sum_{\ell\in\varUpsilon} \sum_{i\in\ell} f_{paging(i)} \\
\text{s.t.} \quad & \text{(C1)}: \quad i,j\in R, 0\leq h_{ij}\leq 1 \\
& \text{(C2)}: \quad i\in R, \ell\in\varUpsilon, 0\leq m_{i\ell}\leq 1 \\
& \text{(C3)}: \quad \forall i\in R, \textstyle\sum_{\ell\in\gamma} m_{i\ell} = 1 \\
& \text{(C4)}: \quad \sum_{i\in R} \sum_{j\in R\wedge i\neq j} f_{RNAU(i,j)} \leq RNAU_{\max} \\
& \text{(C5)}: \quad \textstyle\sum_{i\in R} f_{paging(i)} \leq PAGING_{\max}
\end{aligned} \tag{5}$$

where ω is the weight factor of the paging and the RNA update overhead in the network, which could dynamically adjust the proportion of these two factors. Specifically, the speed-priority type UEs will be assigned with a larger ω than the rate-priority type UEs. The set of constraint (C3) assures that the sum of the proportional usage of the RAN lists in RNA i equals to one. The constraint (C4) guarantees that the sum of all RNA update overhead should not exceed the maximum $RANU_{\max}$, the constraint (C5) indicates that the sum of all paging overhead in the network should not exceed the maximum $PAGING_{\max}$.

In this paper, the discrete Markov chain is used to analyze the RNA update and the paging overhead in the network, which can be obtained by the solution of the balance equations of the discrete Markov chain. The detail process refers to [7].

5 Simulation results

In this section, we verify the performance of the proposed user assisted dynamic RAN configuration scheme (UD-RNA) algorithm by simulations. We focus on the impact of RNA update and paging overhead on the UD-RNA scheme. In order to qualify the proposed algorithm, the following two algorithms are used for comparison: the cell list configuration scheme (C-RNA) and the RAN area ID list configuration scheme (R-RNA). C-RNA scheme could optimize the paging overhead while R-RNA could optimize the RNA update overhead. The RNA update rate of UEs is represented by ν, $\frac{1}{\nu}$ refers to the average duration time of UEs in each RNA. The paging rate of UEs is represented by p, which is the average arrival packets of UEs. The following three scenarios is considered in the simulation: scenario one, $1 \leq p \leq 10$, $\nu = 5$ and $\omega = 5$; scenario two $1 \leq \nu \leq 10$, $p = 0.5$ and $\omega = 0.5$; scenario three, we vary the $0.1 \leq \omega \leq 1$.



(a)

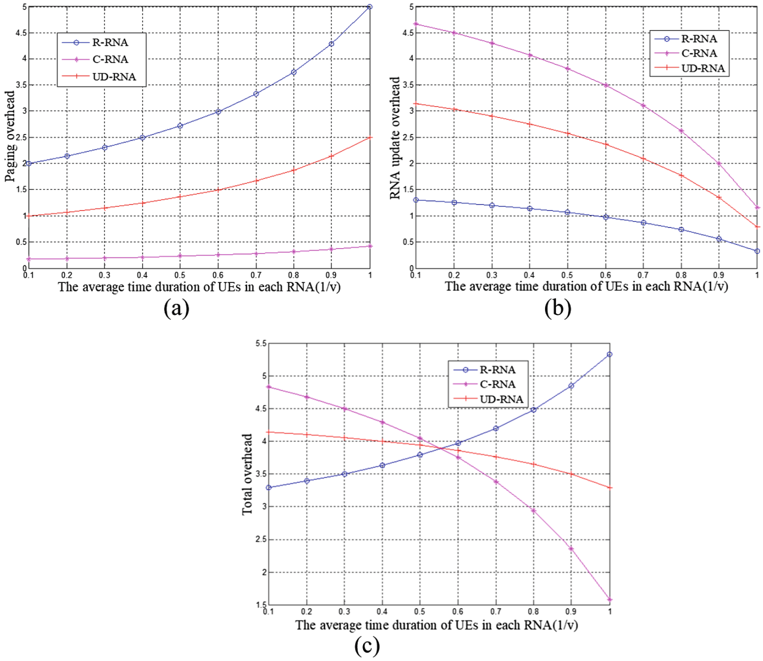
(b)

(c)

Fig. 4. Performance comparison of three schemes as a function of average arrival packets p

Figures 4 and 5 show the paging overhead, the RNA update overhead and the total overhead of C-RNA, R-RNA and UD-RNA algorithm versus the average arrival packets p and the average time duration of UEs in each RNA, respectively. Figure 4a,b show that the average arrival packets p of UEs have a negative impact on paging but a positive impact on RNA update overhead, this is due to the rate-priority type UEs generate more paging overhead than the RNA update overhead. Thus, the larger the p value is, the higher the paging overhead becomes. As depicted in Fig. 5a,b, the increase of the average duration time UE also has a negative impact on paging and a positive impact on RNA update overhead. The longer a UE resides in a RNA, the lower its mobility and the less RNA update overhead is generated.

Figures 4a and 5a illustrate that C-RNA has a better performance than UD-RNA and R-RNA in terms of paging overhead regardless of the vary of p and $\frac{1}{\nu}$. It proves that the C-RNA scheme can effectively reduce the paging overhead because of the small granularity of RNA configuration. Figures 4b and 5b demonstrate that R-RNA has a better performance than UD-RNA and C-RNA in terms of the paging overhead regardless of the vary of p and $\frac{1}{\nu}$. R-RNA scheme can effectively reduce the RNA update overhead because of the big granularity of RNA configuration. Figures 4c and 5c show that the proposed UD-RNA scheme has a better performance for different values of p and $\frac{1}{\nu}$ and reduce the overall signaling message for both the paging and the RAN update overhead. It can be seen from the figures, when $p < 4.7$ and $\frac{1}{\nu} < 0.55$, R-RNA scheme has better performance than the other two schemes. However, after that point C-RNA scheme is the best compared with other two schemes. Especially, UD-RNA always finds an optimal tradeoff between the paging and the RNA update overhead by maintaining the total overhead to the optimal value.



(a) (b) (c)

Fig. 5. Performance comparison of three schemes as a function of average duration time ν

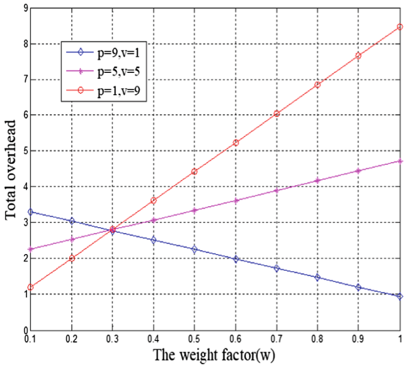


Fig. 6. The impact of the weight factor on the total overhead

Figure 6 illustrates the change of the total overhead in the network versus the weight factor. The following three scenarios are used for comparison: (1) $p = 9$ and $v = 1$, when the paging overhead is larger than the RNA update overhead; (2) $p = 5$ and $v = 5$, when the paging overhead equals to the RNA update overhead; (3) $p = 1$ and $v = 9$, when the paging overhead is smaller than the RNA update overhead. With the increase of ω, the proportion of the RNA update overhead increases, while the proportion of the paging overhead decrease. For scenario 1, the larger the ω is, the small the paging overhead achieves, thus the total overhead is declined. For scenario 2, with the increase of ω, the RNA update overhead is increasing and the paging overhead is decreasing, result in slowly increasing of the total overhead. For scenario 3, the larger the ω is, the bigger the paging overhead becomes, result in increasing of the total overhead.

6 Conclusions

In this paper, a UE assisted based dynamic RNA configuration scheme was proposed to reduce the total overhead of the paging and the RNA update signaling. Simulation results illustrated the effectiveness of the proposed scheme.

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